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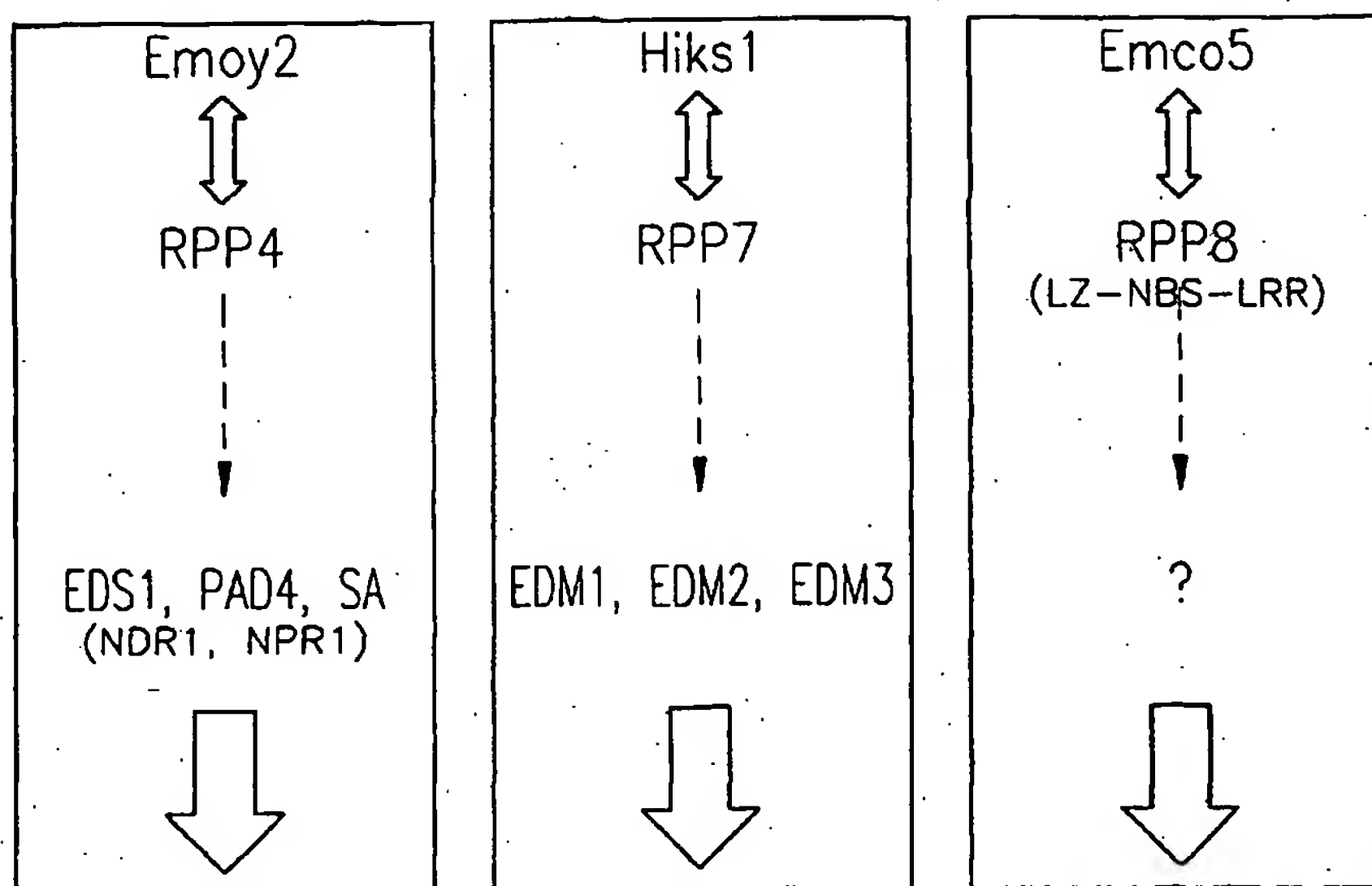
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(54) Title: PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

### RPP-DEPENDENT DEFENSE PATHWAYS



R E S I S T A N C E

(57) Abstract: Methods to identify genes, the expression of which is altered in response to pathogen infection, are provided, as well as the genes identified thereby.

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## PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

5

### Cross-Reference to Related Applications

This application is a continuation-in-part application of U.S. application Serial No. 60/232,778, filed on September 15, 2000, and of U.S. application Serial No. 60/300,183, filed on June 22, 2001, the disclosures of which are  
10 incorporated by reference herein.

### Field of the Invention

The present invention generally relates to the field of plant molecular biology, and more specifically to the regulation of gene expression in plants in response to stress, e.g., to pathogen exposure.

15

### Background of the Invention

Plants are capable of activating a large array of defense mechanisms in response to pathogen attack. A crucial factor determining the success of these mechanisms is the speed of their activation. Consequently, there is considerable  
20 interest in understanding how plants recognize pathogen attack and control expression of defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*) gene that triggers specific recognition by a corresponding host resistance  
25 (*R*) gene. *R* gene specificity is generally quite narrow, in most cases only pathogens carrying a particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

30 One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the  
35 plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component

of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

#### **R gene signal transduction**

Genes such as *NDR1* and *EDS1*, as well as *DND1* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr* recognition. *NDR1* and *EDS1* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDS1* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDR1* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDS1* or *NDR1*, so

the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect. Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

5        *NDR1* encodes a protein with two predicted transmembrane domains (Century et al. 1997). *RPM1*, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1*  
10        encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

15        It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it  
20        triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger  
25        defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDR1*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COI1*, which affect ethylene or jasmonic acid signaling, or in  
30        *coil/npr1* or *coil/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

### SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of PR gene expression and enhanced disease resistance.

- 5 Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of *PR* genes in response to SA is blocked;
- 10 *cpr1*, *cpr5*, and *cpr6*, which constitutively express *PR* genes; the *npr1* suppressor *ssil*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in *PR1* expression.

- Expression of the defense genes *PR1*, *BG2*, and *PR5* in response to SA treatment requires a gene called *NPR1* or *NIM1*. Mutations in *npr1* abolish
- 15 SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). *NPR1* appears to be a positive regulator of *PR* gene expression that acts downstream from SA. *NPR1* encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al.,
- 20 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998). Consequently, it is unlikely that *NPR1* acts as a transcription factor to directly control *PR* gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

- PAD4* appears to act upstream from SA. In *pad4* plants infected with a
- 25 virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and *PR1* expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not affect SA levels,
- 30 camalexin synthesis, or *PR1* when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that *PAD4* is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

### JA-dependent signaling

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jar1* and *coil* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COII* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al., 1998; Zhao et al., 1996) and *coil* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

### Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jar1* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.



Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that *NPR1* was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, *NPR1* mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, *NPR1* mediates a different resistance response. It is difficult to imagine how this could occur, unless *NPR1* is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in *NPR1* could function in protein-protein interactions between *NPR1* and adapter proteins. Identification of proteins that interact with *NPR1*, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how *NPR1* acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

#### Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Thus, what is needed is the systematic identification of genes useful to confer resistance to pathogens.

### Summary of the Invention

The invention provides an isolated nucleic acid molecule (polynucleotide), e.g., DNA, comprising a plant or fungal nucleotide sequence, the expression of which is altered in response to stress, e.g., pathogen infection.

5 For example, the invention provides a nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in

10 combination with other sequences, to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) from an inducible promoter including a promoter which is responsive to external stimuli, such as chemical application, or to

15 pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth. In one embodiment of the invention, the promoter employed to express the nucleotide sequence of the invention may be one that mediates rapid and transient transcription after pathogen infection. Thus, the invention also provides an isolated nucleic acid molecule comprising a plant nucleotide

20 sequence which alters, e.g., increases or decreases, the transcription of plant genes, e.g., open reading frames, in response to stress, e.g., pathogen infection.

As described herein, *Arabidopsis* plants of differing genotypes were infected with different strains of an oomycete, *P. parasitica*. RNA was isolated from each plant/pathogen pair and employed to prepare probes which were hybridized to a gene

25 chip having nucleic acid sequences (probe sets) corresponding to approximately 8,200 *Arabidopsis* genes. Genes were then identified that were upregulated or downregulated in response to infection, including genes that were dependent on *RPP7* or *RPP8*, which act via unconventional signaling cascades and are not dependent on defense regulators such as EDS1, NDR1, PAD4, NPR1, RAR1, PBS3 or salicylic acid (SA). Among the

30 genes showing strong *Peronospora*-induced expression changes, clusters of genes were identified that were specifically upregulated by *RPP7* or *RPP8*, or both. In particular in one analysis, the expression of 184 genes (SEQ ID NOs:1-211 and 792) related to 217 probe sets was upregulated by either *RPP7* or *RPP8*, or both, while in another analysis the expression of genes related to 194 probe sets (SEQ ID NOs:212-399 and 793) was



upregulated by either *RPP7* or *RPP8*, or both. Further, as described below, promoters of genes that were rapidly and transiently transcribed after *P. parasitica* infection and were *RPP7/8*-dependent were significantly enriched with both novel sequence motifs and potential binding sites of known transcription factors. Specifically, the promoters were significantly enriched with two novel sequence motifs (referred to as "motif 1" and "motif 2"), one of which was similar to binding sites for Myb transcription factors, sequence motifs related to WRKY binding sites, and two other novel sequence motifs ("motif 3" and "motif 4"). Moreover, comparisons between expression signatures of wild type plants as well as the *RPP7* loss of function mutants, and *edm1*, *edm2* and *edm3* mutants, allow for predictions regarding the *RPP7* pathway hierarchy.

In addition, more than 200 genes (SEQ ID NOs:75, 214, 228, 301, 339, 400-684, 792-795) were identified that were specifically controlled by the *RPP4*-dependent pathway, which mediates resistance of the *Arabidopsis* ecotype Col-0 to the *Peronospora* isolate Emoy2. According to their response to SA, an important mediator of local and systemic defense responses, and the protein biosynthesis inhibitor cycloheximide (CHX), these genes were further subcategorized into immediate early and secondary response genes. A set of immediate early SA responsive genes (SEQ ID NOs:150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615, and 526) was found to consist exclusively of regulatory genes. Such genes are likely controlled by transcription factors acting closely downstream of SA. One highly conserved motif in the promoters of these immediate early genes was similar to binding sites of WRKY transcription factors (SEQ ID NOs:757-765). Other conserved promoter motifs appeared to be novel and may facilitate the cloning of their cognate transcription factors. A cluster of SA/CHX super-induced genes was found to show elevated expression ground states in the *npr1* mutant (SEQ ID NOs:214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447 and 551) suggesting an NPR1-dependent de-repression mechanism in the control of some SA responsive immediate early genes.

Thus, the invention provides an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to a pathogen that induces a response mediated by *R* genes, including pathogens such as bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones (1997), which is specifically incorporated by

reference herein). For example, the plant or fungal nucleotide sequence encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to infection by an oomycete such as *Peronospora*, and is *RPP4*-,  
5 *RPP7*-, and/or *RPP8*-dependent. These sequences can be identified by employing an array of nucleic acid samples, e.g., a plurality of oligonucleotides, each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid from pathogen-infected (e.g., wild-type) plant cells and to nucleic acid from uninfected plant cells or  
10 plant cells having a mutation which alters the response to pathogen infection. Thus, genes, the expression of which are altered by pathogen infection, can be systematically identified. Preferably, the nucleotide sequence is from plant DNA, either a dicot or a monocot, which encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading  
15 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. More preferably, the nucleotide sequence is from plant DNA that is substantially similar to an *Arabidopsis* nucleic acid segment having any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. The term "substantially similar", when used herein with respect to a polypeptide  
20 means a polypeptide corresponding to a reference polypeptide, wherein the polypeptide has substantially the same structure and function as the reference polypeptide, e.g., where only changes in amino acid sequence are those which do not affect the polypeptide function. When used for a polypeptide or an amino acid sequence, the percentage of identity between the substantially similar and  
25 the reference polypeptide or amino acid sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, where the reference polypeptide is an *Arabidopsis* polypeptide encoded by an open reading  
30 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. However, the percent of identity between the substantially similar and the reference polypeptide may be less than 65% as long as the two polypeptides have the same or similar function, e.g., catalyze the same or similar reaction. Another indication that two polypeptides are substantially similar to

each other is that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence  
5 corresponding to a reference nucleotide sequence, wherein the corresponding sequence is from a gene that encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by a gene comprising the reference nucleotide sequence. The term "substantially similar" is specifically intended to include nucleotide sequences wherein the sequence has been  
10 modified to optimize expression in particular cells. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%,  
15 96%, 97%, 98%, up to at least 99%, wherein the reference sequence is preferably any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www.hto.usc.edu/software/seqaln/index.html>). The localS program, version 1.16, is  
20 preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C,  
25 more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC,  
30 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

Hence, the isolated nucleic acid molecules of the invention also include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*,

including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat or rice, as well as rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugarbeet, and in fungi. An ortholog is a gene from a different species that  
5 encodes a product having the same function as the product encoded by a gene from a reference organism. The encoded ortholog products likely have at least 70% amino acid sequence identity to each other. Hence, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or  
10 more of the *Arabidopsis* sequences, although it is also envisioned that orthologous genes to those disclosed herein may encode a polypeptide with less than 70%, e.g., less than 65% amino acid sequence identity, but which polypeptide has the same or similar function. Databases such GenBank or one found at <http://bioserver.myongjiac.kr/rjce.html> (for rice) may be employed to  
15 identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences.

Thus, the invention preferably includes an isolated nucleic acid molecule  
20 comprising a plant or fungal nucleotide sequence that encodes a polypeptide that has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, amino acid sequence identity to an *Arabidopsis* polypeptide encoded by an open reading  
25 frame comprising any one of SEQ ID NOs: 1-684 and 792-795, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795. In one embodiment, the isolated nucleic acid molecule is not SEQ ID NOs: 1-684 and  
30 792-795. The invention also provides anti-sense nucleic acid molecules corresponding to the open reading frames or genes identified as responsive to pathogen infection. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention in either sense or antisense orientation.



Also provided is an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising a nucleic acid sequence having at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, nucleic acid sequence similarity to an *Arabidopsis* open reading frame comprising any one of SEQ ID NOs: 1-684 and 792-795, the complement thereof, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are useful to provide resistance to pathogens and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression of one or more of the nucleic acid molecules of the invention or one or more of the polypeptides encoded thereby. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant or fungal nucleotide sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. The resistance or tolerance may be accomplished by decreasing or eliminating expression of a plant gene necessary for pathogen infection and/or replication or by overexpressing a gene product that inhibits pathogen infection and/or replication. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence having at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more

preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism. Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields under conditions of pathogen infection and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also includes recombinant nucleic acid molecules which have been modified so as to comprise codons other than those present in the unmodified sequence. The recombinant nucleic acid molecules of the invention include those in which the modified codons specify amino acids that are the same as those specified by the codons in the unmodified sequence, as well as those that specify different amino acids, i.e., they encode a variant polypeptide having one or more amino acid substitutions relative to the polypeptide encoded by the unmodified sequence.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The present invention also provides a method to identify a gene, the expression of which is altered in response to an external stimulus, e.g., pathogen infection. The method comprises contacting a plurality of samples comprising portions or fragments of isolated nucleic acid molecules with a probe which corresponds to a population of a nucleic acid sequences, the expression of which is altered in response to an external stimulus, so as to form a binary complex. Each sample corresponds to a different gene. Then complex formation is detected or determined. The method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. For example, the method comprises contacting a solid substrate comprising a plurality of samples comprising portions or fragments of isolated plant nucleic acid with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from a pathogen infected plant so as to form a complex. Preferred pathogens are those which induce an *R*-gene dependent resistance response. Each individual sample comprises one or more nucleic acid sequences corresponding to a plant gene, e.g., a pool of oligonucleotides corresponding to the same gene or a portion of that gene. The plurality of samples is provided on a DNA chip. A second plurality of samples on a solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising portions or fragments of



isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from an uninfected or mutant plant or plant cells so as to form a complex. Then complex formation with nucleic acid from infected cells and from uninfected or mutant cells is compared.

5       The invention also provides a method for identifying a plant cell infected with a pathogen, e.g., one that induces a *RPP4*-, *RPP7*- and/or *RPP8*-dependent resistance response. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with the pathogen with at least one, preferably at least two, oligonucleotides under conditions effective to amplify at  
10   least a portion of a nucleotide sequence in the isolated plant nucleic acid which is substantially similar to at least one of SEQ ID NOs: 1-684 and 792-795, so as to yield an amplified product. Then the presence of the amplified product is detected or determined. The presence of the amplified product, e.g., in an amount that is different than the amount of the corresponding amplified product  
15   from an uninfected or mutant plant, corresponding to one or more of SEQ ID NOs: 1-684 and 792-795 or an ortholog thereof, is indicative of pathogen infection.

      The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected  
20   from SEQ ID NOs: 1-684 and 792-795 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a pathogen is compared to hybridization of the probe to nucleic acid isolated from an uninfected or mutant cell. A change in the amount of the hybridized probe in  
25   nucleic acid isolated from a cell suspected of being infected by a pathogen relative to the amount of hybridized probe in nucleic acid isolated from an uninfected or mutant cell is indicative of infection.

      Also provided is an isolated nucleic acid molecule comprising a nucleotide sequence that directs transcription, e.g., a promoter, of a linked  
30   nucleic acid segment in a host cell, such as a plant cell, wherein transcription is altered, e.g., increased, in response to a pathogen infection. Preferably, the pathogen is *R*-dependent, and more preferably, one that triggers a response that is dependent on *RPP4*, *RPP7* and/or *RPP8*, such as an oomycete (for example, *Peronospora*). It is preferred that the nucleotide sequence is from plant genomic

DNA which has at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, nucleotide sequence identity to a sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, e.g., SEQ ID NOs: 774-788, or comprising motifs such as one of SEQ ID NOs: 685-773. Thus, the invention also includes orthologs of *Arabidopsis* promoters. Preferably, the nucleotide sequence includes the promoter region from a gene corresponding to SEQ ID NOs: 1-770 and 792-795, which region preferably includes at least one copy of at least one of the following, e.g., a nucleic acid sequence comprising one of SEQ ID NOs: 685-697 ("motif 1"), SEQ ID NOs: 698-709 ("motif 2"), GGT/CCCA ("motif 3"), GNCCAAA ("motif 4"), or SEQ ID NOs: 710-713, 714-756, or 757-773. The promoter sequence is preferably about 25 to 2000, e.g., 50 to 500 or 100 to 1400, nucleotides in length.

In one embodiment of the invention, the isolated nucleic acid molecule comprises a plant nucleotide sequence which is the promoter region for any one of SEQ ID NOs: 1-684 and 792-795, or is structurally related to the promoter for SEQ ID NOs: 1-684 and 792-795, i.e., is an orthologous promoter, and is linked to a plant structural gene or open reading frame. Hence, the present invention further provides an expression cassette or a recombinant vector containing the nucleic acid molecule, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid segment in the plant, plant tissue or plant cell. Transcription of the linked segment is altered in response to pathogen infection, including *Peronospora* infection. For promoters with motif 1, transcription of linked segments may be altered in response to agents or other stimuli that induce Myb-like transcription factors.

Generally, the promoters of the invention may be employed to express a nucleic acid segment that is operably linked to the promoter, for example, an open reading frame or a portion thereof, an anti-sense construct or a transgene. The open reading frame may be obtained from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a

mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a positive selectable marker, a gene affecting plant agronomic characteristics, i.e., yield, standability and the like, or an environment or stress resistance gene, i.e., one or more genes  
5 that confer herbicide resistance or tolerance, insect resistance or tolerance, disease resistance or tolerance (viral, bacterial, fungal, oomycete, or nematode), stress tolerance or resistance (as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress, or oxidative stress), increased yields, food content and makeup, physical appearance, male  
10 sterility, drydown, standability, prolificacy, starch properties or quantity, oil quantity and quality, amino acid or protein composition, and the like.

— Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500; contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743;  
15 250 to about 743, 400 to about 743, 600 to about 743, of the promoter sequences from genes comprising any one of SEQ ID NOs:685-788, 714-756; and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

In a particular embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500,  
20 contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95% sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500; contiguous nucleotides, e.g., 40  
25 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

The expression cassettes or vectors of the invention may optionally  
30 include other regulatory sequences, e.g., transcription terminator sequences, introns and/or enhancers, and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may

be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell protoplast. Further, the expression cassette can be contained in a plant, plant cell or plant tissue from a dicot or a monocot. In particular, the plant may be a cereal plant.

5       The present invention further provides a method of augmenting a plant genome by contacting plant cells with an expression cassette or vector of the invention, i.e., one having a nucleotide sequence that directs transcription of a linked nucleic acid segment in a plant cell, wherein transcription of the linked segment is altered in response to a pathogen such as an oomycete, e.g.,  
10   *Peronospora*, infection, and wherein the nucleic sequence is from plant DNA that has at least 65%, and more preferably at least 70%, identity to the sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the  
15   differentiated transformed plant expresses the linked fragment in the cells of the plant in response to infection. The present invention also provides a plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in  
20   which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and  
25   probes.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid  
30   molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.



The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these  
5 crossed fertile transgenic plants.

The present invention also provides a method to identify a nucleotide sequence that directs transcription of nucleic acid in the genome of a plant cell in response to pathogen exposure, by contacting a probe comprising plant nucleic acid, e.g., cRNA, isolated from tissues of a plant contacted with the pathogen,  
10 with a plurality of isolated nucleic acid samples on a plurality of solid substrates, wherein each sample is a plurality of oligonucleotides corresponding to at least a portion of a plant gene, so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Then complex formation is determined or  
15 detected to determine which samples represent genes comprising promoters that are responsive to infection with the pathogen. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

A method to shuffle the nucleic acid molecules of the invention is provided. This method involves fragmentation of a (parent) nucleic acid  
20 molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-684 and 792-795, the ortholog thereof, or the corresponding gene thereof, followed by religation. This method allows for the production of polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule. Accordingly, the invention provides cells and transgenic plants  
25 containing nucleotide sequences produced through shuffling that encode polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule.

A computer readable medium containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are  
30 provided. This medium allows a nucleic acid molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence

corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795, and the corresponding gene or polypeptide encoded by the nucleic acid sequence.

5

### Brief Description of the Figures

Figure 1 depicts *RPP*-dependent defense pathways.

Figure 2 depicts nucleotide sequences including the promoter region and motifs therein for genes, the expression of which is altered in response to pathogen infection (SEQ ID NOs: 774-788).

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Figure 3 is a schematic of the overlap in genes that are induced early after *P. parasitica* infection and in a *RPP8*-specific manner, genes that are induced late after infection and in a *RPP8*-specific manner, and genes induced early and late after infection in a *RPP7*-specific manner.

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Figure 4 shows a schematic of *RPP4*-pathway, *RPP7*-pathway and *RPP8*-upregulated transcription factor genes.

### Detailed Description of the Invention

#### Definitions

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The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated.

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Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., 1991; Ohtsuka et al., 1985; Rossolini et al., 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic

acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid", "nucleic acid molecule", "nucleic acid fragment" or "nucleic acid sequence or segment" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals. Fragments and variants of the disclosed nucleotide sequences and proteins or partial-length proteins encoded thereby are also encompassed by the present invention. By "fragment" or "portion" is meant a full length or less than



full length of the nucleotide sequence encoding, or the amino acid sequence of, a polypeptide or protein. Alternatively, fragments or portions of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment proteins retaining biological activity. Thus, fragments or portions of a nucleotide sequence may range from at least about 9 nucleotides, about 12 nucleotides, about 20 nucleotides, about 50 nucleotides, about 100 nucleotides or more.

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA, functional RNA, or specific protein, including regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

"Naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

A "marker gene" encodes a selectable or screenable trait.

"Selectable marker" is a gene whose expression in a cell gives the cell a selective advantage. The selective advantage possessed by the cells transformed with the selectable marker gene may be due to their ability to grow in the presence of a negative selective agent, such as an antibiotic or a herbicide, compared to the growth of non-transformed cells. The selective advantage possessed by the transformed cells, compared to non-transformed cells, may also be due to their enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. Selectable marker gene also refers to a gene or a combination of genes whose expression in a cell gives the cell both a negative and/or a positive selective advantage.

The term "chimeric" refers to any gene or DNA that contains 1) DNA

sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are  
5 derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for  
10 example, DNA that is either heterologous or homologous to the DNA of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host  
15 organism but that is introduced by gene transfer.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

By "variants" is intended substantially similar sequences. For nucleotide sequences, variants include those sequences that, because of the degeneracy of  
20 the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those  
25 generated, for example, by using site-directed mutagenesis which encode the native protein, as well as those that encode a polypeptide having amino acid substitutions. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g.,  
30 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98%, sequence identity to the native (endogenous) nucleotide sequence.

"DNA shuffling" is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The

DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may  
5 have an altered biological activity with respect to the polypeptide encoded by the template DNA.

The nucleic acid molecules of the invention can be optimized for enhanced expression in plants of interest. See, for example, EPA035472; WO91/16432; Perlak et al., 1991; and Murray et al., 1989. In this manner, the  
10 genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may  
15 also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are  
20 generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Crameri et al., 1997; Moore et al., 1997; Zhang et al., 1997; Crameri et al., 1998; and  
25 U.S. Patent Nos. 5,605,793 and 5,837,458.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences.  
30 Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the

encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will  
5 recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

"Recombinant DNA molecule" is a combination of DNA sequences that  
10 are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1989).

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," each refer to a sequence that originates from a  
15 source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the  
20 terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" DNA sequence is a DNA sequence that is naturally  
25 associated with a host cell into which it is introduced.

"Wild-type" refers to the normal gene, or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or  
30 *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).



Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

5 "Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically  
10 include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of  
15 interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the  
20 nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under  
25 the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

Such expression cassettes will comprise the transcriptional initiation  
30 region of the invention linked to a nucleotide sequence of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerinneau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

An oligonucleotide corresponding to a nucleic acid molecule of the invention may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16-24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters. However, some suitable regulatory sequences useful in the present invention will include, but are not limited to constitutive plant promoters, plant tissue-specific promoters, plant development specific promoters, inducible plant promoters and viral promoters.

"5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.



The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

The term "intracellular localization sequence" or "signal sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA- box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate

element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e. further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the gene that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of  $\geq 1\%$  of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and

include both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al., 1989. Since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.

Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysone-inducible systems.

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Altered levels" refers to the level of expression in transgenic cells or organisms that differs from that of normal or untransformed cells or organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed cells or organisms.

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

"Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes. (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al., 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

"Transcription stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.



"Translation stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as one or more termination codons in all three frames, capable of terminating translation. Insertion of a translation stop fragment adjacent to or near the initiation codon at the 5' end of the coding sequence will result in no translation or improper translation. Excision of the translation stop fragment by site-specific recombination will leave a site-specific sequence in the coding sequence that does not interfere with proper translation using the initiation codon.

The terms "*cis*-acting sequence" and "*cis*-acting element" refer to DNA or RNA sequences whose functions require them to be on the same molecule. An example of a *cis*-acting sequence on the replicon is the viral replication origin.

The terms "*trans*-acting sequence" and "*trans*-acting element" refer to DNA or RNA sequences whose function does not require them to be on the same molecule.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al., 1981; the homology alignment algorithm of Needleman and Wunsch, 1970; the search-for-similarity-method of Pearson and Lipman, 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al., 1988; Higgins et al., 1989; Corpet et al., 1988; Huang et al., 1992; and Pearson et al., 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find

longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always  $> 0$ ) and N (penalty score for mismatching residues; always  $< 0$ ). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ( $P(N)$ ), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al., 1997. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100,  $M=5$ ,  $N=-4$ , and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By

5 "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two  
10 nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions  
15 which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted  
20 upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity.  
25 Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

30 (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal



alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%,

75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, 1970. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-

hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the  $T_m$  can be approximated from the equation of Meinkoth and Wahl, 1984;  $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$ ; where  $M$  is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and  $L$  is the length of the hybrid in base pairs.  $T_m$  is reduced by about  $1^\circ\text{C}$  for each 1% of mismatching; thus,  $T_m$ , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the  $T_m$  can be decreased  $10^\circ\text{C}$ . Generally, stringent conditions are selected to be about  $5^\circ\text{C}$  lower than the thermal melting point ( $T_m$ ) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or  $4^\circ\text{C}$  lower than the thermal melting point ( $T_m$ ); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or  $10^\circ\text{C}$  lower than the thermal melting point ( $T_m$ ); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or  $20^\circ\text{C}$  lower than the thermal melting point ( $T_m$ ). Using the equation, hybridization and wash compositions, and desired  $T$ , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a  $T$  of less than  $45^\circ\text{C}$  (aqueous solution) or  $32^\circ\text{C}$  (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about  $5^\circ\text{C}$  lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at  $72^\circ\text{C}$  for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at  $65^\circ\text{C}$  for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at  $45^\circ\text{C}$  for 15 minutes.

An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long robes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the  $T_m$  for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5



M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with  
5 washing in 0.1X SSC, 0.1% SDS at 65°C.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native  
10 protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides of the invention may be altered in various ways  
15 including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U.  
20 S. Patent No. 4,873,192; Walker and Gastra, 1983, and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff et al., 1978, herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar  
25 properties, are preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the polypeptides of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to  
30 possess the desired activity. The deletions, insertions, and substitutions of the polypeptide sequence encompassed herein are not expected to produce radical changes in the characteristics of the polypeptide. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of

doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%,  
5 more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative  
10 substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition,  
15 individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue  
20 consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

The word "plant" refers to any plant, particularly to seed plant, and "plant cell" is a structural and physiological unit of the plant, which comprises a cell  
25 wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds,  
30 tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al., 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host cell or organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995; and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

"Transient expression" refers to transgene expression in cells, e.g., after transformation with recombinant virus or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

5 "Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

"Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of  
10 primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Significant increase" is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

15 "Significantly less" means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

#### I. The Nucleic Acid Molecules of the Invention and Polypeptide Encoded

##### 20 Thereby

This invention relates to isolated plant, e.g., *Arabidopsis* and rice, nucleic acid molecules, sequences and segments (fragments), the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those expressed molecules, sequences or segments. However, the  
25 expression of these genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by "knocking out" the expression of at  
30 least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic



plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

Preferred sources for the nucleic acid molecules of the invention include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Wolffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wolffella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, *Biosystematic Investigation on the Family of Duckweeds: The family of*

Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula,

Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia.

- Other vegetable sources (and databases to identify orthologs of the invention) for the nucleic acid sequences of the invention include those are shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		<a href="http://www.cucurbit.org/">http://www.cucurbit.org/</a>
	<i>Cucumis melo</i>	Melon		<a href="http://genome.cornell.edu/cgc/">http://genome.cornell.edu/cgc/</a>
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash - winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				<a href="http://www.nal.usda.gov/pgdic/Map_proj/">http://www.nal.usda.gov/pgdic/Map_proj/</a>
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> <li>• 15x BAC on variety Heinz 1706 order from Clemson Genome center (<a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a>)</li> <li>• 11.6x BAC of <i>L. cheesmanii</i> (originates from J. Giovannoni) available from Clemson genome center (<a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a>)</li> <li>• EST collection</li> </ul>	<a href="http://genome.cornell.edu/solgenes">genome.cornell.edu/solgenes</a> <a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes">http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes</a> <a href="http://genome.cornell.edu/tgc/">http://genome.cornell.edu/tgc/</a> <a href="http://tgrc.ucdavis.edu/">http://tgrc.ucdavis.edu/</a>

			<p>from TIGR (<a href="http://www.tigr.org/tigrdb/lgi/index.html">www.tigr.org/tigrdb/lgi/index.html</a>)</p> <ul style="list-style-type: none"> <li>• EST collection from Clemson Genome Center (<a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a>)</li> <li>• TAG 99:254-271, 1999 (esculentum x pennelli)</li> <li>• TAG 89:1007-1013, 1994 (peruvianum)</li> <li>• Plant Cell Reports 12:293-297, 1993 (RAPDs)</li> <li>• Genetics 132:1141-1160, 1992 (potato x tomato)</li> <li>• Genetics 120:1095-1105, 1988 (RFLP potato and tomato)</li> <li>• Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs)</li> </ul>	
	<i>Capsicum annuum</i>	Pepper		<a href="http://neptune.netimages.com/~chile/science.html">http://neptune.netimages.com/~chile/science.html</a>
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	( <i>Nicotiana tabacum</i> )	(Tobacco)		
	( <i>Solanum tuberosum</i> )	(Potato)		
	( <i>Petunia x hybrida hort. ex E. Vilm.</i> )	(Petunia)	4x BAC of <i>Petunia hybrida</i> 7984 available from	



			Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	
Total				<a href="http://www.nal.usda.gov/pgdic/Map_proj/">http://www.nal.usda.gov/pgdic/Map_proj/</a>
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		<a href="http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm">http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm</a> <a href="http://geneous.cit.cornell.edu/cabbage/aboutcab.html">http://geneous.cit.cornell.edu/cabbage/aboutcab.html</a>
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	( <i>Brassica napus</i> )	(Oilseed rape)		<a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb">http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb</a>
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	<a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr">http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr</a>
Total				<a href="http://www.nal.usda.gov/pgdic/Map_proj/">http://www.nal.usda.gov/pgdic/Map_proj/</a>
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	( <i>Beta vulgaris</i> )	(Sugar Beet)		
Total				

Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	<a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beangen">http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beangen</a>
	<i>Pisum sativum</i>	Pea		
	( <i>Glycine max</i> )	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	<a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase">http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase</a>
Total			<a href="http://www.nal.usda.gov/pgdic/Map_projects/">http://www.nal.usda.gov/pgdic/Map_projects/</a>	
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	
	( <i>Zea mays</i> )	(Field Corn)		<a href="http://www.agron.missouri.edu/mnl/">http://www.agron.missouri.edu/mnl/</a>
Total			<a href="http://www.nal.usda.gov/pgdic/Map_projects/">http://www.nal.usda.gov/pgdic/Map_projects/</a>	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			<a href="http://www.nal.usda.gov/pgdic/Map_projects/">http://www.nal.usda.gov/pgdic/Map_projects/</a>	

Preferred forage and turf grass nucleic acid sources for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Preferably, the nucleic acid sources are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence obtained or obtainable

from any plant gene which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by SEQ ID NOs. 1-684 or 789-795, or a promoter for said gene. Thus, based on the *Arabidopsis* nucleic acid sequences of the present invention, orthologs of those sequences may be identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the *Arabidopsis* coding sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular *Arabidopsis* sequence is used as a probe that selectively hybridizes to other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g., Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from which the probe sequence is derived. The application of these methods using the *Arabidopsis* coding sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art as discussed hereinabove.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as  $^{32}\text{P}$ , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the

sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al., 1989. In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about 5 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for 10 example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

## II. Expression Cassettes of the Invention

15 The present invention also encompasses expression cassettes, preferably in the form of a recombinant vectors comprising the nucleic acid sequences of the invention. In such vectors, the expression cassette comprises regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise 20 promoter and termination signals and preferably also comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be 25 effective in plants. Joshi (1987) has suggested an appropriate consensus for plants and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensus are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst 30 leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, e.g., as extrachromosomal molecules, and are



therefore used to amplify the nucleic acid sequences of this invention in the host cells. In a preferred embodiment, host cells for such vectors are plant cells.

#### A. Promoters and Enhancers

Expression of the nucleotide sequences in transgenic plants is driven by promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In many cases, expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, chemically regulated, stress-responsive, tissue-preferred and tissue-specific promoters. Promoter sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the  $P_{tac}$  promoter can be induced to varying levels of gene expression depending on the level of isothiopyrogalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Preferred technology for chemical induction of gene expression is detailed in the published application EP

0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Tissue-specific or tissue-preferential promoters useful in the present invention. Also useful are promoters which confer seed-specific expression, such as those disclosed by Schernthaner et al., 1988; anther (tapetal) specific promoter B6 (Huffman et al.); and pistil-specific promoters such as a modified S13 promoter (Dzelkalns et al., 1993).

Preferred tissue specific expression patterns include green tissue-specific, root-specific, stem-specific, and flower-specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, 1989). A preferred promoter for root-specific expression is that described by de Framond (1991; EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in U.S. Patent No. 5,625,136 (to Ciba-Geigy) and which drives expression of the maize *trpA* gene.

Other promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs*, *nos*, and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Bonchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Preferred plant promoters include, but are not limited to, a promoter such as the CaMV 35S promoter, an enhanced 35S promoter or others such as CaMV 19S, *nos*, *Adh1*, sucrose synthase,  $\alpha$ -tubulin, ubiquitin, actin, *cab*, PEPCase or those associated with the R gene complex. Further suitable promoters include the U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein

protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea *rbcS* gene and the actin promoter from rice; seed specific promoters, such as the phaseolin promoter from beans, may also be used. Other promoters useful in the practice of the invention are known to those of skill in the art.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990,) corn alcohol dehydrogenase 1 (Vogel et al., 1992; Dennis et al., 1984), corn light harvesting complex (Simpson, 1985; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985; Rochester et al., 1986), pea small subunit RuBP carboxylase (Poulsen et al., 1986; Cashmore et al., 1983), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991),  $\alpha$ -tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), and chalcone synthase promoters (Franken et al., 1991).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearoyl-ACP desaturase, and fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific

expression is the pea vicilin promoter (Czako et al., 1992. (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995, 270 (5244), 1986-8).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674, the disclosure of which is hereby incorporated by reference. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996 and 1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama, 1997) and ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol- (WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to



environmental stress or stimuli such as increased salinity, drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986).

Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have  
5 been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and air  
10 borne pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous or homologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA  
15 sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the  
20 mRNA of the native DNA sequence.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by DNA binding proteins such as zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO  
25 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific  
30 DNA sequence.

#### B. 5' and 3' Sequences

In addition to promoters, a variety of 3 transcriptional terminators are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA

polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the tml terminator, the nopaline synthase terminator, the pea rbcS E9<sup>+</sup> terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed.

The 5' regulatory region of the expression cassette may also include other enhancing sequences. Numerous sequences have been found to enhance gene expression in transgenic plants. These include sequences which have been shown to enhance expression such as intron sequences (e.g., from *Adh1*, *bronzel* or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al., 1986); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

### C. Targeting Sequences

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle, e.g., the nucleus, may be preferred. Subcellular

localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

#### D. Marker Genes

10 In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the preselected nucleic acid sequence or segment. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. 15 Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait). Of course, many examples of suitable 20 marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include 25 markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g.,  $\alpha$ -amylase,  $\beta$ -lactamase, phosphinothricin 30 acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a polypeptide that becomes sequestered in the cell wall, and which polypeptide

includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and  
5 would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

Elements of the present disclosure are exemplified in detail through the use of particular marker genes. However in light of this disclosure, numerous other  
10 possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth herein below. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the  
15 introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant cell, e.g., a monocot cell.

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene, which codes for kanamycin resistance and can be selected for using kanamycin, G418, a gene encoding  
20 resistance to bleomycin, and the like; a *bar* gene which codes for bialaphos resistance; a gene which encodes an altered EPSP synthase protein thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonylurea or other  
25 ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene; a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; or a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a  
30 suitable chloroplast transit peptide, CTP (European Patent Application 0 218 571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces*



*hygroscopicus* or the *pat* gene from *Streptomyces viridochromogenes* (U.S. Patent No. 5,550,318). The enzyme phosphinothricin acetyltransferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Screenable markers that may be employed include, but are not limited to, a  $\beta$ -glucuronidase or *uidA* gene (GUS) which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a  $\beta$ -lactamase gene, which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xyIE* gene which encodes a catechol dioxygenase that can convert chromogenic catechols; an  $\alpha$ -amylase gene; a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a  $\beta$ -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene, which allows for bioluminescence detection; or an aequorin gene, which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein.

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. Maize strains can have one, or as many as four, R alleles which combine to regulate pigmentation in a developmental and tissue specific manner. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22

which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, Pl. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening.

#### E. Other Sequences

A vector of the invention can also further comprise plasmid DNA. Plasmid vectors include additional DNA sequences that provide for easy selection, amplification, and transformation of the expression cassette in prokaryotic and eukaryotic cells, e.g., pUC-derived vectors such as pUC8, pUC9, pUC18, pUC19, pUC23, pUC119, and pUC120, pSK-derived vectors, pGEM-derived vectors, pSP-derived vectors, or pBS-derived vectors. The additional DNA sequences include origins of replication to provide for autonomous replication of the vector, additional selectable marker genes, preferably encoding antibiotic or herbicide resistance, unique multiple cloning sites providing for multiple sites to insert DNA sequences or genes encoded in the expression cassette, and sequences that enhance transformation of prokaryotic and eukaryotic cells.

Another vector that is useful for expression in both plant and prokaryotic cells is the binary Ti plasmid (as disclosed in Schilperoort et al., U.S. Patent No. 4,940,838) as exemplified by vector pGA582. This binary Ti plasmid vector has been previously characterized by An, cited *supra*. This binary Ti vector can be replicated in prokaryotic bacteria such as *E. coli* and *Agrobacterium*. The *Agrobacterium* plasmid vectors can be used to transfer the expression cassette to dicot plant cells, and under certain conditions to monocot cells, such as rice cells. The binary Ti vectors preferably include the nopaline T DNA right and left borders to provide for efficient plant cell transformation, a selectable marker gene, unique multiple cloning sites in the T border regions, the *col/E1* replication of origin and a wide host range replicon. The binary Ti vectors carrying an

expression cassette of the invention can be used to transform both prokaryotic and eukaryotic cells, but is preferably used to transform dicot plant cells.

Virtually any DNA may be used for delivery to recipient cells to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instance containing only the DNA element to be expressed in the plant, and the like, may be employed.

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

### 20 III. Transformation

The expression cassettes of the present invention can be introduced into a host cell, e.g., a plant cell, in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of cell, e.g., monocotyledonous or dicotyledonous, targeted for transformation. Vectors which may be used to transform plant tissue with the expression cassettes of the present invention include both *Agrobacterium* vectors and ballistic vectors, as well as vectors suitable for DNA-mediated transformation, e.g., direct uptake or via electroporation. However, cells other than plant cells may be transformed with the expression cassettes of the invention.

Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), direct DNA transfer to plant cells by PEG precipitation; liposomes; electroporation (Riggs et al., 1986, *Agrobacterium*-mediated transformation (Hinchee et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using

devices available from Agracetus, Inc., Madison, Wis. and BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat).

In one embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994.

The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a



homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

*Agrobacterium tumefaciens* cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known. For example, U.S. Pat. No. 4,459,355 discloses a method for transforming susceptible plants, including dicots, with an *Agrobacterium* strain containing the Ti plasmid. The transformation of woody plants with an *Agrobacterium* vector is disclosed in U.S. Patent No. 4,795,855. Further, U.S. Patent No. 4,940,838 to Schilperoort et al. discloses a binary *Agrobacterium* vector (i.e., one in which the *Agrobacterium* contains one plasmid having the vir region of a Ti plasmid but no T region, and a second plasmid having a T region but no vir region) useful in carrying out the present invention.

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium spp.* Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Lorz et al., 1985; Potrykus, 1985; Park et al., 1985; Hiei et al., 1994. The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An. et al., 1985. For introduction into plants, the nucleotide sequences of the invention can be inserted into binary vectors as described in the examples.



Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention.

Numerous transformation vectors are available for plant transformation, and the  
 5 expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

Preferred plant cells for transformation include, but are not limited to, cells from plant such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B.*  
 10 *juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus*  
 15 *tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa  
 20 (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.),  
 25 oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L.*  
 30 *valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofieldia* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

5 Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis*

10 such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and

15 chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*);

20 redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils,

25 chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula,

30 blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry,

nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,  
 5 Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other vegetables are in Table 1.

10 Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Preferably, plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean,  
 15 barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, and the like), and even more preferably rice, corn and soybean.

In a preferred embodiment, the host cells are monocot or dicot cells, including, but are not limited to, wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince,  
 20 cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage, brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry,  
 25 chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut, nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g.,  
 30 lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia,

Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. More preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be  
5 regenerated into a transgenic plant.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the  
10 term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen,  
15 embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem).

The choice of plant tissue source for transformation will depend on the nature of the host plant and the transformation protocol. Useful tissue sources  
20 include callus, suspension culture cells, protoplasts, leaf segments, stem segments, tassels, pollen, embryos, hypocotyls, tuber segments, meristematic regions, and the like. The tissue source is selected and transformed so that it retains the ability to regenerate whole, fertile plants following transformation, i.e., contains totipotent cells. Type I or Type II embryonic maize callus and  
25 immature embryos are preferred *Zea mays* tissue sources. Selection of tissue sources for transformation of monocots is described in detail in U.S. Application Serial No. 08/112,245 and PCT publication WO 95/06128 (incorporated herein by reference).

For certain plant species, different antibiotic or herbicide selection markers  
30 may be preferred. Selection markers used routinely in transformation include the nptII gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982); Bevan et al., 1983), the *bar* gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the *hph* gene which confers resistance to the antibiotic hygromycin



(Blochinger & Diggelmann), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis et al., 1983).

Thus, the present invention also provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including, but not limited to, a transformed plant cell

5 from plants such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet

10 (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos*

15 *nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond

20 (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L.*

25 *miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofieldia* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*,

30 *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,



Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, as well  
 5 as from vegetables including those described in Table 1.

In a preferred embodiment, the transformed cells, include, but are not limited to, transformed wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage,  
 10 brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut,  
 15 nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field  
 20 bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura,  
 25 Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. Preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be regenerated into a transgenic plant.

#### 30 IV. Identification of Transgenic Plants

To confirm the presence of the preselected nucleic acid segment(s) or "transgene(s)" in the regenerating plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ*

hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the  
5 phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

10 The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discrete fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not  
15 prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments  
20 of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be  
25 identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into  
30 the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

5 Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The  
10 nonchimeric nature of the callus and the parental transformants ( $R_0$ ) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus,  $R_0$  plants and  $R_1$  progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated  
15 from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes  
20 such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information  
25 about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected  
30 DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.



Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or  
5 denaturing gel electrophoresis or isoelectric focussing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western  
10 blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally  
15 used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the  
20 generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical  
25 composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

## 30 V. Utility

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention



include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements

encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order  
5 to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can  
10 be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of viruses or other pests, or other stresses. The various breeding steps are characterized by  
15 well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding,  
20 variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain  
25 properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can  
30 be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

## VI. A Computer Readable Medium

The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-795 as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

The invention will be further described by the following examples which is not intended to limit the scope of the invention.

Example 1GeneChip Standard ProtocolQuantitation of total RNA

Total RNA from plant tissue is extracted and quantified.

- 5        1. Quantify total RNA using GeneQuant  
            $1\text{OD}_{260}=40\text{ mg RNA/ml}$ ;  $A_{260}/A_{280}=1.9$  to about 2.1
2. Run gel to check the integrity and purity of the extracted RNA

Synthesis of double-stranded cDNA

- 10        Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019)

was employed to prepare cDNAs. T7-(dT)<sub>24</sub> oligonucleotides were prepared

and purified by HPLC. (5'-

- 15        GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)<sub>24</sub>-3'(SEQ ID NO:800).

Step 1. Primer hybridization:

Incubate at 70°C for 10 minutes

Quick spin and put on ice briefly

- 20        Step 2. Temperature adjustment:

I        Incubate at 42°C for 2 minutes

Step 3. First strand synthesis:

DEPC-water- 1 µl

RNA (10 µg final)-10 µl

- 25        T7=(dT)<sub>24</sub> Primer (100 pmol final)-1 µl pmol

5X 1st strand cDNA buffer-4 µl

0.1M DTT (10 mM final)- 2 µl

10 mM dNTP mix (500 µM final)-1 µl

Superscript II RT 200 U/µl- 1 µl

- 30        Total of 20 µl

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

- DEPC-water- 91  $\mu$ l  
 5X 2nd strand cDNA buffer- 30  $\mu$ l  
 mM dNTP mix (250 mM final) - 3  $\mu$ l  
*E. coli* DNA ligase (10 U/ $\mu$ l)-1  $\mu$ l  
 5 *E. coli* DNA polymerase 1-10 U/ $\mu$ l- 4  $\mu$ l  
 RnaseH 2U/ $\mu$ l -1  $\mu$ l  
 T4 DNA polymerase 5 U/ $\mu$ l-2  $\mu$ l  
 0.5 M EDTA (0.5 M final)---10  $\mu$ l  
 Total 162  $\mu$ l  
 10 Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- 15 1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233)  
 at 14,000X, transfer 162  $\mu$ l of cDNA to PLG  
 2. Add 162  $\mu$ l of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge  
 2 minutes  
 3. Transfer the supernatant to a fresh 1.5 ml tube, add  
 20 Glycogen (5 mg/ml) 2  
 0.5 M NH<sub>4</sub>OAc (0.75xVol) 120  
 ETOH (2.5xVol, -20 °C) 400  
 4. Mix well and centrifuge at 14,000X for 20 minutes  
 5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)  
 25 6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes  
 7. Add 44  $\mu$ l DEPC H<sub>2</sub>O

Analyze of quantity and size distribution of cDNA

Run a gel using 1  $\mu$ l of the double-stranded synthesis product

30 Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

Purified cDNA	22 $\mu$ l
10X Hy buffer	4 $\mu$ l
10X biotin ribonucleotides	4 $\mu$ l



10X DTT	4 $\mu$ l
10X Rnase inhibitor mix	4 $\mu$ l
20X T7 RNA polymerase	2 $\mu$ l
Total	40 $\mu$ l

- 5 Centrifuge 5 seconds, and incubate for 4 hours at 37°C  
Gently mix every 30-45 minutes

#### Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

- 10 Determine concentration and dilute to 1  $\mu$ g/ $\mu$ l concentration

#### Fragmentation of cRNA

cRNA (1 $\mu$ g/ $\mu$ l)	15 $\mu$ l
5X Fragmentation Buffer*	6 $\mu$ l
DEPC H <sub>2</sub> O	9 $\mu$ l
	30 $\mu$ l

#### \*5x Fragmentation Buffer

1M Tris (pH8.1)	4.0 ml
MgOAc	0.64 g
KOAc	0.98 g
DEPC H <sub>2</sub> O	
Total	20 ml
Filter Sterilize	

25

#### Array wash and staining

Stringent Wash Buffer\*\*

Non-Stringent Wash Buffer\*\*\*

SAPE Stain\*\*\*\*

30 Antibody Stain\*\*\*\*\*

Wash on fluidics station using the appropriate antibody amplification protocol

\*\*Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H<sub>2</sub>O 910 ml,

Filter Sterilize

\*\*\*Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H<sub>2</sub>O 698 ml,  
Filter Sterilize, Antifoam 1.0.

\*\*\*\*SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H<sub>2</sub>O 540 µl.

5 \*\*\*\*\*Antibody Stain: 2X Stain Buffer 300 µl, H<sub>2</sub>O 266.4 µl, BSA 24 ul, Goat  
IgG 6 µl, Biotinylated Ab 3.6 µl

### Example 2

#### Identification of *Arabidopsis* Genes Induced by *Peronospora* Infection

10

To define the transcriptional profile for *Peronospora*-induced and/or *RPP7*- and *RPP8*- dependent genes, four *Arabidopsis* lines were infected with one of two different *P. parasitica* isolates (see Table 2). One *Arabidopsis* line was Col-0::*RPP8* which carries the cloned *RPP8* genomic clone (*RPP8* mediates resistance of the ecotype La-er against Emco5; McDowell et al. 1998) and is  
15 Emco5 resistant. Wild-type Col-0 plants are Emco5 susceptible. *RPP7* mediates resistance of *Arabidopsis* against the *Peronospora* isolate Hiks1, and occurs naturally in Col-0. Another *Arabidopsis* line had a loss of function *rpp7* mutant allele (Col-0 (*rpp7*)) (McDowell et al., 2000). Finally, three mutants in the  
20 signaling pathway for *RPP7*, i.e., they lack a *RPP7*-mediated response, were identified, i.e., *edm1*, *edm2* and *edm3*, and a line with one of the mutant alleles, i.e., *edm1*, was used.

RNA samples were collected from two week old seedlings at three time points, 0, 12 and 24 hours post infection with 100,000 spores/ml. Twelve hours  
25 post-inoculation was determined to be an appropriate time point for analysis of both incompatible interactions, based on trypan blue staining of HR sites and *PR-1* and *sen1* induction. Forty-eight hours post-inoculation was determined to be a time point where both compatible interactions exhibit dense hyphal growth and both *PR-1* and *sen1* expression. Three independent sets of RNA were  
30 pooled.

Table 2

	<u>Plant</u>	<u><i>Peronospora</i> isolate</u>	<u>Time of RNA collection</u>
	Col-0 ( <i>RPP7</i> , <i>incomp.</i> )	Hiks1	0, 12, 48 hours
35	Col-0 ( <i>rpp7</i> , <i>comp.</i> )	Hiks1	0, 12, 48 hours

Col-0 ( <i>edml</i> , <i>comp.</i> )	Hiks1	0, 12, 48 hours
Col-0 ( <i>tgRPP8</i> , <i>incomp.</i> )	Emco5	0, 12, 48 hours
Col-0 ( <i>rpp8</i> , <i>comp.</i> )	Emco5	0, 12, 48 hours

5 RNAs were labeled as described in Example 1 and hybridized to an Affymetrix Gene Chip having sequences corresponding to about 8,200 *Arabidopsis* genes. The data collected from these chips was employed to determine:

- 1) the difference, if any, between *RPP7* and *RPP8* triggered signaling (and how these profiles compare to other profiles, for example, to the profiles of *RPM1* and *RPS2*);
- 2) which portion of the transcriptional response is *R* dependent;
- 3) which genes are either commonly or uniquely induced during two different compatible interactions;
- 4) which genes are specifically activated during the incompatible interactions (gleaned by comparison with isogenic compatible controls) and, hence, may be important for the plant's defense against *Peronospora*;
- 5) which genes whose expression is a prerequisite for induced defense reactions against *Peronospora*; and
- 6) which genes are specifically repressed during the incompatible interactions, which may be required for successful Oomycete infections.

## Results

### Genes Expressed Early and Transiently After Infection

The normalized "average difference" (AD) from the chip experiments were processed as follows. All values together with the respective gene identifiers were loaded in EXCEL. Genes having, for a given treatment, AD values of 25 or less were considered as being not expressed. To reduce spurious background fluctuation, this cut off level was elevated to 75 for most of the analyses and normalized all AD values of 75 or less. For all five infection time courses, the AD values were divided by the corresponding 0 hour time point AD value. To visualize differences in gene expression ground states between the four experimental *Arabidopsis* lines, the following ratios were calculated for the 0 hour AD values: Col-0 (from Emco5 series)/Col-0-*RPP8* and *rpp7*/Col-0 (from Hiks1 series) and *edml*/Col-0 (from Hiks1 series). These ratios indicate whether

a given gene is up- or down-regulated by the *RPP7* or *RPP8* pathway, respectively. The resulting set of 18 expression ratio series was then loaded into CLUSTER (Eisen et al., 1998). The AD values were log transformed (base 2) and filtered to include only genes in the final data set that showed at least a 3-  
 5 fold expression change (which equals a 1.6-fold change of the log transformed values). These criteria were fulfilled by 464 genes that define the final data set. With this data set Average linkage clustering was performed (uncentered correlation). The resulting clustergram was displayed using TREEVIEW (Eisen et al., 1998). A second clustergram was generated in the same way applying a cut  
 10 off value of 50 on the normalized AD values. This clustergram includes 619 genes (probe sets).

Based on these clustergrams, gene clusters showing distinct expression behaviors were defined. Cluster cR7/R8 (see Table 3) contained genes that are early and transiently upregulated early and transiently after *P. parasitica*  
 15 infection of *Arabidopsis* in an *RPP7/8* dependent manner. Upregulation by the *RPP8* pathway was generally stronger. Strong induced expression of cR7/R8 genes was detectable 12 hours after Emco5 infection in Col-0(*tgRPP8*) plants (incompatible interaction), whereas no elevated expression can be observed 48  
 20 hours post infection in the same plants (as compared to untreated control plants). Only weakly elevated or no elevated expression was detected at all tested time points in Col-0 plants (compatible interaction). After Hiks1 infection, elevated expression of these genes was only observed in Col-0 plants (incompatible  
 25 interaction) after 12 hours. At no other time point following Hiks1 infection was substantially elevated expression of these genes observed. The expression ground state of these genes is similar in all four *Arabidopsis* lines.

Table 3

20245 s at	cut off = 75
18716 At	
18022 at	
14609 at	
17014 s at	
17051 s at	
19640 at	
14248 at	
13176 _at	

15978 at cut off +50  
 17014 s at  
 14609 at  
 13764 at  
 16649 s at Subcluster A  
 13215 s at  
 17653 at  
 17008 at  
 15042 at  
 12778\_r\_at

14614 at  
 17051 s at  
 14248 at Subcluster B  
 20245 s at  
 19640 at  
 18716 at  
 18022\_at

17500 s at  
 13217 s at  
 18928 at

The cR7/R8 cluster was originally defined using the clustergram based on a cut off value of 75 and comprised only 9 genes. Applying a cut off value of 50, the cluster became larger, comprising 21 genes, which could be divided into two subclusters (Table 4). Subcluster cR7/R8 A includes genes strongly and transiently upregulated by the *RPP8* pathway, but either not, or only faintly, upregulated by the *RPP7* pathway. Members of subcluster B showed pronounced upregulation by both *RPP* pathways after 12 hours and also elevated expression during compatible *Emco5* infections in Col-0.

10

Table 4

Subcluster AGene-identifier (probe set)

15978\_at

17014\_s\_at\*

14609\_at

16649\_s\_at+

13215\_s\_at+

17653\_at

17008\_at

Related to

X68592.6\_at

atu05206\_s\_at

AC002340.147\_at

athorf\_s\_at

CafferoylCoAmethyltrans\_s\_a  
t

AL035679.144\_at

AC006585.212\_at



15042_at	AL021961.3_at
12778_r_at	AC006577.16_r_at

Subcluster B

<u>Gene-identifier (probe set)</u>	<u>Related to</u>
14614_at	AC004165.66_at
17051_s_at	af098947_s_at
14248_at	PAD3_at
20245_s_at	AC005309.97_s_at
19640_at	AC004561.78_at
18716_at	X91916_at
18022_at	AJ010971_at
17500_s_at <sup>†</sup>	athcallga_s_at
13217_s_at <sup>†</sup>	calmodulinlike_s_at
18928_at	AC002333.181_at

\*Genes printed in **bold** were identified using a cut off value of 75; all others were identified using a cut off value of 50.

<sup>†</sup>The probe sets 16649 and 13215 as well as 17500 and 13217 correspond to the same genes.

Thus, the predominant feature of genes of the cR7/R8 cluster is more pronounced expression along with *RPP7* and *RPP8* mediated *Peronospora* resistance in comparison to the corresponding compatible interactions. Expression of these genes peaks in around 12 hours post infection and returns to ground state by 48 hours post infection. Hence, increased transcript levels of these genes coincide with the time window of decision between disease or resistance. Within 48 hours after infection with each tested *Peronospora* isolate, the plant either responds with HR and hinders development of oomycete hyphae or allows successful infection.

Identification of Conserved Sequence Motifs Within cR7/R8 Upstream Regions

To identify potential *cis*-elements involved in the specific regulation of cR7/R8 genes, stretches comprising 1.1 to 1.2 kb localized directly upstream of the translation start sites of coding regions from this cluster were collected from genomic *Arabidopsis* sequences (see Figure 2). Two motif search algorithms were used to recognize conserved motifs: AlignAce (Roth et al., 1998) and MEME (Bailey and Elkan, 1994). A search with AlignAce (default settings) revealed two conserved motifs within a set of 8 promoters comprising 7 from the originally defined cR7R8 using a cut off value of 75 and the promoter of a gene encoding a putative Myb-like transcription factor (Martin & Paz-Ares, 1997)

(probe set 13176, SEQ ID NO:36), which shows a similar expression behavior as cR7/R8. The AlignAce output is shown below in Table 5:

Table 5

Motif 1	MAP Score:	SEQ ID NO.	Corresponding Probe Set
*****	6.87857		
CAACAATTAT	0 36 1	685	17014
CAACTATGTC	0 981 1	686	17014
CAACAATGAC	1 934 0	687	20245
CAACAATGAC	2 271 1	688	14609
AAACAATGAT	2 1184 1	689	14609
CAACATTGAC	3 163 0	690	17051
CAACATTGTT	3 298 0	691	17051
CAACAATGTT	4 613 1	692	19640
CAACTATGAT	4 791 0	693	19640
CAACAATGAT	4 1064 0	694	19640
CAAAAATGAT	7 397 0	695	17008
CAACATTGAT	7 415 1	696	17008
CATATCA/TA/TTGAC (Consensus)		697	N.A.

5

Motif 2	MAP Score:	SEQ ID NO.	Corresponding Probe Set
***** **	2.22382		
TTTGGGCAAAA	1 368 0	698	20245
GTTGGGTCAAA	1 739 0	699	20245
GATGGGCACAA	2 691 0	700	14609
GATGGGCCAAA	3 700 0	701	17051
GATGGGTATAA	4 344 0	702	19640
GATGGGACTAA	5 98 1	703	14248
TTTGGGCCTAA	5 971 1	704	14248
TATGGGCCCAA	5 1012 0	705	14248
CTTGGGACAAA	7 579 1	706	17008
GATGGGTCAAC	7 1009 0	707	17008
CATGGGAATAA	7 1072 1	708	17008
NATTGGGNC/ANAA (Consensus)		709	N.A.

For each motif, examples from cR7/R8 promoters are listed. Nucleotides evaluated by AlignAce as being conserved are indicated by a "\*" above the examples. Besides motifs 1 and 2, a variety of additional ones were found by AlignAce, which, however, consisted almost exclusively of Ts and As. These motifs probably do not constitute functional *cis*-elements. Promoter sequences

10

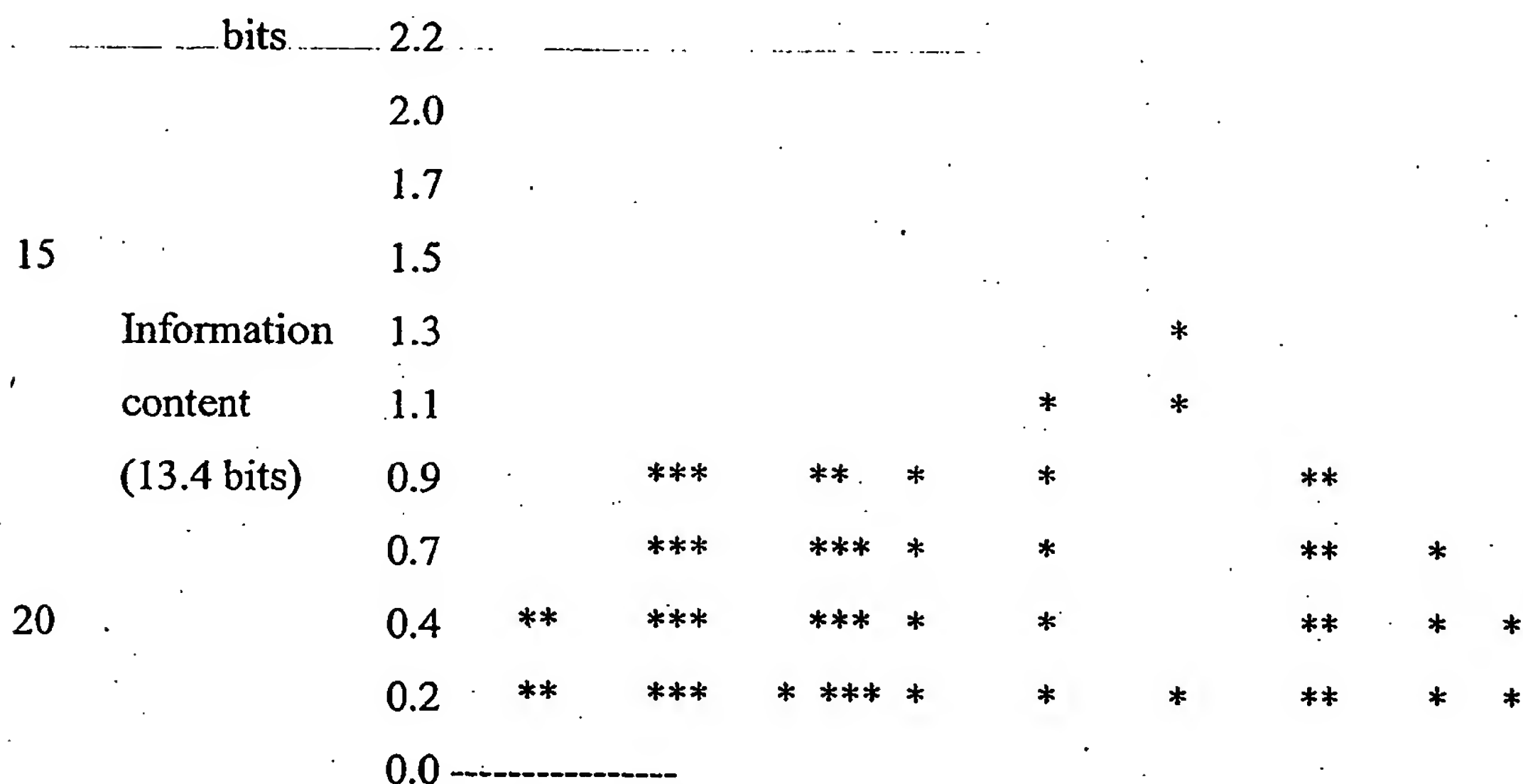
are generally enriched in As or Ts (A/T content in cR7R8 promoters is 70%) and regulatory *cis*-elements usually contain also Cs or Gs.

Motif 1 (CAACA/TA/TTGA/TC/T, SEQ ID NO:710) resembles the type I Myb binding site consensus (MBS;T/CAACT/GG), which is bound by animal and some plant Myb transcription factors (Yang & Klessig, 1996). The 3' portion of the motif 1 consensus allows overlap with binding sites of WRKY (TTTGACC/T; Eulgem et al., 2000) or TGA-bZIP transcription factors (TGACG; Schindler et al. 1992). Interestingly, a gene encoding a putative Myb-like transcription factor (gene identification number 13176) is upregulated along with cR7/R8 genes in an *RPP7/RPP8*-dependent, early and transient manner. The factor encoded by this gene may be a regulator of cR7/R8 genes. Motif 1 is particularly enriched in promoters of the originally defined cR7/R8 cluster (cut off = 75). This motif, which consists of six strictly defined positions and four positions allowing two base pairs each, should occur by random roughly once per 20,000 bp in each of both possible orientations (assuming a T/A content of 70% and a G/C content of 30%). In the 8,441 bp of cR7/R8 promoter sequences, the motif occurs 9 times (roughly 20 times the statistically expected frequency). Consistent with the statistical expectation, motif 1 occurs only two times within 15,873 bp from a set of control promoters of genes showing no defense related expression (data not shown).

In the extended set of cR7/R8 genes (cut off = 50), the enrichment of motif 1 is less striking. It occurs only 9 times within 16,519 bp in total and, more importantly, none of the promoters added to the set by lowering the cut off value contains this motif. Thus, if motif 1 is involved in the specific regulation of cR7/R8 genes it cannot alone be responsible for the particular expression features of these genes, and may rather be responsible for the more pronounced cR7/R8-triggered expression of members of the originally defined cluster (cut off = 75).

Motif 2 (A/TTGGGNC/ANAA; SEQ ID NO:711) does not resemble any other known plant *cis*-element. The consensus sequence consists of six strictly defined positions, two positions with two alternatives and two positions with four alternatives; and, hence, should occur by random once per 10,000 bp. Motif 2 can be found 10 times within 8,441 bp of the promoters from the originally defined cR7/R8 (cut off = 75) and 14 times within 16,519 bp of the extended

cR7/R8 promoter set. Thus, its occurrence in cR7/R8 promoters is roughly 10 times the statistical expectation. Motif 2 is absent in the 15,873 bp of promoters of genes showing no defense related expression (data not shown). It is, however, also enriched in the promoters of previously defined clusters of defense related genes, such as the PR1 regulon (SAR genes) and SOMc3 (genes up regulated in Ws-0 after infection with avirulent Noco2; data not shown). The latter two clusters may also include genes sharing expression features with cR7/R8 genes. In addition to AlignAce, a motif 2-like sequence was also recognized by MEME. Within the extended set of cR7/R8 promoters, MEME found the following sequence stretch to be conserved:



Multilevel Consensus sequence T/C TTT G/C A/T/G C/T  
 25 CCAAG/A/CAA/GAC/A (SEQ ID NO:712)

The reverse complement of this consensus sequence is (positions with three alternatives were given as "N") given below with motif 2 for comparison:

30 MEME motif: G/T T C/T T N T T G G G N G/C A A A A/C (SEQ ID NO:713)  
 Motif 2: T G G G N A N/C A A (SEQ ID NO:714)

MEME was run using the default settings of “advanced MEME” choosing the options “one motif per sequence”, “narrow motifs” and “additional strand: reverse complement”.

To confirm these results, Northern blots using probes of representatives of each cluster are performed. In addition, T-DNA lines are screened for knock out in Myb-like gene (AL031394.56\_at) and selected members of cR7/R8, such as RNS1 (atu05206\_s\_at) or the gene encoding a calmodulin-like protein (identification number 13217\_s\_at). Also, yeast one hybrid screens are performed to clone transcription factors binding to motifs 1 and 2, or other identified motifs. Transgenic *Arabidopsis* plants carrying fusions of GUS with a representative promoter from cR7/R8 can be used to further evaluate the functional significance of motifs 1 and 2, and to perform a genetic screening for mutants impaired in regulation of cR7/R8 genes.

#### 15 Genes Induced by *Peronospora* Infection in a Manner that Requires *RPP7* or *RPP8*

The data sets described above were employed to identify genes that were induced by *Peronospora* infection and were RPP7/8-dependent. All expression values less than 5 were set to 5. Using ratios calculated in Excel, and database sorting using Access, a subset of genes was identified whose expression depends on RPP7 or RPP8 using the following criteria:

Col Hiks1 12 hour/Col untreated > 2.5 AND Col Hiks1 12 hour > 30  
AND Col Hiks1 12 hour/Col rpp7 Hiks1 12 hour > 2  
OR  
25 Col Hiks1 48 hour/Col untreated > 2.5 AND Col Hiks1 48 hour > 30  
AND Col Hiks1 48 hour/Col rpp7 Hiks1 48 hour > 2  
OR  
Col RPP8 Emco5 12 hour/Col RPP8 no treatment > 2.5 AND Col RPP8  
Emco5 12 hour > 30 AND Col RPP8 Emco5 12 hour/Col (rpp8) Emco5  
30 12 hour > 2  
OR  
Col RPP8 Emco5 48 hour/Col RPP8 no treatment AND Col RPP8  
Emco5 48 hour > 30 AND Col RPP8 Emco5 48 hour/Col (rpp8) Emco5  
48 hour > 2



This yielded 217 probe sets ("RPP7 or 8") which correspond to sequences, the expression of which were increased by at least 2.5 fold and were *RPP7*- or *RPP8*-dependent (Table 6).

5

Table 6

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1  (Z99708) putative protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	gb AAC64313.1  (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1  (AL033545) extensin-like protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1  (AL078579) putative protein [Arabidopsis thaliana]
12278_at (AJ011674.2_AT)	emb CAA09731.1  (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12307_at (AC002392.162_AT)	gb AAD12037.1  (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1  (AB023448) basic endochitinase [Arabidopsis thaliana]
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1  (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1  (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12360_at (AL022347.131_AT)	emb CAA18468.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1  (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
12521_at (AF049236.28_AT)	gb AAC14413.1  (AF049236) unknown [Arabidopsis thaliana]
12538_at (AF033205.2_AT)	gb AAC02973.1  (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1  (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1  (X82624) SRG2At [Arabidopsis thaliana]
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]

12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12779_f_at (AC006577.16_F_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1  (U40856) AIG1 [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1  (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12891_at (ATACS6_AT)	gb AAC63850.1  (U73786) ACC synthase [Arabidopsis thaliana]
12892_g_at (ATACS6_G_AT)	gb AAC63850.1  (U73786) ACC synthase [Arabidopsis thaliana]
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1  (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1  (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1  (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12933_r_at (ATPRITAN_R_AT)	emb CAA65420.1  (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1  (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1  (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1  (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1  (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from this gene. [Arabidopsis thaliana]

13154_s_at (AC002333.210_S_AT)	gb AAB64047.1  (AC002333) putative endochitinase [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1  (AL031394) putative protein [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	emb CAA16892.1  (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13215_s_at (CAFFEROYLCOAMETHYLTRANNS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1  (AL049862) calmodulin-like protein [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1  (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1  (M62984) heat shock protein 83 [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	gb AAC49775.1  (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1  (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13627_at (AL035394.196_AT)	emb CAA23036.1  (AL035394) putative Na <sup>+</sup> /H <sup>+</sup> -exchanging protein [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	gb AAB82634.1  (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13697_at (NI16_AT)	No hits found.

13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1  (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1  (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1  (AL022023) putative protein [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1  (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found.
14110_i_at (AL035528.279_I_AT)	emb CAB36854.1  (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	emb CAB36854.1  (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	gb AAC26243.1  (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15.
14145_at (NOVARTIS35_AT)	dbj BAA22813.1  (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14201_at (NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15.
14223_at (NOVARTIS9_AT)	emb CAA19683.1  (AL024486) putative protein [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]

14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14249_i_at (PAD4_I_AT)	emb CAB43438.1  (AL050300) putative protein [Arabidopsis thaliana]
14250_r_at (PAD4_R_AT)	emb CAB43438.1  (AL050300) putative protein [Arabidopsis thaliana]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2  (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2  (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1  (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1  (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1  (AC000348) T7N9.22 [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	gb AAC02748.1  (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	gb AAC16958.1  (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1  (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1  (AC004747) putative antifungal protein [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1  (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
14638_s_at (PRXCB_S_AT)	emb CAA50677.1  (X71794) peroxidase [Arabidopsis thaliana]
14672_s_at (TSA1_S_AT)	gb AAC49117.1  (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
14673_s_at (TSB2_S_AT)	gb AAA32879.1  (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
14682_i_at (WT1012A_RC_I_AT)	No hits found.
14691_at (WT1096_AT)	No hits found.



14704_s_at (WT768_RC_S_AT)	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14763_at (X86958.1_AT)	emb CAA60521.1  (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14838_s_at (M96073.6_S_AT)	gb AAA32835.1  (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14882_at (AL022605.63_AT)	emb CAA18753.1  (AL022605) putative protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1  (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	gb AAB53975.1  (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1  (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1  (AF000657) hypothetical protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	emb CAA19722.1  (AL030978) putative protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1  (AL078637) putative protein [Arabidopsis thaliana]
15532_r_at (AL078637.191_R_AT)	emb CAB45069.1  (AL078637) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	dbj BAA24440.1  (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15641_s_at (AF117063_S_AT)	gb AAD10829.1  (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	gb AAB80922.1  (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1  (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1  (X98676) zinc finger protein [Arabidopsis thaliana]
15846_at (AC006067.63_AT)	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]

15847_g_at (AC006067.63_G_AT)	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1  (AC006587) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1  (X71794) peroxidase [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1  (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1  (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1  (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1  (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1  (AL049730) pEARLI 1 [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1  (AL080252) putative protein [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1  (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1  (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1  (AL024486) putative protein [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1  (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1  (AC003974) putative disease resistance protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1  (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1  (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1  (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	dbj BAA32419.1  (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1  (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1  (AL049500) osmotin precursor [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1  (AC002391) unknown protein [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	gb AAC48925.1  (U05206) ribonuclease [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1  (AF098947) CTF2B [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1  (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1  (U66345) calreticulin [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1  (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1  (X99097) peroxidase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1  (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1  (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]

17487_s_at (U18993.2_S_AT)	gb AAC49117.1  (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1  (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1  (AL049862) calmodulin-like protein [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1  (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	dbj BAA28538.1  (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAC49282.1  (U40856) AIG1 [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	emb CAB38823.1  (AL035679) putative protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1  (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1  (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1  (AC002333) putative endochitinase [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	gb AAB87109.1  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1  (Z97339) hypothetical protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1  (AJ006960) peroxidase [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1  (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	emb CAB52675.1  (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1  (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1  (AL021890) putative protein [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAB87112.1  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAC34217.1  (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

18590_at (AJ222713.4_AT)	emb CAA10955.1  (AJ222713) unnamed protein product [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1  (X74756) ATAF2 [Arabidopsis thaliana] gb AAC72125.1  (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	gb AAC33239.1  (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC62611.1  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC16927.1  (AC002338) putative laccase [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	emb CAA72484.1  (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	emb CAB41722.1  (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAA65053.1  (X95738) proline transporter 2 [Arabidopsis thaliana]
19158_at (X95738.2_AT)	gb AAB64325.1  (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1  (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1  (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAD10694.1  (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAC27173.1  (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	emb CAB45805.1  (AL080253) putative protein [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAA66965.1  (X98321) peroxidase [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	



19640_at (AC004561.78_AT)	gb AAC95192.1  (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1  (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19672_at (AC005687.19_AT)	gb AAC36019.1  (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1  (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1  (AC005770) putative protease inhibitor [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1  (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1  (AC005727) unknown protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1  (AC005395) unknown protein [Arabidopsis thaliana]
19982_at (AC002986.28_AT)	gb AAC17040.1  (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1  (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1  (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1  (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1  (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	gb AAB82640.1  (AC002387) putative pectinesterase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1  (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1  (Y14590) class IV chitinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1  (M92353) anthranilate

	synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1  (AC005314) putative serpin [Arabidopsis thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1  (AL024486) putative chitinase [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1  (Z97336) hypothetical protei [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1  (AC005896) putative C2H2- type zinc finger protein [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1  (AL049658) hypothetical protein [Arabidopsis thaliana]

The functions of RPP7 and RPP8 are independent of *PAD4*, *NDR1*, *NahG*, *COI1*, and *EDS1*. Consequently, it is unlikely that genes whose expression is reduced in *pad4* or *NahG* backgrounds are important for RPP7- or RPP8- mediated resistance. Although data from *Peronospora* infection of *pad4* or *nahG* plants was not available, data from *Pseudomonas syringae* (ES4326) infection of *pad4* and *NahG* plants was available and employed to determine which genes depended on *PAD4* or were interfered with by *NahG*. Resistance to *P. syringae* mediated by *RPS2* requires *NDR1* function. Genes whose expression requires *RPS2* are less likely to be important for RPP7 or RPP8 mediated resistance than genes whose expression is independent of *RPS2*. Gene expression data was available for wild-type plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, and *rps2* mutant plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, 6 hours after infection.

*EDM1* is required for resistance mediated by RPP7. Thus, genes whose expression requires *EDM1* are likely to be important for RPP7-mediated resistance. Gene expression data was available for an *edm1* mutant (see above).

The data from the 7 additional data sets (Col Psm ES4326 30 hour; Col Mock 30 hour; Col *NahG* Psm ES4226 30 hour; Col *pad4* Psm ES4326 30 hour; Col water control; Col DC3000 *avrRpt2* and *rps2* DC3000 *avrPrt2* was added to the 217 probe sets in "RPP7 or 8". The following sets were identified:

*edm1*:

Col edm1 Hiks1 12 hour/Col Hiks1 12 hour < 0.5 OR Col edm1 Hiks1  
48 hour/Col Hiks1 48 hour < 0.5.

rps2:

5 Col DC3000 *avrRpt2* 6 hour/Col water control > 2 AND *rps2* DC3000  
*avrRpt2* 6 hour/Col DC3000 *avrRpt2* 6 hour < 0.5.

pad4 or NahG:

10 Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col pad4 Psm  
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.  
OR  
Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col NahG Psm  
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

15 There are 8 possible combinations of these three sets. Access was used to divide  
the 217 probe sets into 8 sets, numbered 2-9 (considering the whole set of 217  
probe sets as set 1) as shown in Tables 7 and 8:

Table 7

20	<u>Set</u>	<u>Content</u>	<u>Number of probe</u>
		<u>sets</u>	
	2	RPP7 or 8 not edm1 not rps2 not pad4 or NahG	62 probe sets
	3	edm1 not rps2 not pad4 or NahG	50 probe sets
	4	rps2 not edm1 not pad4 or NahG	14 probe sets
25	5	pad4 or NahG not edm1 not rps2	21 probe sets
	6	edm1 and rps2 not pad4 or NahG	23 probe sets
	7	edm1 and pad4 or NahG not rps2	25 probe sets
	8	rps2 and pad4 or NahG not edm1	8 probe sets
	9	edm1 and rps2 and pad4 or NahG	<u>14 probe sets</u>
30	Total		217 probe sets

Table 8

2 RPP7 or 8 not edm1 not rps2  
not pad4 or NahG

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1  (Z99708) putative protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1  (AL078579) putative protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1  (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12538_at (AF033205.2_AT)	gb AAC02973.1  (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1  (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
12777_i_at (AC006577.16_I_AT)	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
12779_f_at (AC006577.16_F_AT)	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1  (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1  (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1  (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1  (AL031394) putative protein [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1  (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1  (AL022023) putative protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	emb CAB36854.1  (AL035528) putative disease resistance protein [Arabidopsis thaliana]

14145_at (NOVARTIS35_AT)	dbj BAA22813.1  (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2  (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1  (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1  (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1  (AC000348) T7N9.22 [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1  (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1  (AC004747) putative antifungal protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1  (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1  (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1  (AF000657) hypothetical protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1  (AL078637) putative protein [Arabidopsis thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1  (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1  (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1  (AL024486) putative protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1  (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1  (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1  (AF098947) CTF2B [Arabidopsis thaliana]



17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1  (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475, gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17487_s_at (U18993.2_S_AT)	gb AAC49117.1  (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1  (X74756) ATAF2 [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAC72125.1  (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC33239.1  (AC005315) putative ligand- gated ion channel protein [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	gb AAC16927.1  (AC002338) putative laccase [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAB41722.1  (AL049730) pEARLI 1- like protein [Arabidopsis thaliana]
19158_at (X95738.2_AT)	emb CAA65053.1  (X95738) proline transporter 2 [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD10694.1  (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAB45805.1  (AL080253) putative protein [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	emb CAA66965.1  (X98321) peroxidase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1  (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1  (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

19982_at (AC002986.28_AT)	gb AAC17040.1  (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1  (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1  (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1  (AC005314) putative serpin [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1  (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]

#### Duplicates

12777 and 12779 (lipase)  
 12889 and 20291 (ASA1)  
 12908 and 16536 (ERF5)  
 17464 and 19982 (RLK5)  
 18216 and 18217 (T22C5.18)  
 18908 and 18909 (subtilisin-like protease)  
 20238 and 20239 (beta-fructofuranosidase)

#### 3 edm1 without rps2 without pad4orNahG

ProbeSet	Description
12091_at (AC004450.116_AT)	gb AAC64313.1  (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1  (AL033545) extensin-like protein [Arabidopsis thaliana]

	gb AAC32192.1  (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
12500_s_at (AF081067.3_S_AT)	[Arabidopsis thaliana]
	gb AAC14413.1  (AF049236) unknown
12521_at (AF049236.28_AT)	[Arabidopsis thaliana]
	emb CAA57944.1  (X82624) SRG2At
12574_at (X82624.2_AT)	[Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	
	gb AAC63850.1  (U73786) ACC synthase
12891_at (ATACS6_AT)	[Arabidopsis thaliana]
	gb AAC63850.1  (U73786) ACC synthase
12892_g_at (ATACS6_G_AT)	[Arabidopsis thaliana]
	dbj BAA32419.1  (AB008104) ethylene responsive element binding factor 2
12905_s_at (ATERF2_S_AT)	[Arabidopsis thaliana]
	gb AAC13947.1  (AF021244) coronatine- induced protein 1 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
	emb CAA16892.1  (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	
	gb AAC49775.1  (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	
	gb AAB82634.1  (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	
14096_at (AC002291.12_AT)	No hits found.
	emb CAA19683.1  (AL024486) putative protein [Arabidopsis thaliana]
14223_at (NOVARTIS9_AT)	
	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	
14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2  (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
	gb AAC16958.1  (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	
14691_at (WT1096_AT)	No hits found.
	gb AAA32835.1  (M96073) phosphoribosylanthranilate transferase
14838_s_at (M96073.6_S_AT)	[Arabidopsis thaliana]
	gb AAB53975.1  (U90522) lysine- ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	

15532_r_at (AL078637.191_R_AT)	emb CAB45069.1  (AL078637) putative protein [Arabidopsis thaliana] dbj BAA24440.1  (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	gb AAB80922.1  (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1  (AL080252) putative protein [Arabidopsis thaliana] dbj BAA32419.1  (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1  (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana] gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAC48925.1  (U05206) ribonuclease [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1  (AL049862) calmodulin- like protein [Arabidopsis thaliana] dbj BAA28538.1  (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	emb CAB38823.1  (AL035679) putative protein [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	gb AAC23646.1  (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAB87109.1  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	emb CAB52675.1  (AJ010971) glucose-6- phosphate 1-dehydrogenase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	gb AAB87112.1  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	emb CAA72484.1  (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAB64325.1  (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1  (X99923) male sterility 2- like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1  (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAC27173.1  (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	

19672_at (AC005687.19_AT)	gb AAC36019.1  (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1  (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1  (AC005770) putative protease inhibitor [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1  (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1  (Z97336) hypothetical protei [Arabidopsis thaliana]
20641_at (X91919.1_AT)	emb CAA63012.1  (X91919) LEA76 homologue type1 [Arabidopsis thaliana] Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.

**Duplicates**

12905 and 16609 (ERF2)

13188 and 16981 (thioredoxin h)

12891 and 12892 (ACC  
synthase)14838 (phosphoribosyl  
anthranilate transferase) has a  
duplicate in set 2 (14620).  
Counted in set 214254 (PAL1) has a duplicate in  
set 2 (14256) Counted in set 2.12778 (lipase) has duplicates in  
set 2 (12777 and 12779) Counted  
in set 2.**4 rps2 without edm1 without  
pad4orNahG****ProbeSet****Description**

12278_at (AJ011674.2_AT)	emb CAA09731.1  (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12360_at (AL022347.131_AT)	emb CAA18468.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13154_s_at (AC002333.210_S_AT)	gb AAB64047.1  (AC002333) putative endochitinase [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15.



15431_at (AL030978.64_AT)	emb CAA19722.1  (AL030978) putative protein [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1  (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1  (AC002391) unknown protein [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1  (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1  (AL021890) putative protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1  (AC005395) unknown protein [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]

#### Duplicates

12360 and 20223 (serine  
threonine kinase)  
13685 and 20365 (similar to  
Mlo)

#### 5 pad4orNahG without rps2 without edm1

##### ProbeSet

	Description
12307_at (AC002392.162_AT)	gb AAD12037.1  (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1  (AB023448) basic endochitinase [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1  (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1  (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]

14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1  (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1  (X98676) zinc finger protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1  (AC006587) unknown protein [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1  (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1  (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1  (AL049500) osmotin precursor [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1  (U66345) calreticulin [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1  (Z97340) beta-1, 3- glucanase class I precursor [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1  (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1  (AL024486) putative chitinase [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1  (AL049658) hypothetical protein [Arabidopsis thaliana]

**Duplicates:**

15778 and 15779 (zinc finger  
protein)

**6 edm1 and rps2 without  
pad4orNahG**

**ProbeSet**

	Description
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1  (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1  (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]

13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1  (AL049862) calmodulin- like protein [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1  (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1  (M62984) heat shock protein 83 [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1  (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	gb AAC26243.1  (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14682_i_at (WT1012A_RC_I_AT)	No hits found.
15641_s_at (AF117063_S_AT)	gb AAD10829.1  (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1  (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1  (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1  (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1  (AC002294) similar to S- linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1  (Z97339) hypothetical protein [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1  (AJ002295) inositol-1,4,5- trisphosphate 5-Phosphatase [Arabidopsis thaliana]

19640\_at (AC004561.78\_AT) gb|AAC95192.1| (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

### Duplicates

13187 and 13189 (thioredoxin h)  
There are two duplicates of this in set 3 (13188 and 16981) Count it in set 3.

13215 and 16649 (putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase)

13285 and 16091 (heat shock protein 83)

13217 (calmodulin-like) has a duplicate in set 3 (17500). Count in set 3

16105 (hsf4) has a duplicate in set 4 (13273) Count in set 4

### 7 pad4orNahG and edm1 without rps2

#### ProbeSet

#### Description

14110\_i\_at  
(AL035528.279\_I\_AT)

emb|CAB36854.1| (AL035528) putative disease resistance protein [Arabidopsis thaliana]

14148\_at (NOVARTIS38\_AT)

gb|AAF34713.1|AF224762\_1 (AF224762) SigA binding protein [Arabidopsis thaliana]

14249\_i\_at (PAD4\_I\_AT)

emb|CAB43438.1| (AL050300) putative protein [Arabidopsis thaliana]

14250\_r\_at (PAD4\_R\_AT)

emb|CAB43438.1| (AL050300) putative protein [Arabidopsis thaliana]

14672\_s\_at (TSA1\_S\_AT)

gb|AAC49117.1| (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]

14673\_s\_at (TSB2\_S\_AT)

gb|AAA32879.1| (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]

14704\_s\_at (WT768\_RC\_S\_AT)

gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]

14709\_at (WT788\_AT)

No hits found less than or equal to 1e-15.

14882\_at (AL022605.63\_AT)

emb|CAA18753.1| (AL022605) putative protein [Arabidopsis thaliana]

15616\_s\_at  
(ATHPRO25A\_S\_AT)

emb|CAA08794.1| (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

15846_at (AC006067.63_AT)	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
15847_g_at (AC006067.63_G_AT)	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1  (X71794) peroxidase [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1  (AL049730) pEARLI 1 [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1  (AC003974) putative disease resistance protein [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1  (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1  (X99097) peroxidase [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1  (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1  (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
18590_at (AJ222713.4_AT)	emb CAA10955.1  (AJ222713) unnamed protein product [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1  (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1  (Y14590) class IV chitinase [Arabidopsis thaliana]

#### Duplicates

14249 and 14250 (PAD4)

14704 and 15846 and 15847  
(unknown protein)

18968 and 18969  
(endoxyloglucan transferase)



20287 and 20288 (class IV chitinase)  
 14110 (putative disease-resistance gene) is an incomplete probe set with very low signal. It has a duplicate (14111) in set 2. Count in set 2.  
 14672 (trp synthase alpha) has a duplicate in set 2 (17487) Counted in set 2.

**8 rps2 and pad4orNahG without edm1**

ProbeSet	Description
13627_at (AL035394.196_AT)	emb CAA23036.1  (AL035394) putative Na <sup>+</sup> /H <sup>+</sup> -exchanging protein [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1  (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1  (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1  (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1  (AJ006960) peroxidase [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1  (AC005727) unknown protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1  (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]

Duplicates:

14635 and 17128 (PR-1)

**9 edm1 and rps2 and pad4orNahG**

ProbeSet	Description
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1  (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1  (U40856) AIG1 [Arabidopsis thaliana]

12989_s_at (AC004077.149_S_AT) 13697_at (NI16_AT)	gb AAC26690.1  (AC004077) putative cytochrome P450 [Arabidopsis thaliana] No hits found.
14201_at (NOVARTIS73_AT) 14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15. No hits found less than or equal to 1e-15.
14609_at (AC002340.147_AT)	gb AAC02748.1  (AC002340) putative cytochrome P450 [Arabidopsis thaliana] emb CAA50677.1  (X71794) peroxidase [Arabidopsis thaliana]
14638_s_at (PRXCB_S_AT)	emb CAA60521.1  (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14763_at (X86958.1_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAC49282.1  (U40856) AIG1 [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAB64049.1  (AC002333) putative endochitinase [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAC34217.1  (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAB82640.1  (AC002387) putative pectinesterase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	
Duplicates 12879 and 17544 (AIG1)	
14201 and 14202 (Novartis 73)	
14638 (peroxidase) has a duplicate in set 7 (15970).	
Counted in set 7.	

The first set (set 2 above) do not require *EDM1* and are not affected by *rps2*, *pad4* or *NahG*. These genes are less likely to be important for resistance mediated by *RPP7* and *RPP8* than the genes in the second set (set 3 above). The

5 genes in the second set require *EDM1* but are not affected by *rps2*, *pad4* or *NahG*. These genes are more likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the third set (set 4 above) are affected by *rps2*, do not require *EDM1*, and are not affected by *pad4* or *NahG*. The genes in the

fourth (set 5 above), seventh (set 8 above) and eight (set 9 above) sets include

10 genes that are affected by *pad4* or *NahG*, and so are less likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the sixth set (set 7 above) require *RPP7* or *RPP8* for increased expression after infection by

*Peronospora* and are affected by *rps2*. These genes are also less likely to be important for resistance mediated by *RPP7* and *RPP8*.

Duplicates were identified by sorting "RPP7 or 8" by description, which put duplicated genes adjacent to one another. Most duplicates were in the same set, but there were nine cases of duplicates that had one probe set in one set, and another in another set. Examination of the data revealed that in these cases, the expression values were close to the cut-offs used to define the various sets. If one copy met the criteria, e.g., for *rps2*-dependent, but the other copy did not, the gene was classified as not *rps2*-dependent. Duplicates are noted. One hundred eighty four unique genes remained (SEQ ID NOs:1-211 and 792, Table 9 and Table 10).

Table 9

SEQ ID NO	ProbeSet	Description
1	12007_at (Z99708.249_AT)	emb CAB16829.1  (Z99708) putative protein [Arabidopsis thaliana]
2	12091_at (AC004450.116_AT)	gb AAC64313.1  (AC004450) unknown protein [Arabidopsis thaliana]
3	12115_at (AL033545.26_AT)	emb CAA22152.1  (AL033545) extensin-like protein [Arabidopsis thaliana]
4	12240_at (AL078579.130_AT)	emb CAB43974.1  (AL078579) putative protein [Arabidopsis thaliana]
5	12278_at (AJ011674.2_AT)	emb CAA09731.1  (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
6	12307_at (AC002392.162_AT)	gb AAD12037.1  (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
7	12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1  (AB023448) basic endochitinase [Arabidopsis thaliana]
8	12341_s_at (AL021637.176_S_AT)	emb CAA16619.1  (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
9	12349_s_at (X84728.6_S_AT)	gb AAA17993.1  (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
10	12360_at (AL022347.131_AT)	emb CAA18468.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
11	20223_at (AL022347.145_AT)	emb CAA18468.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

- 12 12500\_s\_at (AF081067.3\_S\_AT) gb|AAC32192.1| (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
- 13 12521\_at (AF049236.28\_AT) gb|AAC14413.1| (AF049236) unknown [Arabidopsis thaliana]
- 14 12538\_at (AF033205.2\_AT) gb|AAC02973.1| (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
- 15 12556\_at (AL079344.155\_AT) emb|CAB45330.1| (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
- 16 12574\_at (X82624.2\_AT) emb|CAA57944.1| (X82624) SRG2At [Arabidopsis thaliana]
- 17 12630\_at (AF024504.13\_AT) gb|AAF18681.1|AF024504\_11 (AF024504) unknown protein [Arabidopsis thaliana]
- 18 12642\_at (AC006920.138\_AT) gb|AAD22285.1|AC006920\_9 (AC006920) unknown protein [Arabidopsis thaliana]
- 19 12777\_i\_at (AC006577.16\_I\_AT) gb|AAD25772.1|AC006577\_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 20 12778\_r\_at (AC006577.16\_R\_AT) gb|AAD25772.1|AC006577\_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 21 12779\_f\_at (AC006577.16\_F\_AT) gb|AAD25772.1|AC006577\_8 (AC006577) Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb|T44453, gb|T04815, gb|T45993, gb|R30138, gb|AI099570 and gb|T22281 come from this gene. [Arabidopsis thaliana]
- 22 12879\_s\_at (AIG1\_S\_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]
- 23 17744\_s\_at (AC004684.168\_S\_AT) gb|AAC23646.1| (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 24 12889\_s\_at (ASA1\_S\_AT) gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
- 25 20291\_s\_at (M92353.4\_S\_AT) gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]

26	12891_at (ATACS6_AT)	gb AAC63850.1  (U73786) ACC synthase [Arabidopsis thaliana]
27	12892_g_at (ATACS6_G_AT)	gb AAC63850.1  (U73786) ACC synthase [Arabidopsis thaliana]
28	12905_s_at (ATERF2_S_AT)	dbj BAA32419.1  (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
29	16609_s_at (AB008104_S_AT)	dbj BAA32419.1  (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
30	12908_s_at (ATERF5_S_AT)	dbj BAA32422.1  (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
31	16536_s_at (AB008107_S_AT)	dbj BAA32422.1  (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
32	12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1  (AF021244) coronatine- induced protein 1 [Arabidopsis thaliana]
33	12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1  (X96600) pathogenesis- related protein 1 [Arabidopsis thaliana]
34	12989_s_at (AC004077.149_S_A T)	gb AAC26690.1  (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
35	13067_s_at (AC003114.16_S_AT)	gb AAC24083.1  (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
36	13100_at (AC003680.50_AT)	gb AAC06158.1  (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
37	13115_at (AC000375.44_AT)	gb AAB60774.1  (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
38	13154_s_at (AC002333.210_S_A T)	gb AAB64047.1  (AC002333) putative endochitinase [Arabidopsis thaliana]
39	13176_at (AL031394.56_AT)	emb CAA20567.1  (AL031394) putative protein [Arabidopsis thaliana]
40	13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
41	13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
42	13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
43	16981_s_at (U35829.2_S_AT)	gb AAC49356.1  (U35829) thioredoxin h [Arabidopsis thaliana]
44	13198_i_at (ATTTS0190_I_AT)	emb CAA16892.1  (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]



45	13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT) T)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
46	16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
47	13217_s_at (CALMODULINLIK E_S_AT)	emb CAB42906.1  (AL049862) calmodulin- like protein [Arabidopsis thaliana]
48	17500_s_at (ATHCALLGA_S_A T)	emb CAB42906.1  (AL049862) calmodulin- like protein [Arabidopsis thaliana]
49	13273_s_at (HSF4_S_AT)	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
50	16105_s_at (ATU68017_S_AT)	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
51	13277_i_at (HSP176A_I_AT)	emb CAA74399.1  (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
52	13285_s_at (HSP83_S_AT)	gb AAA32822.1  (M62984) heat shock protein 83 [Arabidopsis thaliana]
53	16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1  (M62984) heat shock protein 83 [Arabidopsis thaliana]
54	13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
55	13435_at (AF003102.3_AT)	gb AAC49775.1  (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
56	13588_at (AL021961.24_AT)	emb CAA17552.1  (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
57	13627_at (AL035394.196_AT)	emb CAA23036.1  (AL035394) putative Na <sup>+</sup> /H <sup>+</sup> -exchanging protein [Arabidopsis thaliana]
58	13631_at (AC002387.185_AT)	gb AAB82634.1  (AC002387) putative transketolase precursor [Arabidopsis thaliana]
59	13659_at (AL022347.46_AT)	emb CAA18462.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
	13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]

	20365_s_at	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
60	(AC005850.19_S_AT)	
61	13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
no cds	13697_at (NI16_AT)	No hits found.
	13751_at	gb AAF16751.1 AC010155_4 (AC010155)
62	(NOVARTIS127_AT)	F3M18.8 [Arabidopsis thaliana]
	13764_at	gb AAD39641.1 AC007591_6 (AC007591)
63	(NOVARTIS22_AT)	F9L1.6 [Arabidopsis thaliana]
	13818_s_at	gb AAD15433.1  (AC006218) putative.
	(AC006218.175_S_A	aspartate aminotransferase [Arabidopsis
64	T)	thaliana]
	13880_s_at	emb CAB39611.1  (AL049480) possible
	(AL049480.183_S_A	apospory-associated like protein
65	T)	[Arabidopsis thaliana]
	13966_at	emb CAA17775.1  (AL022023) putative
66	(AL022023.172_AT)	protein [Arabidopsis thaliana]
		gb AAC78535.1  (AC005662) putative
	14083_at	embryo-abundant protein [Arabidopsis
67	(AC005662.56_AT)	thaliana]
	14096_at	
68	(AC002291.12_AT)	No hits found.
	14110_i_at	emb CAB36854.1  (AL035528) putative
	(AL035528.279_I_AT	disease resistance protein [Arabidopsis
69	)	thaliana]
	14111_s_at	emb CAB36854.1  (AL035528) putative
	(AL035528.279_S_A	disease resistance protein [Arabidopsis
70	T)	thaliana]
		gb AAC26243.1  (AF077407) contains
	14116_at	similarity to sugar transporters (Pfam:
71	(AF077407.30_AT)	sugar_tr.hmm, score: 395.39) [Arabidopsis
	14141_at	thaliana]
72	(NOVARTIS31_AT)	No hits found less than or equal to 1e-15.
		dbj BAA22813.1  (D26015) CND41,
	14145_at	chloroplast nucleoid DNA binding protein
73	(NOVARTIS35_AT)	[Nicotiana tabacum]
	14146_at	gb AAD25550.1 AC005850_7 (AC005850)
74	(NOVARTIS36_AT)	Hypothetical protein [Arabidopsis thaliana]
	14148_at	gb AAF34713.1 AF224762_1 (AF224762)
75	(NOVARTIS38_AT)	SigA binding protein [Arabidopsis thaliana]
	14201_at	
76	(NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
	14202_at	
	(NOVARTIS73_RC_	
77	AT)	No hits found less than or equal to 1e-15.
	14223_at	emb CAA19683.1  (AL024486) putative
78	(NOVARTIS9_AT)	protein [Arabidopsis thaliana]

79	14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
80	14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
81	14249_i_at (PAD4_I_AT)	emb CAB43438.1  (AL050300) putative protein [Arabidopsis thaliana]
82	14250_r_at (PAD4_R_AT)	emb CAB43438.1  (AL050300) putative protein [Arabidopsis thaliana]
83	14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2  (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
84	14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2  (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
85	14278_at (AL022373.295_AT)	emb CAA18503.1  (AL022373) hypothetical protein [Arabidopsis thaliana]
86	14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
87	14381_at (AC002521.68_AT)	gb AAC05341.1  (AC002521) unknown protein [Arabidopsis thaliana]
88	14443_at (AC000348.23_AT)	gb AAB61498.1  (AC000348) T7N9.22 [Arabidopsis thaliana]
89	14609_at (AC002340.147_AT)	gb AAC02748.1  (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
90	14614_at (AC004165.66_AT)	gb AAC16958.1  (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
91	14620_s_at (PAT1_S_AT)	gb AAA32835.1  (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
92	14838_s_at (M96073.6_S_AT)	gb AAA32835.1  (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
93	14621_at (PDF1.2_AT)	gb AAC31244.1  (AC004747) putative antifungal protein [Arabidopsis thaliana]
94	14635_s_at (PR.1_S_AT)	gb AAC69381.1  (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
95	17128_s_at (ATHRPRP1A_S_AT )	gb AAC69381.1  (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
96	14638_s_at (PRXCB_S_AT)	emb CAA50677.1  (X71794) peroxidase [Arabidopsis thaliana]

97	15970_s_at (X71794.2_S_AT)	emb CAA50677.1  (X71794) peroxidase [Arabidopsis thaliana]
98	14672_s_at (TSA1_S_AT)	gb AAC49117.1  (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
99	17487_s_at (U18993.2_S_AT)	gb AAC49117.1  (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
100	14673_s_at (TSB2_S_AT)	gb AAA32879.1  (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana] thaliana]
101	14682_i_at (WT1012A_RC_I_AT )	No hits found.
102	14691_at (WT1096_AT)	No hits found.
103	14704_s_at (WT768_RC_S_AT)	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
104	15846_at (AC006067.63_AT)	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
105	15847_g_at (AC006067.63_G_AT )	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
106	14709_at (WT788_AT)	No hits found less than or equal to 1e-15. emb CAA60521.1  (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
107	14763_at (X86958.1_AT)	
108	14882_at (AL022605.63_AT)	emb CAA18753.1  (AL022605) putative protein [Arabidopsis thaliana]
109	15042_at (AL021961.3_AT)	emb CAA17549.1  (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
110	15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
111	15161_s_at (ATU90522_S_AT)	gb AAB53975.1  (U90522) lysine- ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
112	15366_at (U93215.38_AT)	gb AAB63077.1  (U93215) unknown protein [Arabidopsis thaliana]
113	15415_at (AF000657.28_AT)	gb AAB72169.1  (AF000657) hypothetical protein [Arabidopsis thaliana]
114	15431_at (AL030978.64_AT)	emb CAA19722.1  (AL030978) putative protein [Arabidopsis thaliana]
115	15523_s_at (AL078637.213_S_A T)	emb CAB45071.1  (AL078637) putative protein [Arabidopsis thaliana]
116	15532_r_at (AL078637.191 R A	emb CAB45069.1  (AL078637) putative protein [Arabidopsis thaliana]

T)

- 117 15616\_s\_at  
(ATHPRO25A\_S\_AT) emb|CAA08794.1| (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]  
) dbj|BAA24440.1| (AB010407)
- 118 15629\_s\_at  
(AB003280\_S\_AT) phosphoglycerate dehydrogenase [Arabidopsis thaliana]  
gb|AAD10829.1| (AF117063) putative
- 119 15641\_s\_at  
(AF117063\_S\_AT) inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]  
gb|AAB80922.1| (AF022658) putative c2h2
- 120; 682 15665\_s\_at  
(AF022658\_S\_AT) zinc finger transcription factor [Arabidopsis thaliana]
- 121 15778\_at  
(X98676.2\_AT) emb|CAA67234.1| (X98676) zinc finger protein [Arabidopsis thaliana]
- 122 15779\_g\_at  
(X98676.2\_G\_AT) emb|CAA67234.1| (X98676) zinc finger protein [Arabidopsis thaliana]
- 123 15859\_at  
(AC006587.164\_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
- 124 15978\_at  
(X68592.6\_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
- 125 16053\_i\_at  
(Y14251.4\_I\_AT) emb|CAA74639.1| (Y14251) glutathione S-transferase [Arabidopsis thaliana]
- 126 16061\_s\_at  
(AB004796\_S\_AT) gb|AAB97145.1| (AF000977) MEK1 [Arabidopsis thaliana] thaliana  
gb|AAD34615.1|AF153283\_1 (AF153283)
- 127 16083\_s\_at  
(AF153283\_S\_AT) putative progesterone-binding protein homolog [Arabidopsis thaliana]
- 128 16150\_s\_at  
(ATHPEAR\_S\_AT) emb|CAB41718.1| (AL049730) pEARLI 1 [Arabidopsis thaliana]
- 129 16232\_s\_at  
(AL080252.77\_S\_AT) emb|CAB45796.1| (AL080252) putative protein [Arabidopsis thaliana]  
gb|AAC32915.1| (AC004138) putative
- 130 16257\_at  
(AC004138.105\_AT) nucleoside triphosphatase [Arabidopsis thaliana]
- 131 16298\_at  
(AL021890.71\_AT) emb|CAA17152.1| (AL021890) putative protein [Arabidopsis thaliana]
- 132 16299\_at  
(AL024486.185\_AT) emb|CAA19705.1| (AL024486) putative protein [Arabidopsis thaliana]  
gb|AAD40144.1|AF149413\_25 (AF149413)  
contains similarity to protein kinase domains.  
(Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)
- 133 16357\_at  
(AF149413.38\_AT) [Arabidopsis thaliana]  
emb|CAA20203.1| (AL031187) receptor-like
- 134 16360\_at  
(AL031187.126\_AT) serine/threonine protein kinase ARK3 [Arabidopsis thaliana]



- 135 16365\_at (AC003974.136\_AT) gb|AAC04495.1| (AC003974) putative disease resistance protein [Arabidopsis thaliana]
- 136 16578\_s\_at (ATHRPRP1B\_S\_AT) emb|CAB68132.1| (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
- 137 16817\_s\_at (AL096882.91\_S\_AT) emb|CAB51412.1| (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
- 138 16914\_s\_at (AL049500.57\_S\_AT) emb|CAB39936.1| (AL049500) osmotin precursor [Arabidopsis thaliana]
- 139 16995\_at (AC002391.188\_AT) gb|AAB87114.1| (AC002391) unknown protein [Arabidopsis thaliana]
- 140 17008\_at (AC006585.212\_AT) gb|AAD23027.1|AC006585\_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
- 141 17014\_s\_at (ATU05206\_S\_AT) gb|AAC48925.1| (U05206) ribonuclease [Arabidopsis thaliana]
- 142 17051\_s\_at (AF098947\_S\_AT) gb|AAD09952.1| (AF098947) CTF2B [Arabidopsis thaliana]
- 143 17068\_s\_at (ATHRLPKA\_S\_AT) gb|AAA32857.1| (M84658) receptor-like protein kinase [Arabidopsis thaliana]
- 144 17083\_s\_at (ATU18770\_S\_AT) gb|AAD25838.1|AC006951\_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
- 145 17097\_s\_at (ATU66345\_S\_AT) gb|AAC49697.1| (U66345) calreticulin [Arabidopsis thaliana]
- 146 17278\_at (AC000107.5\_AT) gb|AAD36959.1|AC000107\_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
- 147 17413\_s\_at (AJ006961.4\_S\_AT) emb|CAA67551.1| (X99097) peroxidase [Arabidopsis thaliana]
- 148 17464\_at (AC000132.72\_AT) gb|AAB60752.1| (AC000132) Similar to A. thaliana receptor-like protein kinase (gb|RLK5\_ARATH). ESTs gb|ATTS0475,gb|ATTS4362 come from this gene. [Arabidopsis thaliana]
- 149 17485\_s\_at (Z97340.345\_S\_AT) emb|CAB10405.1| (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]
- 150 17499\_s\_at (AF107726\_S\_AT) gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
- 151 17511\_s\_at (AF067605\_S\_AT) gb|AAB71482.1| (AC002294) similar to S-linalool synthase gp|U58314|1491939 [Arabidopsis thaliana]
- 152 17522\_s\_at (D78606\_S\_AT) dbj|BAA28538.1| (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
- 153 17544\_s\_at (ATU40856\_S\_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]

- 154 17653\_at (AL035679.144\_AT) emb|CAB38823.1| (AL035679) putative protein [Arabidopsis thaliana]  
gb|AAC28500.1| (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. [Arabidopsis thaliana]
- 155 17775\_at (AC004392.2\_AT)
- 156 17840\_s\_at (AC002333.223\_S\_A T) gb|AAB64049.1| (AC002333) putative endochitinase [Arabidopsis thaliana]
- 157 17843\_s\_at (AC002391.150\_S\_A T) gb|AAB87109.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 158 17899\_at (Z97339.197\_AT) emb|CAB10339.1| (Z97339) hypothetical protein [Arabidopsis thaliana]
- 159 17930\_s\_at (AJ006960.4\_S\_AT) emb|CAA07352.1| (AJ006960) peroxidase [Arabidopsis thaliana]
- 160 18012\_s\_at (AJ002295\_S\_AT) emb|CAB59428.1| (AJ002295)-inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
- 161 18022\_at (AJ010971\_AT) emb|CAB52675.1| (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
- 162 18054\_at (AJ238846\_AT) emb|CAB54517.1| (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
- 163 18216\_at (X95573.2\_AT) gb|AAF24959.1|AC012375\_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 164 18217\_g\_at (X95573.2\_G\_AT) gb|AAF24959.1|AC012375\_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 165 18551\_at (AC002391.163\_AT) gb|AAB87112.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 166 18567\_at (AC004411.25\_AT) gb|AAC34217.1| (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 167 18590\_at (AJ222713.4\_AT) emb|CAA10955.1| (AJ222713) unnamed protein product [Arabidopsis thaliana]
- 168; 665 18591\_at (X74756.2\_AT) emb|CAA52772.1| (X74756) ATAF2 [Arabidopsis thaliana]
- 169 18625\_at (AC005278.22\_AT) gb|AAC72125.1| (AC005278) ESTs gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene. [Arabidopsis thaliana]
- 170 18716\_at (X91916\_AT) gb|AAF26754.1|AC007396\_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
- 171 18844\_at (AC005315.131\_AT) gb|AAC33239.1| (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
- 172 18908\_i\_at (AF055848.2\_I\_AT) gb|AAC62611.1| (AF055848) subtilisin-like protease [Arabidopsis thaliana]

173	18909_s_at (AF055848.2_S_AT)	gb AAC62611.1  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
174	18946_at (Y11788.1_AT)	emb CAA72484.1  (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
175	18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
176	18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
177	18983_s_at (AL049730.104_S_A T)	emb CAB41722.1  (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
178	19158_at (X95738.2_AT)	emb CAA65053.1  (X95738) proline transporter 2 [Arabidopsis thaliana]
179	19171_at (AC002335.160_AT)	gb AAB64325.1  (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
180	19177_at (X99923.1_AT)	emb CAA68191.1  (X99923) male sterility 2-like protein [Arabidopsis thaliana]
181	19182_at (AL031804.245_AT)	emb CAA21214.1  (AL031804) putative protein [Arabidopsis thaliana]
182	19229_at (AC003027.39_AT)	gb AAD10694.1  (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
183	19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
184	19284_at (AC003028.196_AT)	gb AAC27173.1  (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
185	19415_at (AL080253.32_AT)	emb CAB45805.1  (AL080253) putative protein [Arabidopsis thaliana]
186	19594_i_at (X98321.2_I_AT)	emb CAA66965.1  (X98321) peroxidase [Arabidopsis thaliana]
187	19640_at (AC004561.78_AT)	gb AAC95192.1  (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
188	19664_at (AL050351.172_AT)	emb CAB43638.1  (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
189	19672_at (AC005687.19_AT)	gb AAC36019.1  (AC005687) RAP2.6 [Arabidopsis thaliana]
190	19762_at (AL035527.204_AT)	emb CAB36812.1  (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
191	19892_at (AC005770.30_AT)	gb AAC79626.1  (AC005770) putative protease inhibitor [Arabidopsis thaliana]
192	19894_at (AJ001809.1_AT)	emb CAA05025.1  (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

193	19914_at (AC005727.175_AT)	gb AAC79593.1  (AC005727) unknown protein [Arabidopsis thaliana]
194	19951_at (AC005395.47_AT)	gb AAC42241.1  (AC005395) unknown protein [Arabidopsis thaliana]
195	19991_at (AC007017.124_AT)	gb AAD21459.1  (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
196	20189_at (AC005489.2_AT)	gb AAD32864.1  AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
197	20232_s_at (AL022347.12_S_AT)	emb CAA18469.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
198	20238_at (X74514.2_AT)	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
199	20239_g_at (X74514.2_G_AT)	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
200	20245_s_at (AC005309.97_S_AT)	emb CAA05625.1  (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
201	20246_s_at (AF084037.3_S_AT)	gb AAC95354.1  (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
202	20269_at (AC002387.237_AT)	gb AAB82640.1  (AC002387) putative pectinesterase [Arabidopsis thaliana]
203	20287_at (Y14590.5_AT)	emb CAA74930.1  (Y14590) class IV chitinase [Arabidopsis thaliana]
204	20288_g_at (Y14590.5_G_AT)	emb CAA74930.1  (Y14590) class IV chitinase [Arabidopsis thaliana]
205	20331_at (AC007168.86_AT)	gb AAD23617.1  AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
206	20368_at (AC005314.38_AT)	gb AAC36163.1  (AC005314) putative serpin [Arabidopsis thaliana]
207	20420_at (AL024486.131_AT)	emb CAA19698.1  (AL024486) putative chitinase [Arabidopsis thaliana]
208	20429_s_at (Z97336.167_S_AT)	emb CAB10219.1  (Z97336) hypothetical protei [Arabidopsis thaliana]
209	20620_g_at (AC005896.161_G_A T)	gb AAC98070.1  (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
210	20625_at (AL049658.102_AT)	emb CAB41131.1  (AL049658) hypothetical protein [Arabidopsis thaliana]
211	20641_at (X91919.1_AT)	emb CAA63012.1  (X91919) LEA76 homologue type1 [Arabidopsis thaliana]
789	18224_s_at (AL021890.57_S_AT)	Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.
790	16522_at (X77500.2_AT)	emb CAA17152.1  (AL021890) putative protein [Arabidopsis thaliana]
		emb CAA54631.1  (X77500) amino acid transporter [Arabidopsis thaliana]

		gb AAC17040.1  (AC002986) Similarity to
		A. thaliana gene product F21M12.20,
		gb AC000132. EST gb Z25651 comes from
		this gene. [Arabidopsis thaliana]
791	19982_at (AC002986.28_AT)	gb AAC16927.1  (AC002338) putative
367	18920_at (AC002338.11_AT)	laccase [Arabidopsis thaliana]
212	12324_i_at	AC007212
793	12345_at	L36246
213	12500_s_at	AF081067
214; 662	12505_s_at	AC005309
215	12608_i_at	S70188
216	12642_at	AC006920
217	12746_i_at	AL096882
218	12748_f_at	AL096882
219	12761_s_at	AC006577
220	12773_at	AC005727
221	12778_r_at	AC006577
222	12798_at	AC003028
223	12802_at	AL022373
	12842_s_at	No hits found less than or equal to 1e-15
224	12843_s_at	AC007195
	12845_s_at	AJ004810
225	12879_s_at	U40856
226	12891_at	U73786
227	12892_g_at	U73786
228; 658	12904_s_at	AB008103
229	12905_s_at	AB008104
230	12908_s_at	AB008107
231	12909_s_at	Z97343
232	12911_s_at	X84229
233	12916_s_at	AF021244
234	13138_at	AL096882
235	13177_at	AL049640
236	13178_at	U93215
237	13187_i_at	U35829
238	13189_s_at	U35829
239	13198_i_at	AL021749
240	13212_s_at	AL137080
241	13217_s_at	AL049862
242	13258_s_at	AC005309
243	13273_s_at	U68017
244	13284_s_at	AJ002551
245	13604_at	AC000104
246	13615_at	AC002332
247	13617_at	AC006592
248	13718_at	Z72152
249	13771_at	AC006593
250	13785_at	AC007087
251	14052_at	AC004122



252	14096_at	AC002291
253	14097_at	AC005309
254	14116_at	AF077407
255	14141_at	AC011437
256; 683	14148_at	AF224762
257	14196_at	AC012563
258	14201_at	AL163972
259	14219_at	AC068667
260	14223_at	AL024486
261	14248_at	AC007357
262	14250_r_at	AL050300
263	14595_at	AL022580
264	14608_at	AC007357
265	14614_at	AC004165
266	14621_at	AC004747
267	14627_i_at	X76609
268	14628_r_at	X76609
269	14635_s_at	AC005398
270	14636_s_at	AC013258
271	14643_s_at	AC006836
272	14672_s_at	U18993
273	14675_s_at	D85191
274	14691_at	AP002046
275	14704_s_at	AC006067
276	14706_r_at	AL137189
277	14709_at	AP002046
278	14711_s_at	AF085279
279	14731_s_at	AF014960
280	14784_at	AC005310
281	14951_at	AL049481
282	15057_at	AL035440
283	15085_s_at	AL031018
284	15105_s_at	Z14987
285	15116_f_at	AF121356
286	15125_f_at	D85190
287	15141_s_at	D85191
288	15145_s_at	D64155
289	15154_s_at	AL096860
290	15161_s_at	U90522
291	15178_s_at	U43489
292	15216_s_at	U75198
293	15431_at	AL030978
294	15496_at	AC006282
295	15523_s_at	AL078637
296	15593_s_at	U54561
297	15611_s_at	L22567
298	15616_s_at	AJ009696
299	15622_s_at	U43945

300	15629_s_at	AB010407
301	15665_s_at	AF022658
302	15680_s_at	D42061
303	15846_at	AC006067
304	15847_g_at	AC006067
305	15866_s_at	AC005770
306	15950_at	AC006429
307	15954_at	U72155
308	15978_at	X68592
309	16038_s_at	L04173
310	16063_s_at	AB008103
311	16105_s_at	U68017
312	16150_s_at	AL049730
313	16153_s_at	AC013258
314	16393_s_at	AC006436
315	16412_s_at	AL022603
316	16442_s_at	AJ002551
317	16504_s_at	Z97335
318	16510_at	AL034567
319	16536_s_at	AB008107
320	16539_s_at	Z97343
321	16569_s_at	L23968
322	16578_s_at	AL137080
323	16609_s_at	AB008104
324	16620_s_at	AF051338
325	16637_s_at	Z97336
326	16817_s_at	AL096882
327	16864_i_at	AL133248
328	16951_i_at	AC005662
329	16952_s_at	AC005662
330	16981_s_at	U35829
331	17014_s_at	U05206
332	17033_s_at	U83179
333	17054_s_at	AF134128
334	17073_s_at	AC006836
335	17119_s_at	AF132212
336	17123_s_at	AF106087
337	17128_s_at	AC005398
338	17187_at	AF128396
339; 669	17303_s_at	AC005499
340; 663	17379_at	AC018721
341	17386_at	AC006264
342	17413_s_at	X99097
343	17499_s_at	AF107726
344	17500_s_at	AL049862
345	17544_s_at	U40856
346	17567_at	AL162751
347	17886_at	AC004484

348	17899_at	Z97339
349	17917_s_at	AC004261
350	17961_at	AC007323
351	17963_at	AL049730
352	18003_at	AF188334
	18064_r_at	No hits found
	18069_at	No hits found
	18070_r_at	No hits found
353	18216_at	AC012375
354	18217_g_at	AC012375
355	18235_at	AC000348
356	18252_at	AL096882
357	18255_at	AC005770
358	18272_at	AF002109
359	18533_at	AL021684
360	18556_at	AC006264
361	18590_at	AJ222713
362	18591_at	X74756
363	18607_s_at	U78721
364	18635_at	AC004005
365	18716_at	AC007396
366	18876_at	AF002109
367	18920_at	AC002338
368	18928_at	AC002338
369	19034_at	AL021768
370	19171_at	AC002335
371	19178_at	AB035137
372	19182_at	AL031804
373	19251_at	AL035538
374	19640_at	AC004561
375	19977_at	AL049659
376	20017_at	AC004521
377	20034_i_at	A71607
378	20201_at	AL078470
379	20227_s_at	AB027252
380	20269_at	AC002387
381	20297_at	AC007153
382	20314_s_at	AL096882
383	20335_s_at	Y14208
384	20429_s_at	Z97336
385	20585_s_at	AC005309
386	20641_at	X91919
387	12333_at	AJ286345
388	14028_at	
389	14295_s_at	Z54356
390	14965_at	AC002329
391	15969_s_a	AJ133036
392	15982_s_a	X98190

393	16461_I_at	AC004683
394	16462_s_a	AC004683
395	16514_at	AL035538
396	17549_s_a	L37126
397	18706_s_a	X75782
398	19594_i_at	X98321
399	20555_s_a	AL080318
400	16212_at	gb AAD17366.1  (AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]
794	14985_s_at	gb AAC32233.2  (AC005168) unknown protein [Arabidopsis thaliana]
401	16411_s_at	emb CAB71046.1  (AL137898) shaggy-like kinase beta [Arabidopsis thaliana]
402	15920_i_at	gb AAD39561.1 AC007067_1 (AC007067) T10O24.1 [Arabidopsis thaliana]
403	16299_at	emb CAA19705.1  (AL024486) putative protein [Arabidopsis thaliana]
404	18445_at	gb AAC98458.1  (AC005851) putative glucosyltransferase [Arabidopsis thaliana]
405	19215_at	gb AAC23400.1  (AC004005) putative methyl chloride transferase [Arabidopsis thaliana]
406	16439_at	emb CAA50905.1  (X72022) ORF1 [Arabidopsis thaliana]
407	16047_at	gb AAD20710.1  (AC006300) unknown protein [Arabidopsis thaliana]
408	18003_at	gb AAF01328.1 AF188334_1 (AF188334) Toll/interleukin-1 receptor-like protein [Arabidopsis thaliana]
409	20429_s_at	emb CAB10219.1  (Z97336) hypothetical protei [Arabidopsis thaliana]
410	17917_s_at	gb AAD12002.1  (AC004261) calcium binding protein (CaBP-22) [Arabidopsis thaliana]
411	17963_at	emb CAB41717.1  (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
412	16150_s_at	emb CAB41718.1  (AL049730) pEARLI 1 [Arabidopsis thaliana]
413	20239_g_at	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
414	20238_at	emb CAA52619.1  (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
415	15616_s_at	emb CAA08794.1  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
416	18591_at	emb CAA52772.1  (X74756) ATAF2 [Arabidopsis thaliana]

417	14116_at	gb AAC26243.1  (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
418	12759_at	gb AAC72120.1  (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb AI100071 come from this gene. [Arabidopsis thaliana]
419	19060_at	gb AAC18809.1  (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
420	12998_at	emb CAB41863.1  (AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]
421	13172_s_at	gb AAD30608.1 AC007369_18 (AC007369) Sugar transporter [Arabidopsis thaliana]
422	14709_at	No hits found less than or equal to 1e-15.
423	15931_at	gb AAD41420.1 AC007727_9 (AC007727) F8K7.9 [Arabidopsis thaliana]
424	20369_s_at	emb CAB41109.1  (AL049656) ammonium transport protein (AMT1) [Arabidopsis thaliana]
425	14201_at	No hits found less than or equal to 1e-15.
426	14691_at	No hits found.
75	14148_at	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
426	16140_s_at	emb CAB42872.1  (AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]
427	13625_s_at	emb CAB42924.1  (AL049862) putative disease resistance protein [Arabidopsis thaliana]
428	13702_s_at	emb CAA19683.1  (AL024486) putative protein [Arabidopsis thaliana]
429	17886_at	gb AAC14530.1  (AC004484) unknown protein [Arabidopsis thaliana]
430	12354_g_at	gb AAC23641.1  (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
431	12353_at	gb AAC23641.1  (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
432	17899_at	emb CAB10339.1  (Z97339) hypothetical protein [Arabidopsis thaliana]



433	18894_at	emb CAB43665.1  (AL050352) Ca <sup>2+</sup> -transporting ATPase-like protein [Arabidopsis thaliana]
434	14978_at	gb AAB64024.1  (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
435	14223_at	emb CAA19683.1  (AL024486) putative protein [Arabidopsis thaliana]
436	16109_s_at	gb AAC05342.1  (AC002521) putative protein kinase [Arabidopsis thaliana]
437	18820_at	gb AAD28055.1 AC007166_3 (AC007166) putative protein kinase [Arabidopsis thaliana]
438	20345_at	gb AAC72865.1  (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]
439	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
440	15143_s_at	gb AAD38519.1 AF138281_1 (AF138281) phospholipase D-gamma-2 [Arabidopsis thaliana]
441	17499_s_at	gb AAD19610.1  (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
442	20590_at	emb CAB37511.1  (AL035540) Phospholipase like protein [Arabidopsis thaliana]
443	14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
444	13550_at	emb CAA18465.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
445	13355_at	emb CAA71371.1  (Y10342) putative amidase [Arabidopsis thaliana]
446	13564_at	gb AAC78521.1  (AC005312) putative glutathione S-transferase [Arabidopsis thaliana]
447	19845_g_at	emb CAB37510.1  (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
448	12764_f_at	gb AAC32912.1  (AC004138) putative glutathione S-transferase [Arabidopsis thaliana]
449	17922_at	gb AAB16855.1  (U71122) pyruvate decarboxylase [Arabidopsis thaliana]

450	15982_s_at	emb CAA66863.1  (X98190) peroxidase ATP2a [Arabidopsis thaliana]
451	12227_at	gb AAD39285.1 AC007576_8 (AC007576) Unknown protein [Arabidopsis thaliana]
452	20555_s_at	emb CAB45975.1  (AL080318) copper amine oxidase like protein (fragment2) [Arabidopsis thaliana]
453	19844_at	emb CAB37510.1  (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
454	13985_s_at	gb AAC31242.1  (AC004747) unknown protein [Arabidopsis thaliana]
455	13548_at	gb AAD41421.1 AC007727_10 (AC007727) ESTs gb N96028, gb F14286, gb T20680, gb F14443, gb AA657300 and gb N65244 come from this gene. [Arabidopsis thaliana]
456	15611_s_at	gb AAA32775.1  (L22567) cor78 [Arabidopsis thaliana]
457	19840_s_at	gb AAD25759.1 AC007060_17 (AC007060) Strong similarity to F19I3.2 gi 3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb AC004238. EST gb R90518 comes from this gene.
458	15985_at	emb CAA67340.1  (X98808) peroxidase ATP3a [Arabidopsis thaliana]
459	14584_at	gb AAD32844.1 AC007658_3 (AC007658) unknown protein [Arabidopsis thaliana]
460	15422_at	gb AAD36948.1 AF069441_8 (AF069441) hypothetical protein [Arabidopsis thaliana]
461	20150_at	gb AAB61076.1  (AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]
462	18844_at	gb AAC33239.1  (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
463	16360_at	emb CAA20203.1  (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
464	20292_at	gb AAB87113.1  (AC002391) putative protein kinase [Arabidopsis thaliana]
465	14554_at	gb AAC18798.1  (AC003671) F17O7.4 [Arabidopsis thaliana]
466	18604_at	gb AAC19273.1  (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]

467	16061_s_at	gb AAB97145.1  (AF000977) MEK1 [Arabidopsis thaliana]
468	14145_at	dbj BAA22813.1  (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
469	16144_s_at	dbj BAA04870.1  (D21843) MAP kinase [Arabidopsis thaliana]
470	17097_s_at	gb AAC49697.1  (U66345) calreticulin [Arabidopsis thaliana]
471	19718_at	gb AAB71447.1  (AC000098) Similar to Arabidopsis Fe(II) transport protein (gb U27590). [Arabidopsis thaliana]
472	14298_g_at	gb AAC25507.1  (AC003979) T22J18.6 [Arabidopsis thaliana]
473	12307_at	gb AAD12037.1  (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
474	20232_s_at	emb CAA18460.1  (AL022347) protein kinase-like protein [Arabidopsis thaliana]
475	19322_at	gb AAF19738.1 AC012463_12 (AC012463) T2E6.14 [Arabidopsis thaliana]
476	14224_at	gb AAF07386.1 AC010675_9 (AC010675) putative peptide transporter [Arabidopsis thaliana]
477	14270_at	gb AAD39269.1 AC007203_1 (AC007203) Putative UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]
478	15479_at	emb CAB39671.1  (AL049483) putative protein [Arabidopsis thaliana]
479	14090_i_at	gb AAD41981.1 AC006438_13 (AC006438) unknown protein [Arabidopsis thaliana]
480	16162_s_at	gb AAB05099.1  (U39944) BELL1 [Arabidopsis thaliana]
481	20149_at	gb AAB70415.1  (AC000106) Similar to Beta integral membrane protein (gb U43629). [Arabidopsis thaliana]
482	12765_at	gb AAD15574.1  (AC006340) unknown protein [Arabidopsis thaliana]
214	12505_s_at	gb AAC63643.1  (AC005309) putative CONSTANS-like B-box zinc finger protein [Arabidopsis thaliana]
483	13140_at	gb AAC79588.1  (AC005727) putative RING zinc finger ankyrin protein [Arabidopsis thaliana]
484	15022_at	gb AAC72124.1  (AC005278) ESTs gb H37641 and gb AA651422 come from this gene. [Arabidopsis thaliana]

485	16306_at	emb CAB41935.1  (AL049751) putative protein [Arabidopsis thaliana] gb AAC26246.1  (AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
486	18611_at	emb CAB43428.1  (AL050300) putative protein [Arabidopsis thaliana]
487	20199_at	emb CAA18626.1  (AL022580) putative protein [Arabidopsis thaliana]
488	14595_at	gb AAD31337.1 AC007354_10 (AC007354) Strong similarity to gb Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF 01326 Pyruvate phosphate dikinase, PEP/pyruvate binding domain. EST gb N96757 comes from this gene.
489	12532_at	[Arabidopsis thaliana] emb CAB41162.1  (AL049659) putative protein [Arabidopsis thaliana]
490	19977_at	gb AAC79594.1  (AC005727) putative membrane channel protein [Arabidopsis thaliana]
491	12773_at	gb AAD32870.1 AC005489_8 (AC005489) F14N23.8 [Arabidopsis thaliana]
492	19632_at	emb CAA16957.1  (AL021811) putative protein [Arabidopsis thaliana]
493	19359_s_at	emb CAA78712.1  (Z14988) glycine rich protein [Arabidopsis thaliana] thaliana]
494	14716_f_at	gb AAC19269.1  (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
495	13648_at	gb AAD41977.1 AC006438_9 (AC006438) unknown protein [Arabidopsis thaliana]
496	12768_at	gb AAC69134.1  (U78721) putative auxin-regulated protein [Arabidopsis thaliana]
497	16422_at	gb AAC26203.1  (AF053747) dormancy-associated protein [Arabidopsis thaliana]
498	15131_s_at	emb CAB38829.1  (AL035679) drought-inducible cysteine proteinase RD19A precursor
499	14659_s_at	emb CAB38829.1  (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
500	14658_s_at	emb CAB36513.1  (AL035440) putative protein [Arabidopsis thaliana]
501	15057_at	emb CAB56039.1  (AJ133786) gigantea protein [Arabidopsis thaliana]
502	17581_g_at	gb AAC34217.1  (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
503	18567_at	

504	17047_s_at	gb AAC68674.1  (AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]
505	15105_s_at	emb CAA78711.1  (Z14987) glycine rich protein [Arabidopsis thaliana]
506	14196_at	gb AAF16557.1 AC012563_10 (AC012563) unknown protein [Arabidopsis thaliana]
507	17599_s_at	gb AAD50976.1 AF170494_1 (AF170494) ionotropic glutamate receptor ortholog GLR6 [Arabidopsis thaliana]
508	18556_at	gb AAD29803.1 AC006264_11 (AC006264) cyclophilin (CYP2) [Arabidopsis thaliana]
509	16486_at	gb AAB04606.1  (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana]
510	18272_at	gb AAB95293.1  (AF002109) unknown protein [Arabidopsis thaliana]
795	12219_at	gb AAD31373.1 AC006053_15 (AC006053) unknown protein [Arabidopsis thaliana]
511	20446_s_at	gb AAC80600.1  (AC005106) T25N20.21 [Arabidopsis thaliana]
512	12561_at	emb CAA16701.1  (AL021687) putative protein [Arabidopsis thaliana]
513	12060_at	gb AAD46000.1 AC005916_12 (AC005916) Contains similarity to gb AF113001 silencing mediator of retinoic acid and thyroid hormone receptor alpha and gb AF109179 cyclin T1 from Mus musculus. ESTs gb N95317, gb Z29139 and gb Z30853 come from this gene. [Arabidopsis thaliana]
514	18235_at	gb AAB61480.1  (AC000348) T7N9.4 [Arabidopsis thaliana]
515	14021_r_at	emb CAA04134.1  (AJ000497) Starch branching enzyme II [Arabidopsis thaliana]
516	14020_i_at	emb CAA04134.1  (AJ000497) Starch branching enzyme II [Arabidopsis thaliana] emb CAA44630.1  (X62818) Metallothionein-like protein [Arabidopsis thaliana]
517	16011_s_at	gb AAD09232.1  (U83179) unknown [Arabidopsis thaliana]
518	17033_s_at	
519	16050_at	gb AAD24630.1 AC006919_10 (AC006919) putative fructose biphosphate aldolase [Arabidopsis thaliana]



520	19692_at	gb AAC14039.1  (AC003981) F22O13.13 [Arabidopsis thaliana]
521	19181_s_at	gb AAC39464.1  (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]
792	13435_at	gb AAC49775.1  (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
522	17128_s_at	gb AAC69381.1  (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
523	14635_s_at	gb AAC69381.1  (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
524	15846_at	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
525	15847_g_at	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
526	14704_s_at	gb AAD15461.1  (AC006067) unknown protein [Arabidopsis thaliana]
527	17456_at	gb AAB80678.1  (AC002332) putative steroid dehydrogenase [Arabidopsis thaliana]
528	14895_s_at	emb CAB10562.1  (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]
529	19979_at	gb AAB95235.1  (AC002130) F1N21.7 [Arabidopsis thaliana]
530	20325_s_at	emb CAA78152.1  (Z12162) protein phosphatase 1A [Arabidopsis thaliana]
531	18234_at	gb AAB61479.1  (AC000348) T7N9.3 [Arabidopsis thaliana]
532	16474_s_at	emb CAA35838.1  (X51474) kin1 [Arabidopsis thaliana]
533	18701_s_at	emb CAA38894.1  (X55053) cold regulated [Arabidopsis thaliana]
534	13785_at	gb AAD23000.1 AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]
535	20387_at	gb AAC23422.1  (AC004005) putative methionine aminopeptidase [Arabidopsis thaliana]
536	13178_at	gb AAB63086.1  (U93215) unknown protein [Arabidopsis thaliana]
537	12103_at	gb AAD30603.1 AC007369_13 (AC007369) Unknown protein [Arabidopsis thaliana]
538	13225_s_at	emb CAA42483.1  (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

539	17003_at	gb AAB95275.1  (AF002109) putative LIM-domain protein [Arabidopsis thaliana]
540	15878_at	emb CAA19880.1  (AL031032) putative protein [Arabidopsis thaliana]
541	13004_at	gb AAD03574.1  (AC003952) putative senescence-related protein [Arabidopsis thaliana]
542	14052_at	gb AAC34333.1  (AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]
543	15798_at	gb AAC05351.1  (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]
793	12345_at	gb AAB67985.1  (L36246) anoxia-induced protein [Arabidopsis thaliana]
544	16818_s_at	emb CAA20206.1  (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
545	13916_at	gb AAC62136.1  (AC005169) unknown protein [Arabidopsis thaliana]
666	20342_at	emb CAB41311.1  (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
546	20421_at	emb CAB10242.1  (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
547	14250_r_at	emb CAB43438.1  (AL050300) putative protein [Arabidopsis thaliana]
548	14249_i_at	emb CAB43438.1  (AL050300) putative protein [Arabidopsis thaliana]
549	17544_s_at	gb AAC49282.1  (U40856) AIG1 [Arabidopsis thaliana]
550	12879_s_at	gb AAC49282.1  (U40856) AIG1 [Arabidopsis thaliana]
551	20017_at	gb AAC16079.1  (AC004521) unknown protein [Arabidopsis thaliana]
552	13177_at	emb CAB40989.1  (AL049640) growth factor like protein [Arabidopsis thaliana]
553	19946_at	gb AAF18611.1  AC005170_1 (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]
554	17894_at	gb AAD08938.1  (AC005724) unknown protein [Arabidopsis thaliana]
555	15855_at	gb AAD15572.1  (AC006340) unknown protein [Arabidopsis thaliana]
556	15558_r_at	emb CAB45807.1  (AL080253) putative protein [Arabidopsis thaliana]
557	15208_s_at	No hits found less than or equal to 1e-15.

558	16153_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
559	14636_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
560	19178_at	dbj BAA86999.1  (AB035137) blue copper binding protein [Arabidopsis thaliana]
561	17580_at	emb CAB56039.1  (AJ133786) gigantea protein [Arabidopsis thaliana]
562	14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
563	18946_at	emb CAA72484.1  (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
564	13009_i_at	emb CAA17138.1  (AL021889) putative protein [Arabidopsis thaliana]
565	18508_s_at	gb AAA33709.1  (L16797) glutamate decarboxylase [Petunia x hybrida]
566	12556_at	emb CAB45330.1  (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
567	13115_at	gb AAB60774.1  (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
568	15046_s_at	gb AAB87120.1  (AC003000) unknown protein [Arabidopsis thaliana]
339	17303_s_at	gb AAC67339.2  (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
569	18597_at	emb CAB45881.1  (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]
570	13908_s_at	emb CAB42588.1  (A71590) unnamed protein product [Arabidopsis thaliana]
571	14553_at	emb CAB41103.1  (AL049655) putative protein [Arabidopsis thaliana]
572	18928_at	gb AAB64044.1  (AC002333) putative endochitinase [Arabidopsis thaliana]

- gb|AAC72119.1| (AC005278) Strong similarity to gb|D14550 extracellular dermal glycoprotein (EDGP) precursor from *Daucus carota*. ESTs gb|H37281, gb|T44167, gb|T21813, gb|N38437, gb|Z26470, gb|R65072, gb|N76373, gb|F15470, gb|Z35182, gb|H76373, gb|Z34678 and gb|Z35387>
- 573 12772\_at emb|CAA18124.1| (AL022141) putative receptor protein kinase [*Arabidopsis thaliana*]
- 574 16326\_at
- 575 20479\_i\_at emb|CAB38908.1| (AL035708) cytochrome P450-like protein [*Arabidopsis thaliana*]  
gb|AAD28318.1|AC006436\_9 (AC006436) putative receptor-like protein kinase
- 576 16393\_s\_at [Arabisidopsis thaliana]
- 577 17413\_s\_at emb|CAA67551.1| (X99097) peroxidase [Arabisidopsis thaliana]  
gb|AAA32835.1| (M96073) phosphoribosylanthranilate transferase
- 578 14620\_s\_at [Arabisidopsis thaliana]
- 579 20480\_s\_at emb|CAB38908.1| (AL035708) cytochrome P450-like protein [*Arabidopsis thaliana*]  
gb|AAC79625.1| (AC005770) unknown protein [Arabisidopsis thaliana]
- 580 15866\_s\_at emb|CAA21214.1| (AL031804) putative protein [Arabisidopsis thaliana]  
gb|AAC79625.1| (AC005770) unknown protein [Arabisidopsis thaliana]
- 581 19182\_at
- 582 18255\_at
- 583 16054\_s\_at emb|CAA74639.1| (Y14251) glutathione S-transferase [Arabisidopsis thaliana]
- 584 14672\_s\_at gb|AAC49117.1| (U18993) tryptophan synthase alpha chain [Arabisidopsis thaliana]
- 585 20291\_s\_at gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabisidopsis thaliana]  
emb|CAA74639.1| (Y14251) glutathione S-transferase [Arabisidopsis thaliana]
- 586 16053\_i\_at
- 587 17083\_s\_at gb|AAD25838.1|AC006951\_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabisidopsis thaliana]
- 588 12889\_s\_at gb|AAA32738.1| (M92353) anthranilate synthase alpha subunit [Arabisidopsis thaliana]  
gb|AAD22285.1|AC006920\_9 (AC006920) unknown protein [Arabisidopsis thaliana]
- 589 12642\_at

590	17487_s_at	gb AAC49117.1  (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
591	14838_s_at	gb AAA32835.1  (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
592	17104_s_at	dbj BAA13640.1  (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]
593	19892_at	gb AAC79626.1  (AC005770) putative protease inhibitor [Arabidopsis thaliana]
594	16105_s_at	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
664	13273_s_at	gb AAC31756.1  (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
595	12892_g_at	gb AAC63850.1  (U73786) ACC synthase [Arabidopsis thaliana]
596	15141_s_at	dbj BAA22096.1  (D85191) vegetative storage protein [Arabidopsis thaliana]
597	18231_at	emb CAA55322.1  (X78585) Di21 [Arabidopsis thaliana]
598	15629_s_at	dbj BAA24440.1  (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
599	15978_at	emb CAA48579.1  (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
600	20269_at	gb AAB82640.1  (AC002387) putative pectinesterase [Arabidopsis thaliana]
601	14614_at	gb AAC16958.1  (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
602	17930_s_at	emb CAA07352.1  (AJ006960) peroxidase [Arabidopsis thaliana]
603	16952_s_at	gb AAC78532.1  (AC005662) calmodulin-like protein [Arabidopsis thaliana]
604	12930_s_at 12842_s_at	gb AAC49679.1  (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana] No hits found less than or equal to 1e-15.
605	16063_s_at	dbj BAA32418.1  (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
228	12904_s_at	dbj BAA32418.1  (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
606	12908_s_at	dbj BAA32422.1  (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]



607	15937_at	emb CAA17127.1  (AL021889) hypothetical protein [Arabidopsis thaliana]
608	17843_s_at	gb AAB87109.1  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
609	18966_at	gb AAC95196.1  (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
610	20519_at	gb AAC80599.1  (AC005106) T25N20.20 [Arabidopsis thaliana]
611	19641_at	gb AAC95189.1  (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
612	17408_at	gb AAD32297.1 AC006533_21 (AC006533) putative glucosyltransferase [Arabidopsis thaliana]
613	15646_s_at	gb AAC37474.1  (L42212) serine acetyltransferase [Arabidopsis thaliana]
614	14731_s_at	gb AAC49988.1  (AF014960) multidrug resistance-associated protein 2; AtMRP2 [Arabidopsis thaliana]
615	20685_at	emb CAB41928.1  (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]
616	16968_at	emb CAA17559.1  (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]
617	18253_s_at	gb AAC78440.1  (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana] thaliana]
618	15496_at	gb AAD20156.1  (AC006282) putative glucosyl transferase [Arabidopsis thaliana]
619	19137_at	emb CAA52771.1  (X74755) ATAF1 [Arabidopsis thaliana]
620	19132_s_at	emb CAA18722.1  (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]
621	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function. [Arabidopsis thaliana]
622	17024_s_at	gb AAB67854.1  (U61231) cytochrome P450 [Arabidopsis thaliana]
623	14705_i_at	emb CAB69849.1  (AL137189) anthranilate N-benzoyltransferase-like protein [Arabidopsis thaliana]
624	17500_s_at	emb CAB42906.1  (AL049862) calmodulin-like protein [Arabidopsis thaliana]

625	13217_s_at	emb CAB42906.1  (AL049862) calmodulin-like protein [Arabidopsis thaliana]
626	15196_s_at	gb AAC49573.1  (U43412) 3'-phosphoadenosine 5'-phosphosulfate reductase [Arabidopsis thaliana]
627	18590_at	emb CAA10955.1  (AJ222713) unnamed protein product [Arabidopsis thaliana]
628	14700_at	No hits found less than or equal to 1e-15.
629	14665_r_at	emb CAA69879.1  (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
630	12630_at	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
631	18953_at	gb AAC69851.1  (AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
632	13514_s_at	emb CAA16793.1  (AL021713) putative protein [Arabidopsis thaliana]
633	12490_at	gb AAF02787.1 AF195115_7 (AF195115) weak similarity to receptor protein kinase [Arabidopsis thaliana]
634	12246_s_at	emb CAB10404.1  (Z97340) phytochrome D [Arabidopsis thaliana]
635	20536_s_at	emb CAB37488.1  (AL035539) putative protein [Arabidopsis thaliana]
636	18409_at	gb AAC72122.1  (AC005278) F15K9.14 [Arabidopsis thaliana]
637	19387_at	gb AAD21475.1  (AC007017) unknown protein [Arabidopsis thaliana]
638	16117_s_at	gb AAB70244.1  (AF016848) WD-40 repeat protein [Arabidopsis thaliana]
639	18347_s_at	emb CAA21480.1  (AL031986) putative protein [Arabidopsis thaliana]
640	15880_at	emb CAB38906.1  (AL035708) putative protein [Arabidopsis thaliana]
667	20471_at	gb AAC49767.1  (AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]
641	16603_s_at	gb AAB58497.1  (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]
642	12049_at	gb AAC13598.1  (AF058914) F21E10.13 gene product [Arabidopsis thaliana]
643	12048_at	gb AAC78704.1  (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

		gb AAB61117.1  (AC002062) ESTs
644	14064_at	gb N38288,gb T43486,gb AA395242 come from this gene. [Arabidopsis thaliana]
645	12149_at	gb AAC04492.1  (AC003974) unknown protein [Arabidopsis thaliana]
646	14295_s_at	emb CAA91183.1  (Z54356) HD-ZIP [Arabidopsis thaliana]
647	19034_at	emb CAA16930.1  (AL021768) TMV resistance protein N-like [Arabidopsis thaliana]
648	18624_at	gb AAC27848.1  (AC004218) unknown protein [Arabidopsis thaliana]
649	13181_at	gb AAC97218.1  (AC005936) unknown protein [Arabidopsis thaliana]
650	18866_at	gb AAD10163.1  (AC005917) putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana]
651	19502_at	emb CAB44686.1  (AL078620) cytochrome P450-like protein [Arabidopsis thaliana]
652	16301_s_at	emb CAA19807.1  (AL031018) hypothetical protein [Arabidopsis thaliana]
653	19411_at	gb AAD32774.1 AC007661_11 (AC007661) unknown protein [Arabidopsis thaliana]
654	20300_g_at	emb CAA71588.1  (Y10556) CONSTANS [Arabidopsis thaliana]
655	20299_at	emb CAA71588.1  (Y10556) CONSTANS [Arabidopsis thaliana]
656	18696_s_at	gb AAB57688.1  (U96045) APS reductase [Arabidopsis thaliana]
657	15186_s_at	gb AAC26980.1  (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana] [Arabidopsis thaliana]
659	16609_s_at	AtERF2 (, BAA32419.1; AB008104)
660	12909_s_at	EREBP4-like, AtERF6 (, CAB10530.1; Z97343)
661	16536_s_at	AtERF5 (, BAA32422.1; AB008107)
301	15665_s_at	put. C2H2 zinc finger transcription factor (, AAB80922.1; AF022658)
668	13176_at	Myb-like (, emb CAA20567.1  (AL031394) putative protein
670	15778_at	X98676.2_at
671	20619_at	AC005896.161_at
672	12966_s_at	AL023094.197_s_at
673	20335_s_at	Y14208.2_s_at
674	18949_at	Z54136.1_at
675	13015_s_at	X98673.2 s at emb CAB41311.1

		(AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
676	19646_s_at	AC005819.55_s_at
677	19855_at	AC007260.16_at
		AC007047.101_at gb AAC49767.1
		(AF003094) AP2 domain containing protein
678	18475_at	RAP2.1 [Arabidopsis thaliana]
		unspecified t-factor gb AAC49775.1
		(AF003102) AP2 domain containing protein
679	13001_at	RAP2.9 [Arabidopsis thaliana]
		AC004665.101_at emb CAA67234.1
		(X98676) zinc finger protein [Arabidopsis thaliana]
680	15219_at	ATTHIRED4_s_at gb AAC98070.1
		(AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
681	13189_s_at	hsp70_s_at emb CAA18838.1  (AL023094)
		bZIP transcription factor ATB2 [Arabidopsis thaliana]
684	13284_s_at	

Table 10

<u>Set</u>	<u>Content</u>	<u>Number of unique genes</u>
2	7 or 8 not edm1 not	55 genes
5	rps2 not pad4 or NahG	
3	edm1 not rps2 not pad4 or NahG	44 genes
4	rps2 not edm1 not pad4 or NahG	12 genes
5	pad4 or NahG not edm1 not rps2	20 genes
6	edm1 and rps2 not pad4 or NahG	17 genes
10	7	edm1 and pad4 or NahG not rps2
	8	rps2 and pad4 or NahG not edm1
	9	edm1 and rps2 and pad4 or NahG
	Total	184 genes

15 For engineering resistance to pathogens whose growth is restricted by RPP7 or RPP8 dependent responses, such as oomycete pathogens, all 184 genes are potentially useful. The 128 genes in sets 2, 3, 4, and 6 are more likely to be useful, as *pad4* and *NahG* do not interfere with resistance mediated by *RPP7* or *RPP8*, so genes under their control should not be important for this type of

20 resistance. The 99 genes in sets 2 and 3 are even more likely to be useful, because they not affected by *rps2*, and *RPP7* and *RPP8* trigger a different kind of resistance response than the one triggered by *RPS2*. The 44 genes in set 3 are

most likely to be useful, as they require *EDM1*, and *EDM1* is required for resistance.

### Example 3

#### 5     Transcriptional Responses Triggered by the RPP7 Defense Signaling Pathway

The *RPP7* defense-signaling pathway (Figure 1) mediates resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Hiks1. In contrast to conventional *R*-gene dependent defense signaling pathways in *Arabidopsis*, such as the *RPP4* pathway, the *RPP7* pathway does not essentially  
10   require salicylic acid accumulation or previously described defense regulators, such as *EDS1*, *NDR1*, *NPR1*, *PAD4* and others.

A comparative analysis of transcriptional responses triggered by the *RPP7* and *RPP8* pathways was performed by gene expression profiling using Affymetrix oligonucleotide chips with roughly 8,200 different *Arabidopsis*  
15   genes, representing roughly a third of the genome. For the analysis, 2 week old seedlings were harvested 0, 12 or 48 hours post infection with a particular *Peronospora* isolate (Table 11). To examine *RPP8* triggered transcriptional responses, a transgenic line Col-0 line carrying the *RPP8* resistance gene from the *Arabidopsis* ecotype Landsberg erecta was infected with the *Peronospora*  
20   isolate Emco5. This interaction is incompatible. The interaction between Emco5 and Col-0 wild type plants served as compatible control. Responses triggered by the *RPP7* pathway were analyzed using the incompatible interaction between the *Peronospora* isolate Hiks1 and Col-0 wild type plants, as well as compatible interactions between Hiks1 and the susceptible mutants *rpp7*, *edm1*,  
25   *edm2* and *edm3*. To compare transcriptional responses triggered by the unconventional *RPP7* and *RPP8* pathways with those triggered by the more conventional *RPP4* pathway, Col-0 wild type plants were infected with the *Peronospora* isolate Emoy2, which is avirulent on this ecotype. The interactions between Emoy2 and NahG plants, as well as the mutants *pad4*, *ndr1* and *npr1*,  
30   served as compatible controls. Whereas *pad4* and NahG plants are fully Emoy2 susceptible, *ndr1* and *npr1* plants are only partly compromised in Emoy2 resistance.



Table 11

	<u>Plant</u>	<u>Peronospora isolate</u>	<u>Interaction type</u>
	Col-0 ( <i>tgRPP8</i> )	Emco5	incompatible
	Col-0 ( <i>rpp8</i> )	Emco5	compatible
5	Col-0 ( <i>RPP7</i> )	Hiks1	incompatible (2x)
	Col-0 ( <i>rpp7</i> ; 3929)	Hiks1	compatible
	Col-0 ( <i>edm1</i> )	Hiks1	compatible
	Col-0 ( <i>edm2</i> )	Hiks1	compatible
	Col-0 ( <i>edm3</i> )	Hiks1	compatible
10	Col-0 ( <i>RPP4</i> )	Emoy2	incompatible
	Col-0 ( <i>ndr-1-1</i> )	Emoy2	intermediate
	Col-0 ( <i>pad4-1</i> )	Emoy2	compatible
	Col-0 ( <i>NahG</i> )	Emoy2	compatible
	Col-0 ( <i>npr1-1</i> )	Emoy2	intermediate

15

ResultsIdentification of Genes Potentially Required for *RPP7* Mediated *Peronospora* Resistance

Genes that play a role in the establishment of resistance may show differences in their regulation or their expression levels between compatible and incompatible interactions (e.g., genes may show lower expression levels in “loss of Hiks-resistance mutants” as compared to Col-0 wild type plants). Thus, for each gene expression, ratios were calculated between Col-0 and each of the four Hiks response mutants (*rpp7*, *edm1*, *edm2* or *edm3*) at each time point (0, 12 and 48 hours). The resulting data set, consisting of 12 expression ratios for each of the 8,775 probe sets on the chip, was first analyzed with “CLUSTER” and “TREE VIEW”, two commonly used programs for chip and micro-array data analysis (Eisen et al., 1998). Genes that demonstrated only minor or less significant expression differences between Col-0 wild type and the mutants were excluded from analysis. Genes that showed at least one 3-fold expression difference over all 12 calculated expression ratios were first considered for further analysis.

Table 12 shows 194 probe sets corresponding to genes having SEQ ID NOs: 301-494, the expression of which is altered after infection of *Arabidopsis* with *P. parasitica* (wild-type relative to *rpp7*, *edm1*, *edm2*, or *edm3*). Table 13

depicts about 100 genes (genes comprising SEQ ID NOs: 373, 385, 242, 369, 306, 232, 346, 367, 212, 221, 307, 322, 240, 313, 270, 252, 383, 245, 377, 212, 327, 297, 375, 263, 250, 282, 358, 257, 332, 560, 284, 220, 259, 355, 248, 281, 215, 236, 309, 386, 253, 333, 336, 296, 319, 414, 354, 353, 293, 278, 324, 339, 345, 225, 249, 264, 310, 228, 214, 311, 343, 298, 384, 277, 314, 372, 331, 338, 370, 352, 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 223, 348, 318, 251, 291, 289, 361, 285, 368, 342, 290, 351, 312, 286, 287, 273, 239, 326, 226, 227, 350, 280, 317, 359, 294, 279, 382, 356, 234, 218, 217, 347, 379, 401, 378, 363, 341, 208, 268, 267, 364, 266, 337, 269, 269, 325, 793 and 224) represented by 137 probe sets that show at least one 3-fold-expression difference in comparisons between wild type *Arabidopsis* Col-0 and mutants *rrp7* or *edm1*, *edm2*, or *edm3* infected with *P. parasitica* Hiks1 (i.e., probe sets that show at least one 3-fold difference in expression levels over all 12 expression ratios calculated between Col-0 wild type and each of the 4 Hiks response mutants at each of the time points). Genes were grouped together according to similarities of their expression characteristics. Expression ratios were color encoded. Positive expression ratios were red and negative ratios were green. Black indicated no expression difference. Genes were represented in rows and infection treatments in columns. Red generally indicated that a gene at a given time point is more strongly expressed in Col-0 wild type plants as compared to the respective mutant. One cluster represented genes that are upregulated in response to Hiks1 infection by the *RPP7* pathway (Table 14; genes comprising SEQ ID NOs: 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 310, 228, 214, 347 and 225, which are induced by Hiks1-infection and which are *RPP7*, *EDM1*, *EDM2*, *EDM3*-dependent genes and so may encode regulators acting downstream of those genes; see probe sets 12505, 13217 and 12904 which correspond to genes that encode potential regulators of Hiks response pathway). Genes in this cluster represent genes that are more strongly expressed in Col-0 wild type than in all four mutants predominantly at the 12 hour time-point in each comparison. The expression difference is less pronounced in the case of *edm2* and *edm3*, but it is consistent over all four comparisons.

Table 12

Affy ID (Probe Set)	Reference No.
12324_i_at	AC007212
12333_at	AJ286345
12345_at	L36246
12500_s_at	AF081067
12505_s_at	AC005309
12608_i_at	S70188
12642_at	AC006920
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12911_s_at	X84229
12916_s_at	AF021244
13138_at	AL096882
13177_at	AL049640
13178_at	U93215
13187_i_at	U35829
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13273_s_at	U68017
13284_s_at	AJ002551
13604_at	AC000104
13615_at	AC002332
13617_at	AC006592
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14028_at	AF075597
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309

14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14295_s_at	Z54356
14595_at	AL022580
14608_at	AC007357
14614_at	AC004165
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14643_s_at	AC006836
14672_s_at	U18993
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
14965_at	AC002329
15057_at	AL035440
15085_s_at	AL031018
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15216_s_at	U75198
15431_at	AL030978
15496_at	AC006282
15523_s_at	AL078637
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15622_s_at	U43945

15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15950_at	AC006429
15954_at	U72155
15969_s_a	AJ133036
15978_at	X68592
15982_s_a	X98190
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16412_s_at	AL022603
16442_s_at	AJ002551
16461_I_at	AC004683
16462_s_a	AC004683
16504_s_at	Z97335
16510_at	AL034567
16514_at	AL035538
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16578_s_at	AL137080
16609_s_at	AB008104
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
16951_i_at	AC005662
16952_s_at	AC005662
16981_s_at	U35829
17014_s_at	U05206
17033_s_at	U83179
17054_s_at	AF134128
17073_s_at	AC006836
17119_s_at	AF132212
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17379_at	AC018721
17386_at	AC006264
17413_s_at	X99097



17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17549_s_a	L37126
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17917_s_at	AC004261
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18255_at	AC005770
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18591_at	X74756
18607_s_at	U78721
18635_at	AC004005
18706_s_a	X75782
18716_at	AC007396
18876_at	AF002109
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19594_i_at	X98321
19640_at	AC004561
19977_at	AL049659
20017_at	AC004521
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20297_at	AC007153
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336

20555_s_a	AL080318
20585_s_at	AC005309
20641_at	X91919

Table 13

Probe Set	Description
12324_i_at	AC007212
12345_at	L36246
12505_s_at	AC005309
12608_i_at	S70188
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12908_s_at	AB008107
12911_s_at	X84229
13138_at	AL096882
13178_at	U93215
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13604_at	AC000104
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309
14116_at	AF077407
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14248_at	AC007357
14250_r_at	AL050300
14595_at	AL022580

14608_at	AC007357
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
15057_at	AL035440
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15431_at	AL030978
15496_at	AC006282
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15846_at	AC006067
15847_g_at	AC006067
15950_at	AC006429
15954_at	U72155
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16504_s_at	Z97335
16510_at	AL034567
16536_s_at	AB008107
16578_s_at	AL137080
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
17014_s_at	U05206
17033_s_at	U83179

17054_s_at	AF134128
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17386_at	AC006264
17413_s_at	X99097
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18607_s_at	U78721
18635_at	AC004005
18716_at	AC007396
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19640_at	AC004561
19977_at	AL049659
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336
20585_s_at	AC005309
20641_at	X91919

Table 14

Probe Set	Description
12505_s_at	AC005309
12879_s_at	U40856
12904_s_at	AB008103
13189_s_at	U35829
13217_s_at	AL049862
14116_at	AF077407
14148_at	AF224762
14201_at	AL163972
14248_at	AC007357
14250_r_at	AL050300
14691_at	AP002046
14704_s_at	AC006067
15846_at	AC006067
15847_g_at	AC006067
16063_s_at	AB008103
17500_s_at	AL049862
17544_s_at	U40856
18716_at	AC007396
19178_at	AB035137
19640_at	AC004561
20269_at	AC002387

Thus, Hiks1 induced upregulation is compromised in all four tested “loss of Hiks1 resistance mutants” and there is a correlation between breakdown of resistance and deregulation of these genes. This may indicate that these genes play important roles in mediating Hiks1 resistance. Furthermore, these genes appear to act downstream of all four genetically defined *RPP7* pathway components, *RPP7*, *EDM1*, *EDM2* and *EDM3*. Some genes of this set may encode important regulators; whereas others may indicate metabolic processes required for Hiks1 resistance.

Seventy-eight genes (Table 15; genes comprising SEQ ID NOs:330, 292, 311, 243, 237, 302, 315, 283, 300, 372, 308, 335, 272, 305, 357, 213, 362, 331, 254, 384, 277, 343, 298, 349, 314, 265, 262, 258, 256, 303, 321, 304, 275, 274, 323, 238, 374, 241, 344, 244, 365, 261, 380, 371, 295, 255, 316, 233, 345, 225, 260, 229, 324, 301, 235, 340, 278, 320, 231, 319, 230, 354, 353, 293, 376, 247, 246, 366, 216, 214, 276, 299, 310, 334, 271, 381 and 228) that show the same, but less pronounced, expression characteristics were selected using relaxed selection criterion (at least one 2-fold expression difference over all 12 calculated expression ratios). With a lower cutoff criterion of at least one 2-fold-expression difference across all twelve expression ratios, this cluster is larger



than that shown in Table 14. Genes that are part of this less stringently defined cluster were included in further analyses so as to not exclude potentially important genes. Potential regulators in this cluster are listed in Table 16 (genes comprising SEQ ID NOs: 220, 323, 231, 319, 214, 301, 340, 243, 227, 321, 235, 315, 298, 314, 328, 344 and 349). Four different ERF transcription factors genes are upregulated by the *RPP7*-pathway. Genes encoding ERFs are known to be upregulated in response to several stress-related stimuli, such as wounding, pathogens or ethylene. Moreover, ERF transcription factors bind to GCC boxes, which are ethylene, wounding and pathogen-responsive *cis*-elements. This cluster also contains a gene encoding an ACC synthase, a component of the ethylene biosynthetic pathway. Therefore, ethylene may play a role in the Hiks response pathway.

Table 15

Probe Set	Description
12500_s_at	AF081067
12505_s_at	AC005309
12642_at	AC006920
12879_s_at	U40856
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12916_s_at	AF021244
13177_at	AL049640
13187_i_at	U35829
13189_s_at	U35829
13217_s_at	AL049862
13273_s_at	U68017
13284_s_at	AJ002551
13615_at	AC002332
13617_at	AC006592
14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14201_at	AL163972
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14614_at	AC004165
14643_s_at	AC006836
14672_s_at	U18993

14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
15085_s_at	AL031018
15216_s_at	U75198
15431_at	AL030978
15523_s_at	AL078637
15616_s_at	AL078637
15622_s_at	U43945
15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15978_at	X68592
16063_s_at	AB008103
16105_s_at	U68017
16393_s_at	AB008103
16412_s_at	U68017
16442_s_at	AJ002551
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16609_s_at	AB008104
16620_s_at	AF051338
16952_s_at	AC005662
16981_s_at	U35829
17073_s_at	AC006836
17119_s_at	AF132212
17379_at	AC018721
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17917_s_at	AC004261
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18255_at	AC005770
18591_at	X74756
18716_at	AC007396
18876_at	AF002109
19178_at	AB035137
19182_at	AL031804
19640_at	AC004561
20017_at	AC004521

20269_at	AC002387
20297_at	AC007153
20429_s_at	Z97336

Additionally, a gene encoding a lipoxygenase, a component of the jasmonic acid biosynthetic pathway, is upregulated. Other regulators potentially acting downstream of RPP7, EDM1, EDM2 and EDM3 include some putative  
 5 zinc finger transcription factors and protein kinases as well as two calmodulin-like proteins and a calcium binding protein, which may point to a role of calcium in the *RPP7*-pathway.

Table 16

10 I. Transcriptional regulators:

- 1.) AtERF1 (12904\_s\_at, BAA32418.1; AB008103)
- 2.) AtERF2 (16609\_s\_at, BAA32419.1; AB008104)
- 3.) EREBP4-like (12909\_s\_at, CAB10530.1; Z97343)
- 4.) AtERF5 (16536\_s\_at, BAA32422.1; AB008107)
- 15 5.) putative CONSTANS-like zinc finger (12505\_s\_at, AAC63643.1; AC005309)
- 6.) putative C2H2 zinc finger transcription factor (15665\_s\_at, AAB80922.1; AF022658)
- 7.) putative C3H zinc finger protein (17379\_at, AAF18728.1; AC018721)
- 20 8.) heat shock transcription factor 4 (13273\_s\_at, AAC31756.1; U68017)
- 9.) SigA binding protein (14148\_s\_at, AAF34713.1; AF224762)

II. Other signaling proteins

- 10.) AtACS-6 (12892\_g\_at, CAB51412.1, AL096882, 35400..37154)
- 11.) lipoxygenase (16569\_s\_at, AAA32749.1; L23968)
- 25 12.) growth factor like protein (13177\_at, CAB40989.1; AL049640)
- 13.) serine/threonine protein kinase (16412\_s\_at, CAA18704.1; AL022603)
- 14.) wall associated kinase 1 (15616\_s\_at, CAB08794.1; AJ009696)
- 15.) putative receptor-like protein kinase (16393\_s\_at, AAD28318.1; AC006436)
- 30 16.) calmodulin-like (16951\_i\_at, AAC78532.1; AC005662)
- 17.) calmodulin-like (17500\_s\_at; CAB42906.1; AL049862)
- 18.) calcium binding protein (17917\_s\_at, AAD12002.1; AC004261)

Twenty-six genes (genes comprising SEQ ID NOs: 300, 308, 272, 213, 362, 265, 374, 241, 261, 380, 310, 228, 233, 330, 311, 243, 237, 254, 230, 244, 365, 216, 316, 345, 225, 301, 278, 354, 353, 293, 335, 271 and 321, also shown in Table 15), represented by 33 probe sets, were found to be commonly

5 upregulated in response to both *Peronospora* isolates, Hiks1 and Emco5, in an *RPP7*- or *RPP8*-dependent (and *EDM1*, *EDM2* and *EDM3*-dependent) manner (Table 17). Elevated expression of these genes may be required for resistance against both *Peronospora* isolates or against *Peronospora parasitica* in general. Among these 26 genes are those encoding ERF1, putative zinc finger

10 transcription factors, two proteins potentially involved in calcium signaling, a lipoxygenase, and a cysteine rich antifungal protein.

Table 17

15	26 <i>Peronospora</i> (Hiks1 and Emco5) induced <i>RPP8</i> , <i>RPP7</i> , <i>EDM1</i> , <i>EDM2</i> , <i>EDM3</i> -dependent genes	
	<b>Transcription factors</b>	
	AtERF1	
	Putative salt-tolerance zinc finger transcription factor (18217_g_at)	
20	(ZFPI) hypothetical Cys-3-His zinc finger protein	
	Putative C2H2 zinc finger transcription factor	
	Heat shock transcription factor 4	
	<b>Other potential proteins</b>	
25	Calmodulin-like protein	
	Similarity to centrin, <i>Marsilea vestita</i> contains EF-hand calcium-binding domain (15431_at)	
	Lipoxygenase	
30	<b>Others</b>	
	heat shock protein 70	
	putative steroid sulfotransferase	tryptophan synthase alpha chain
	putative glucosyltransferase	similar to xyloglucan fucosyltransferase (12642_at)
35	phosphoglycerate dehydrogenase	Pad3 (Cytochrome P450)
	ATAF2	putative pectinesterase
	OPDA-reductase homolog	AIG1
	coronatine-induced protein 1	putative glutathione S-transferase
	thioredoxin h	adenosine nucleotide translocator
40	IAA-amino acid hydrolase	contains similarity to sugar transporters
		CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 PRECURSOR (AFP1) (18716_at)

Thirteen of these 26 genes (genes comprising SEQ ID NOs: 308, 300, 272, 362, 265, 242, 261, 380, 228, 243, 254, 216 and 225, *Peronospora* (Hiks1, Emco5 and Emoy2) induced and *RPP4*, *RPP8* and *RPP7* dependent) were also found to be more strongly expressed during the incompatible interaction between the *Peronospora* isolate Emoy2 and Col-0 plants as compared to Emoy2 infections of the compatible or intermediate type (see Table 18). These 13 genes may play an important role in defense against *Peronospora parasitica* in general. Among these genes is PAD3, which was previously demonstrated to be required for pathogen-induced phytoalexin production. Strikingly, Hiks1 resistance is, partially compromised in the *pad1-1/pad3-1* double mutant, whereas Emoy2 resistance is reduced in the *pad3-1* single mutant (Glazebrook et al. 1997).

Table 18

13 *Peronospora* (Hiks1, Emco5 and Emoy2) induced  
RRP4-pathway, RPP7-pathway, and RPP8-dependent genes

- adenosine nucleotide translocator (15978\_at)
- phosphoglycerate dehydrogenase (15629\_s\_at)
- tryptophan synthase alpha chain (14672\_s\_at)
- ATAF2 (18591\_at)
- putative glucosyltransferase (14614\_at)
- calmodulin-like protein (13217\_s\_at)
- pad3 (cytochrome P450)(14248\_at)
- putative pectinesterase (20269\_at)
- ethylene responsive element binding factor 1 (12904\_s\_at)
- heat shock transcription factor 4 (13273\_s\_at)
- sugar transporter-like (14116\_at)
- similar to xyloglucan fucosyltransferase (12642\_at)
- AIG1 (12879\_s\_at)

Identification of promoter motifs common to *RPP7* and *RPP8* controlled genes



Sequence motifs conserved in the promoters of genes co-regulated by the *RPP7* or *RPP8* pathways may lead to information about the types of transcription factors controlling expression of these genes and may serve as starting points for isolating and/or cloning of such factors. Sub-categorization of *RPP7*-  
 5 upregulated genes by K-means clustering, based on the absolute expression levels of the genes, revealed the existence of only a few basic expression profiles. K-means clustering into five gene sets gave the most consistent and tight clusters. For each of the five gene sets (Table 19), the expression changes in two repetitions of the Col-0 wild type/Hiks1 interaction are shown as well as  
 10 in the *rpp7* mutant and *edm1*, *edm2* and *edm3*.

The first set comprises genes (genes comprising SEQ ID NOs: 292, 302, 315, 300, 308, 213, 265, 374, 241, 344, 261, 299, 365 and 276) that show early and transient upregulation. The genes peak at 12 hours and return to their ground-states at approximately the 48 hours post infection. Genes of the second  
 15 set (genes comprising SEQ ID NOs: 267, 305, 357, 362, 380, 310, 228, 295, 233, 329, 312, 243, 237, 283, 372, 254, 314, 323, 216, 260, 229 and 235) are also rapidly upregulated, but show a less pronounced or no decline after the peak. In both sets, the response is weaker in the mutants. Only a few genes in the first set respond almost as strongly in *edm2* and *edm3* plants as in wild type plants.  
 20 Genes of the third (genes comprising SEQ ID NOs: 258, 256, 303, 304, 275, 244, 316, 354 and 225) and fifth (genes comprising SEQ ID NOs: 330, 384, 277, 343, 298, 349, 262, 274, 238 and 301) set show an almost linear increase of transcript level in wild type. In the mutants, this increase is delayed and in some cases less steep. In the fourth set (genes comprising SEQ ID NOs: 432, 347,  
 25 370, 412, 323, 411, 322, 449, 448, 385, 471, and 339) the expression levels rise in the first repetition of the Col-0 wild type/Hiks interaction, but respond very little in the second one. In *edm3*, the transcript levels drop from a high ground state. The probe sets and genes corresponding to each of these K-means cluster sets are shown in Table 19.

30

Table 19

K-means set 1	Description	K-means set2	Description
12500_s_at	AF081067	12642_at	AC006920
13217_s_at	AL049862	12904_s_at	AB008103
14248_at	AC007357	12905_s_at	AB008104

14614_at	AC004165	12916_s_at	AF021244
14706_r_at	AL137189	13177_at	AL049640
15216_s_at	U75198	13187_i_at	U35829
15622_s_at	U43945	13273_s_at	U68017
15629_s_at	AB010407	14116_at	AF077407
15680_s_at	D42061	14223_at	AL024486
15978_at	X68592	14672_s_at	X76609
16412_s_at	U68017	15085_s_at	AL031018
17500_s_at	AL049862	15523_s_at	AL078637
18070_r_at		15866_s_at	AC005770
18716_at	AC007396	16063_s_at	AB008103
19640_at	AC004561	16105_s_at	AL049730
		16393_s_at	AC006436
		16609_s_at	AB008104
		16952_s_at	AC005662
		18255_at	AC005770
		18591_at	X74756
		19182_at	AL031804
		20269_at	AC002387
<b>K-means set 3 Description</b>			
12879_s_at	U40856		
13284_s_at	AJ002551		
14148_at	AF224762		
14201_at	AC068667		
14704_s_at	AC006067		
15846_at	AC006067		
15847_g_at	AC006067		
16442_s_at	AJ002551		
17544_s_at	U40856		
<b>K-means set 5 Description</b>			
		13189_s_at	U35829
		14250_r_at	AL050300
		14691_at	AP002046
		14709_at	AP002046
		15616_s_at	AJ009696
		15665_s_at	AF022658
		16981_s_at	U35829
		17499_s_at	AF107726
		17917_s_at	AC004261
		20429_s_at	Z97336
<b>K-means set 4 Description</b>			
12908_s_at	AB008107		
12909_s_at	Z97343		
13617_at	AC006592		
14141_at	AC011437		
14711_s_at	AF085279		
15431_at	AL030978		
16536_s_at	AB008107		
16539_s_at	Z97343		
17379_at	AC018721		
18216_at	AC012375		
18217_g_at	AC012375		
20017_at	AC004521		

Recently, the plant specific family of WRKY transcription factors has been implicated in the regulation of defense-associated genes. Promoters of genes upregulated during systemic acquired resistance were found to be strongly enriched in potential WRKY binding sites. WRKY factors comprise a large family of 72 different members in *Arabidopsis*. Generally these factors appear to bind to sequence motifs containing the core T G A C (W box). It has not yet

been determined whether individual WRKY family members differ in their preferences for distinct W box variations. However, it is probable that a given WRKY protein has a binding preference for a certain variation of the W box motif.

5        Using the program AlignACE, three variations of potential WRKY binding sites were found to be conserved in sub-sets of *RPP7* controlled genes. Two of these motifs are highly enriched in promoters of genes from K-means cluster 3, representing genes that show a linear increase in transcript level after *Peronospora* infection (Table 20; genes comprising SEQ ID NOs: 384, 298, 349, 10 262 and 238 for W box I and genes comprising SEQ ID NOs: 384, 349, 262, 238 and 301 for W box II). These motifs are also present in promoters of K-means cluster 5, which represents a similar expression profile. Focusing on sustained up-regulated genes, that show a particularly pronounced expression difference between Col-0 wild type plants and the Hiks1 response mutants, a third variation 15 of potential WRKY binding sites was found to be significantly enriched (Table 21; genes comprising SEQ ID NOs: 397, 371, 238, 262, 256, 275, 254, 214 and 225). In all three cases, sequence conservation clearly exceeds the core motif of WRKY binding sites that appears to be recognized by all members of this family. These additionally conserved positions may confer specificity for 20 certain WRKY family members. They may provide a highly defined binding site preferentially recognized by a distinct WRKY factor or may serve as binding sites for another transcription factor binding closely adjacent to and specifically interacting with a distinct WRKY factor. In any case, the high conservation of extended potential WRKY binding motifs strongly suggests that specific 25 members of this family participate in the regulation of certain sub-sets of *RPP7*-controlled genes.

Table 20

<u>W box I</u>		MAP Score: 8.98114		
30	GTCATCTTTTAATCTCTGG	0	638	1
	GTCATCTTTTAATCGCCGG	0	932	1
	GCCTTTGCTTATTTATAGG	0	1036	1
	GTCATTTGTTACAAAGAGG	1	318	1
	GTCATTGATCATAAACTGT	1	389	0
35	GCCACTGCTGAATTGTCGG	1	494	1
	GTCCATTGTCAATAAATGG	2	689	1
	GTCCATTGTAAATAAATGT	2	949	1

5  
 GTCATCTTTTAATCTCTGT 3 475 0  
 GTCACGTATGAATGGAAGG 4 73 1  
 GTCAACGTTTAGTTCATGT 4 226 0  
 GTCAAGTTTTAAATTGTGG 4 352 1  
 GTCAACGTTTAGTTCATGT 4 401 0

\*\*\* \* \* \* \*

GTCANNTNTNANTNNNNGG

G A T

Expected frequency by chance: 0.02/1kb  
 10 Observed frequency: 1.2/1kb  
 Enrichment: ~60 fold

W box II MAP Score: 15.2966

15  
 ATTAAAAGATGAC 0 638 0  
 ATTAAAAGATGAC 0 932 0  
 ATTAAATGCTGTC 2 752 0  
 ATTAAATGCTGTC 2 1011 0  
 AGCAAAAGCTGAC 2 1092 1  
 ATTAAAAGATGAC 3 481 1  
 ATCAAAAGTTGTC 3 829 1  
 20 ACTAAACGTTGAC 4 232 1  
 ACTAAACGTTGAC 4 407 1  
 ACTAAAAAGTGAC 5 755 1  
 \* \* \* \* \*

25 W II ANTAAANGNTGAC  
 C A T

W I: CCNNNNANTNANCNNTGAC  
 A T A

30 Expected frequency by chance: 0.04/1kb  
 Observed frequency: 1.35/1kb  
 Enrichment: ~30 fold  
 Table 21

35 ATAGGTGGTCAAGT 1 106 0  
 AATTGTGGTCATTT 1 823 0  
 ACTTGTGGTCAATT 2 804 0  
 AAAAGGGGTCATTT 2 970 1  
 ATATGTCGTCTCTT 2 994 0  
 AGTTGTGGTCTACC 3 502 0  
 40 AAAAGTTGTCAATT 3 732 1  
 AGACGTCGTAATTT 4 400 0  
 ACGTGGCGTCATAT 5 179 0  
 ATGTGGCGTCTCCT 6 249 1  
 AGTTGGTGTACCGT 6 925 1  
 45 ATTCGTGGTCAACT 7 582 1  
 ATATGTCGTCACTT 7 875 1

\* \* \* \* \*

ANNNGTNGTCANNT

G

50

expected: 0.05/1kb;  
 in random set: 0/1kb;  
 this set: 1/1kb;  
 enrichment: 10-20 fold;

5

Novel, conserved promoter motifs were also found. Genes of K-means set 1, which are early and transient *RPP7*-pathway specific genes, share two similar highly conserved promoter motifs, G G T/C C C A (SEQ ID NO:714; genes comprising SEQ ID NOs: 302, 315, 308, 265, 374, 241, 261, 299 and 365) and G N C C A A A (SEQ ID NO:715; genes comprising SEQ ID NOs: 292, 302, 308, 265, 374, 241, 261, 299, 365 and 276) (Table 22). Both motifs are almost perfectly conserved and are represented in nearly all promoters of this gene set. They are compact six- or seven-mers, which is typical for transcription factor binding sites. For the second motif, the permutations G A C C A A A and G T C C A A A are strongly represented. These permutations may constitute the preferred binding site of a so far unknown transcription factor.

15

Table 22

Two related novel motifs are highly enriched in all  
 11 promoters of K-means set1

20

	GGTCCA	1	232	0
	GGCCCA	1	289	1
	GGTCCA	1	597	1
25	GGTCCA	2	517	0
	GGTCCA	3	211	1
	GGCCCA	3	360	1
	GGTCCA	4	597	1
	GGCCCA	4	681	1
30	GGTCCA	5	352	0
	GGTCCA	5	1060	1
	GGTCCA	6	358	0
	GGCCCA	7	776	0
	GGCCCA	7	816	0
35	GGTCCA	8	285	0
	GGTCCA	9	888	1
	*****			
	GGTCCA	C		
	Expected frequency by chance: 0.22/1kb			
40	Observed frequency:		1.2/1kb	
	Enrichment: 5.4 fold			
	GCCCAA	0	601	1
	GTCCAA	10	1186	1
	GTCCAA	9	562	1



5 GACCAAA 8 640 0  
 GCCCAA 7 774 0  
 GTCCAA 7 717 1  
 GTCCAA 6 712 1  
 GACCAAA 5 970 1  
 GTCCAA 5 350 0  
 GACCAAA 4 1164 1  
 GACCAAA 4 1072 1  
 GTCCAA 4 784 0  
 10 GACCAAA 4 714 0  
 GGCCAA 4 698 0  
 GCCCAA 3 361 1  
 GACCAAA 1 920 0  
 GTCCAA 1 230 0  
 15 \*\*\*\*\*  
 GNCCAA  
 Expected frequency by chance: 0.32/1kb  
 Observed frequency: 1.3/1kb  
 Enrichment: 4 fold

20

Following a similar approach as for the Hiks1-induced *RPP7* pathway controlled genes, a cluster of early and transiently Emco5-induced *RPP8*-dependent genes were defined (Table 23). In Col-0-*RPP8* plants these genes (genes comprising SEQ ID NOs: 364, 341, 288, 378, 363, 379 and 219) show a  
 25 very pronounced upregulation 12 hours post Emco5 infection, after which they return to expression ground states. Using AlignACE, two different motifs (see Example 2) were found to be strongly enriched in the promoters of this cluster. The first motif strongly resembles the type I consensus binding site of Myb transcription factors. This motif is also almost identical to a recently identified  
 30 *cis*-element conferring rapid elicitor responsive gene expression in parley cell culture (Kirsch et al., 2001). Interestingly, a gene encoding a Myb-like transcription factor (highlighted in yellow) is co-regulated with other genes of this cluster. The Myb-like transcription factor gene is the only gene of this cluster that does not contain this conserved motif in its promoter. This MYB-  
 35 like factor could be a regulator of this cluster. The second motif does not resemble any known stress responsive plant *cis* element or transcription factor binding site. However, the second motif was found to be strongly represented in promoters from other defense related genes, such as SAR genes. As is typical of many transcription factor binding sites, certain permutations of its consensus

sequence may constitute palindromes. This motif was also found to be conserved by the program MEME.

Table 23

5	Glutathione-conjugate transporter AtMRP4 putative GST putative cytochrome P450 (AC002340) PAD3 (similar to cytochrome P450) CTF2B (similarity to proteins involved in Hydroxylation and oxidation of aromatic rings)	
10	Ribonuclease RNS1 Putative Myb-like protein	
	AlignACE Motif 1:	CAACTTTGAC AA TT
15	type I Myb binding site:	CAACTG T G
	Frequency by chance: 0.05/1kb Observed frequency in control cluster: 0.13/1kb	
20	Observed frequency in this cluster: 1.10/1kb	
	AlignACE Motif2:	TTGGGNCNAA A A
	MEME motif:	GTCTNTTGGGNCAAAA T T A G C
25	Frequency by chance: 0.13/1kb Observed frequency in control cluster: 0/1kb Observed frequency in this cluster: 1.2/1kb	

Different types of transcription factors may participate in the control of distinct *RPP7*-pathway dependent expression profiles. Promoters of genes showing a linear sustained increase of transcript are enriched in different variations of WRKY binding sites. However, no *WRKY*-pathway gene was found to be upregulated by the *RPP7* pathway. Therefore, WRKY factors involved in *RPP7* mediated up-regulation of K-means cluster 3 and 5 genes may already be pre-formed when the pathogen signal is perceived. However, only 21 *WRKY* genes out of 72 members of this family in *Arabidopsis* are represented on the oligonucleotide chip. Upregulated WRKY factors participating in *RPP7* mediated gene regulation may not be present on the chip. A novel type of transcription factor may be involved in regulation of early and transient *RPP7*-controlled genes (K-means cluster 1). Promoter stretches containing this motif may be used in yeast one hybrid screenings for novel factors. In addition, transgenic plants carrying appropriate promoter-reporter constructs could be used

as a basis for mutant screenings with the aim of identifying regulators acting on this motif.

A Myb-like transcription factor appears to be involved in the regulation of early and transient *RPP8*-controlled genes. A gene showing a similar pattern of regulation may encode a candidate factor controlling this cluster. The potential role of this factor in regulating *RPP8*-controlled genes may be examined using T-DNA insertion mutants.

#### Potential constitutive effects of the *RPP7*-pathway

In order to focus on genes showing multiple expression differences between Col-0 wild type plants and Hiks response mutants, all genes that showed at least four 1.8-fold expression differences across all comparisons were selected. The resulting clustergram contains the majority of *RPP7* pathway-dependent Hiks1-induced genes. Two more clusters of genes behaving consistently in all four tested Hiks1-response mutants were found. The first cluster comprises genes that show at all tested time points (including the 0 hpi time point) elevated transcript levels in Col-0 wild type plants as compared to all four mutants (Table 24; genes comprising SEQ ID NOs: 364, 288, 378, 363, 379, 219, 399, 389 and 390). In most cases, expression levels are not affected by Hiks1 infection. These elevated expression levels may be directed by constitutive (non Hiks1-triggered) signal flow via the *RPP7* pathway. This signal flow is disrupted in the *rpp7*, *edm1*, *edm2* and *edm3* mutants. Constitutive expression of these genes may be required for effective disease resistance and may be a prerequisite for induction of subsequent defense responses. A HD-ZIP transcription factor, which is included in this cluster, may act as a pre-formed regulator controlling genes responding to Hiks1-recognition. Its potential role in regulating *RPP7* pathway-dependent genes may be examined using T-DNA insertion mutants.

Table 24

The *RPP7* pathway constitutively activates a cluster of genes including a HD-ZIP transcription factor

PROBE SET	DESCRIPTION
14965 at	AC002329
18635 at	AC004005
14295 s at	Z54356
17386 at	AC006264

15145 s at	D64155
20201 at	AL078470
18607 s at	U78721
20227 s at	AC007153
12761 s at	AC006577
20555 s a	AL080318

Genes of the second cluster show the opposite behavior (Table 25). Their transcript levels are elevated in all four Hiks1 response mutants as compared to Col-0 wild type plants. Hiks1-infection does also not affect their expression levels. Surprisingly, this cluster contains six genes encoding peroxidases. Since peroxidases are believed to play roles in conferring disease resistance, the biological significance of this phenomenon is obscure. Perhaps the mutant plants “realize” disruption of the *RPP7*-defense pathway and compensate for their reduced defense capacity by constitutively up-regulating some defense mechanisms. Alternatively, elevated expression of these peroxidases may be advantageous for invading *Peronospora* hyphae. Therefore, expression of these genes could be constitutively reduced by the *RPP7* pathway.

Table 25

Probe Set	Description
15982_s_at	X98190
15954_at	U72155
12333_at	AJ286345
19594_i_at	X98321
15969_s_at	AJ133036
16462_s_at	AC004683
16461_i_at	AC004683
12324_i_at	AC007212
12778_r_at	AC006577
16514_at	AL035538
17549_s_at	L37126
14028_at	AF075597
17054_s_at	AF134128

#### Predictions about *RPP7*-pathway hierarchy

Clustering of the Hiks1-infection data in the “treatment” dimension, instead of the “gene” dimension, revealed that at all three infection time points, gene expression profiles of the *rpp7* mutant resemble most those of the *edm1* mutant. Similarly, expression profiles of the *edm2* mutant resemble those of the

*edm3* mutant. This may indicate that RPP7 and EDM1 closely act together at a certain level in the *RPP7* signalling cascade, whereas EDM2 and EDM3 may act closely together at a different level of the pathway. Close interaction of RPP7 and EDM1 is also suggested by a T-DNA tagged *rpp7* mutant that

5 phenotypically resembles the *edm1* mutant. In contrast to *rpp7*, *edm2* and *edm3*, which appear only to be compromised in resistance against the *Peronospora* isolate Hiks1, *edm1* is also compromised in resistance to other *Peronospora* isolates that are avirulent on Col-0 plants. Like *edm1*, the putatively T-DNA tagged *rpp7* mutant is also susceptible to a variety of normally Col-0

10 incompatible *Peronospora* isolates. This observation may indicate that the EDM1 protein requires a portion of the RPP7 protein for proper function, which is disrupted in the T- DNA tagged *rpp7* mutant. Assuming that RPP7, which appears to constitute an NBS-LRR receptor, acts at the top of the Hiks1 recognition pathway hierarchy, EDM1 could act at a high level as well and

15 EDM2 and EDM3 may act more downstream in the cascade.

Table 26



Table 27 shows the plant and fungal orthologs of the *Arabidopsis* sequences identified herein.



Table 27

Query= AIG1\_s\_at 12879\_s\_at /id\_source genbank /description  
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1.00e-150

5 (1381 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

	Score	E	
Sequences producing significant alignments:		(bits)	Value
15	gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ...	260	1e-68
	emb AW625701 AW625701 EST319608 tomato radicle, 5 d post-imbibit...	228	6e-59
	emb AW720227 AW720227 LjNEST17c4r Lotus japonicus nodule library...	219	4e-56
	emb AW220184 AW220184 EST302667 tomato root during/after fruit s...	208	7e-53
	emb AI774580 AI774580 EST255680 tomato resistant, Cornell Lycope...	173	2e-42
20	emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t...	171	2e-41
	emb AI443867 AI443867 sa44d09.y1 Gm-c1004 Glycine max cDNA clone...	170	3e-41
	emb AW397252 AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone...	168	1e-40
	emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon...	162	5e-39
	emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two...	153	4e-36
25	emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco...	138	9e-32
	emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycop...	111	2e-23
	emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco...	86	7e-16
	emb AW164180 AW164180 Ljimpest21-672-c8 Ljimp Lambda HybriZap ...	84	2e-15
	emb AI781596 AI781596 EST262475 tomato susceptible, Cornell Lyco...	75	1e-12
30	emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo...	62	7e-09
	emb AW348781 AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ...	54	2e-06
	emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersic...	29	0.010
	emb AW651526 AW651526 EST329980 tomato germinating seedlings, TA...	29	0.011
	emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ...	29	0.011
35	emb AW926585 AW926585 HVSMEG0007J19 Hordeum vulgare pre-anthesis...	29	0.025
	emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon...	28	0.026
	emb AW736598 AW736598 EST333090 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW736597 AW736597 EST333089 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW713727 AW713727 h1f12ne.fl Neurospora crassa evening cDNA ...	35	1.0
40	emb AW711542 AW711542 f3g07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AB009972 AB009972 Aspergillus oryzae gene for beta-1,4-xylos...	35	1.0
	emb AW713709 AW713709 h1e09ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW712721 AW712721 g3a07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW709185 AW709185 d3e02ne.fl Neurospora crassa evening cDNA ...	35	1.0
45	emb Y09354 SPABC1 S.pombe ABC1 gene.	35	1.4
	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9.	35	1.4
	emb AJ225108 STA225108 Solanum tuberosum (cultivar Bintje) mitoc...	35	1.4
	emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ...	26	1.5
	emb Z25870 CACDC10G C.albicans CDC10 gene for cell division cycl...	31	1.5
50	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso...	35	1.9
	emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom...	35	1.9
	emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso...	35	1.9
55	emb AQ643883 AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano...	35	1.9
	emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom...	35	1.9
	emb AW727289 AW727289 GA__Ea0011H24 Gossypium arboreum 7-10 dpa ...	35	1.9
	emb AW729536 AW729536 GA__Ea0025E24 Gossypium arboreum 7-10 dpa ...	35	1.9
	gb L36856 PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR...	28	2.1
60	emb Z28341 PSCLOEP P.sativum (miranda) mRNA for chloroplast oute...	28	2.1

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 emb|AW685649|AW685649 NF032G04NR1F1000 Nodulated root Medicago t... 28 2.2  
 emb|AW690755|AW690755 NF037H10ST1F1000 Developing stem Medicago ... 28 2.2  
 emb|AW256896|AW256896 EST305033 KV2 Medicago truncatula cDNA clo... 28 2.3  
 5 emb|AV422565|AV422565 AV422565 Lotus japonicus young plants (two... 28 2.3  
 emb|AW832303|AW832303 sm07c04.y1 Gm-cl027 Glycine max cDNA clone... 27 2.3  
 emb|AL136538|SPAC30 S.pombe chromosome I cosmid c30. 34 2.6  
 emb|AI724721|AI724721 RHIZ1\_26\_C05.y2\_A001 Rhizome1 Sorghum hale... 34 2.6  
 emb|AW256609|AW256609 EST304746 KV2 Medicago truncatula cDNA clo... 34 2.6  
 10 emb|AI775696|AI775696 EST256796 tomato resistant, Cornell Lycopen... 28 3.1  
 emb|Z71682|SCYNR067C S.cerevisiae chromosome XIV reading frame O... 34 3.6  
 emb|AI776315|AI776315 EST257415 tomato resistant, Cornell Lycopen... 34 3.6  
 emb|AF230371|AF230371 Lycopersicon esculentum allene oxide synth... 34 3.6  
 emb|AA741645|AA741645 LmLv39p3/255A Leishmania major promastigot... 34 3.6  
 15 gb|U08843|PPU08843 Porphyra purpurea putative polysaccharide bin... 34 3.6  
 emb|AF124792|AF124792 Sporothrix schenckii protein kinase C (PCK... 29 4.7  
 emb|AQ399149|AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P... 33 5.0  
 emb|AW615911|AW615911 EST325409 tomato flower buds 0-3 mm, Corne... 33 5.0  
 emb|AW035453|AW035453 EST281191 tomato callus, TAMU Lycopersicon... 33 5.0  
 20 emb|AF051695|AF051695 Trypanosoma cruzi sialidase homolog (P85.1... 33 5.0  
 emb|Z37538|LTGRR4-L.tarentolae mRNA encoding putative NADH subun... 28 5.5  
 emb|X85021|SCXLTORFS S.cerevisiae DNA from left arm of chromosom... 33 6.8  
 gb|L25088|YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi... 33 6.8  
 emb|AQ443826|AQ443826 GSSTc01287 Trypanosoma cruzi random genom... 33 6.8  
 25 emb|AQ502942|AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc... 33 6.8  
 emb|Z85962|MSZ85962 Musa sp. DNA for sequence tagged microsatell... 33 6.8  
 emb|Z49377|SCYJL102W S.cerevisiae chromosome X reading frame ORF... 33 6.8  
 emb|AW224537|AW224537 EST302980 tomato root, plants pre-anthesis... 31 7.5  
 emb|AW257183|AW257183 EST305320 KV2 Medicago truncatula cDNA clo... 32 9.4  
 30 emb|AQ642922|AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos... 32 9.4  
 emb|AW738509|AW738509 EST339936 tomato flower buds, anthesis, Co... 32 9.4  
 emb|AW217351|AW217351 EST296174 tomato flower buds 0-3 mm, Corne... 32 9.4  
 emb|AW219255|AW219255 EST301737 tomato root during/after fruit s... 32 9.4  
 emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 32 9.4  
 35 emb|AW684118|AW684118 NF012F02NR1F1000 Nodulated root Medicago t... 32 9.4  
 emb|AW622239|AW622239 EST313037 tomato root during/after fruit s... 32 9.4  
 emb|AQ651543|AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom... 32 9.4  
 emb|Y11565|NC11565 N.crassa acu-15 gene. 32 9.4  
 emb|AW775944|AW775944 EST335009 DSIL Medicago truncatula cDNA cl... 32 9.4  
 40 emb|AB014493|AB014493 Gibberella zeae gene for reductase, partia... 32 9.4

Query= ASA1\_s\_at 12889\_s\_at /id\_source genbank /description  
 gb|aaa32738.1| (m92353) anthranilate synthase alpha subunit  
 45 [arabidopsis thaliana] /blast\_score 0 /ec\_number /family /chip nova  
 /gb\_link /ncgi  
 (1788 letters)

Database: plantfungal  
 50 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E
55 Sequences producing significant alignments:	(bits)	Value
gb L34344 RTAANTSYNB Ruta graveolens anthranilate synthase alpha...	772	0.0
gb L34343 RTAANTSYNB Ruta graveolens anthranilate synthase alpha...	467	0.0
emb AF079168 AF079168 Nicotiana tabacum feedback-insensitive ant...	365	0.0
60 emb AW931942 AW931942 EST357785 tomato fruit mature green, TAMU ...	356	3e-97
emb AW218352 AW218352 EST303535 tomato radicle, 5 d post-imbibit...	210	1e-73

	emb AL031966 SPCC1442 <i>S.pombe</i> chromosome III cosmid c1442.	209	6e-69
	emb AW651095 AW651095 EST329549 tomato germinating seedlings, TA...	222	2e-64
	dbj D89256 D89256 <i>Schizosaccharomyces pombe</i> mRNA, partial cds, c...	205	5e-64
	emb AW982499 AW982499 HVSMEg0003G22f <i>Hordeum vulgare</i> pre-anthesi...	215	2e-58
5	emb AW460005 AW460005 si07d11.y1 <i>Gm-c1029</i> Glycine max cDNA clone...	116	1e-57
	gb U18839 SCE9747 <i>Saccharomyces cerevisiae</i> chromosome V cosmids ...	123	4e-48
	emb X68327 SCTRP2 <i>S.cerevisiae</i> TRP2 gene for anthranilate syntha...	123	4e-48
	emb AW719463 AW719463 LjNEST5b1r <i>Lotus japonicus</i> nodule library,...	184	1e-45
	emb AI736775 AI736775 sb33d01.y1 <i>Gm-c1012</i> Glycine max cDNA clone...	104	2e-40
10	gb K01388 YSCTRP2 Yeast ( <i>S.cerevisiae</i> ) TRP2 gene coding for anth...	122	4e-38
	emb AL032684 SPBP8B7 <i>S.pombe</i> chromosome II pl p8B7.	95	6e-25
	emb AW509018 AW509018 si39b01.y1 <i>Gm-r1030</i> Glycine max cDNA clone...	113	5e-24
	gb T14852 T14852 crs299 lambdaZAPST <i>Ricinus communis</i> cDNA clone ...	107	2e-22
	emb AW223881 AW223881 EST300692 tomato fruit red ripe, TAMU Lyco...	103	4e-21
15	emb AF119554 AF119554 <i>Plasmodium falciparum</i> para-aminobenzoic ac...	67	6e-10
	emb AL111470 CNS019CM <i>Botrytis cinerea</i> strain T4 cDNA library un...	45	2e-05
	emb AI329873 AI329873 b9g02ne.r1 <i>Neurospora crassa</i> evening cDNA ...	48	3e-04
	emb AW224247 AW224247 EST300974 tomato fruit red ripe, TAMU Lyco...	46	7e-04
	emb AF149719 AF149719 <i>Aspergillus fumigatus</i> para aminobenzoic ac...	42	0.012
20	emb AQ448372 AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ324360 AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P...	39	0.15
	emb AQ160089 AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P...	39	0.15
	emb AW599019 AW599019 gb01b03.y1 Moss EST library PPN Physcomitr...	37	0.38
	emb AW599000 AW599000 ga99h03.y1 Moss EST library PPN Physcomitr...	37	0.38
25	emb AW678847 AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S...	35	0.88
	emb AW680390 AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ...	35	0.89
	emb AW678385 AW678385 WS1_15_H06.g1_A002 Water-stressed 1 (WS1) ...	35	0.89
	emb AW747146 AW747146 WS1_66_E07.b1_A002 Water-stressed 1 (WS1) ...	35	0.89
	emb AW678361 AW678361 WS1_15_H06.b1_A002 Water-stressed 1 (WS1) ...	35	0.90
30	emb AW745749 AW745749 WS1_37_D12.b1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW747427 AW747427 WS1_68_B09.b1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW678071 AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW747468 AW747468 WS1_68_B09.g1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW672427 AW672427 LG1_359_A06.g1_A002 Light Grown 1 (LG1) So...	35	0.90
35	emb AW744836 AW744836 LG1_384_E07.g1_A002 Light Grown 1 (LG1) So...	35	0.90
	emb AW746170 AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ...	35	0.90
	emb AW922317 AW922317 DG1_17_E06.g1_A002 Dark Grown 1 (DG1) Sorg...	35	0.91
	emb AQ648582 AQ648582 RPCI93-EcoRI-1M22.TP RPCI93-EcoRI Trypanos...	36	0.99
	emb AQ643551 AQ643551 RPCI93-EcoRI-3I24.TJ RPCI93-EcoRI Trypanos...	36	0.99
40	emb AI443370 AI443370 sa31b05.x1 <i>Gm-c1004</i> Glycine max cDNA clone...	35	1.4
	emb AW101313 AW101313 sd77d08.y1 <i>Gm-c1009</i> Glycine max cDNA clone...	35	1.4
	emb AW678030 AW678030 WS1_12_B10.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW349006 AW349006 GM210004A12H10R <i>Gm-r1021</i> Glycine max cDNA ...	35	1.4
	emb AW309961 AW309961 sf27b12.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	1.4
45	emb AW678582 AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW317198 AW317198 sf38f03.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	1.4
	emb AW678305 AW678305 WS1_14_G05.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
	emb AW680905 AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S...	35	1.4
	emb AW679666 AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
50	emb AL031746 PFMAL1P3 <i>Plasmodium falciparum</i> MAL1P3, complete seq...	35	1.9
	emb AI959816 AI959816 sc94f02.y1 <i>Gm-c1019</i> Glycine max cDNA clone...	35	1.9
	emb AW924277 AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ...	35	1.9
	gb J03998 PFAGAR <i>Plasmodium falciparum</i> glutamic acid-rich protei...	35	1.9
	emb AW696796 AW696796 NF109A07ST1F1052 Developing stem <i>Medicago</i> ...	35	1.9
55	emb AW396753 AW396753 sf37c11.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	2.6
	gb M98871 SOYCHS7A Glycine max chalcone synthase (chs7) gene, co...	35	2.6
	emb AI460797 AI460797 sa69d02.y1 <i>Gm-c1004</i> Glycine max cDNA clone...	35	2.6
	emb AW348617 AW348617 GM210002B22G1R <i>Gm-r1021</i> Glycine max cDNA 3...	35	2.6
	emb AW310362 AW310362 sf35a09.x1 <i>Gm-c1028</i> Glycine max cDNA clone...	35	2.6
60	emb AI437832 AI437832 sa40c07.y1 <i>Gm-c1004</i> Glycine max cDNA clone...	35	2.6
	gb BE023927 BE023927 sm94c05.y1 <i>Gm-c1015</i> Glycine max cDNA clone ...	35	2.6



	emb AW424189 AW424189 sh62b04.y1 Gm-c1015 Glycine max cDNA clone...	35	2.6
	emb AW101907 AW101907 sd72d01.y1 Gm-c1008 Glycine max cDNA clone...	35	2.6
	emb AW102370 AW102370 sd86h01.y1 Gm-c1009 Glycine max cDNA clone...	35	2.6
	emb AW309356 AW309356 sf16d02.x1 Gm-c1028 Glycine max cDNA clone...	35	2.6
5	emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC ...	34	3.5
	emb AQ652663 AQ652663 Sheared DNA-20A9.TR Sheared DNA Trypanosom...	34	3.5
	emb Z98056 SPAC5D6 S.pombe chromosome I cosmid c5D6.	34	3.5
	emb AW348286 AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3...	34	4.9
	emb AB018422 AB018422 Pisum sativum mRNA for DNA binding zinc fi...	34	4.9
10	emb AW734949 AW734949 sk93b10.y1 Gm-c1035 Glycine max cDNA clone...	34	4.9
	emb AW679089 AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) ...	34	4.9
	emb AW306776 AW306776 sf48c12.y1 Gm-c1009 Glycine max cDNA clone...	34	4.9
	gb M36941 BLYHORDCA Hordeum vulgare C-hordein gene, complete cds.	29	5.3
	gb BE034677 BE034677 ML01H08 ML Mesembryanthemum crystallinum cD...	33	6.7
15	emb Z26877 SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro...	33	6.7
	emb AW267708 AW267708 EST305836 DSIR Medicago truncatula cDNA cl...	33	6.7
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	emb AW980990 AW980990 EST392143 GVN Medicago truncatula cDNA clo...	33	6.7
	gb BE037412 BE037412 MP20G03 MP Mesembryanthemum crystallinum cD...	33	6.7
20	emb Z28161 SCYKL161C S.cerevisiae chromosome XI reading frame OR...	33	6.7
	emb AI726247 AI726247 BNLGH15399 Six-day Cotton fiber Gossypium ...	33	6.7
	emb AE001401 AE001401 Plasmodium falciparum chromosome 2, sectio...	33	6.7
	emb AW573801 AW573801 EST316392 GVN Medicago truncatula cDNA clo...	33	6.7
	emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque...	33	9.2
25	emb AQ659747 AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom...	33	9.2
	gb BE021269 BE021269 sm56h04.y1 Gm-c1028 Glycine max cDNA clone ...	33	9.2
	emb AW222457 AW222457 EST299268 tomato fruit red ripe, TAMU Lyco...	33	9.2
	emb AB012116 AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl...	33	9.2
	emb AW725836 AW725836 GA__Ea0019N24 Gossypium arboreum 7-10 dpa ...	33	9.2
30	emb AQ324451 AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P...	33	9.2
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN...	33	9.2
	emb AW132634 AW132634 se06h07.y1 Gm-c1013 Glycine max cDNA clone...	33	9.2
	emb AI166186 AI166186 a032p32u Hybrid aspen plasmid library Popu...	33	9.2
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35			

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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|atacs6|/ncgi)  
<http://www.ncgr.org/cgi-bin/ff?atacs6>  
(1567 letters)

45 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

50 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
	emb X82273 BOACCS B.oleracea mRNA for ACC synthase.	944	0.0
55	emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo...	833	0.0
	emb AB034992 AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc...	725	0.0
	emb AF057563 AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-...	729	0.0
	emb AJ005002 NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro...	726	0.0
	emb AB034993 AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc...	723	0.0
60	gb U72389 LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1...	724	0.0
	gb U72390 LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1...	720	0.0

	gb U68216 CPU68216	Carica papaya ACC synthase mRNA, complete cds.	435	0.0
	emb AB033503 AB033503	Populus euramericana peacs-2 mRNA for 1-am...	713	0.0
	emb AF061605 AF061605	Nicotiana glutinosa ACC synthase mRNA, com...	712	0.0
	emb AJ012551 CSI012551	Citrus sinensis mRNA for ACC synthase.	420	0.0
5	emb AB033502 AB033502	Populus euphratica peacs-1 mRNA for 1-amin...	591	0.0
	emb AB013100 AB013100	Lycopersicon esculentum LE-ACS6 mRNA for 1...	706	0.0
	emb AB013346 AB013346	Lycopersicon esculentum mRNA for 1-aminocy...	704	0.0
	gb U88971 PHU88971	Pelargonium hortorum 1-aminocyclopropane-1-ca...	423	0.0
	emb Z11613 VRACCSYNM	V.radiata mRNA for ACC synthase.	428	0.0
10	emb X98492 NTACCS	Nicotiana tabacum mRNA for ACC-synthase (clone...	425	0.0
	emb X67100 GMCACCS1	G.max mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSI012696	Citrus sinensis mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY	P.hybrida mRNA for 1-aminocyclopropane 1-ca...	424	0.0
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15	emb Z18952 DCAMCRBSY	D.caryophyllus mRNA for 1-aminocyclopropane...	686	0.0
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	emb AF080258 AF080258	Musa acuminata 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459	Pisum sativum 1-aminocyclopropane-1-carbox...	415	0.0
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20	emb X65982 NTXACCSYN	N.tabacum mRNA for 1-aminocyclopropane-1-ca...	417	0.0
	emb AF109927 AF109927	Musa acuminata 1-aminocyclopropane-1-carbo...	676	0.0
	emb AB006803 AB006803	Cucumis sativus CS-ACS1 mRNA for ACC synth...	676	0.0
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25	emb AF129508 AF129508	Musa acuminata 1-aminocyclopropane-1-carbo...	671	0.0
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	emb AB031026 AB031026	Prunus mume PM-ACS1 mRNA for ACC synthase,...	405	0.0
	emb Y11357 CP1A1CS	C.papaya mRNA for 1-aminocyclopropane-1-carbo...	404	0.0
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	gb M58323 CUCACCSYN	Cucurbita pepo 1-aminocyclopropane-1-carboxy...	663	0.0
35	emb AF057562 AF057562	Nicotiana glutinosa 1-aminocyclopropane-1-...	412	0.0
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50	gb U73815 MDU73815	Malus domestica ACC synthase (MdACS-2) mRNA, ...	623	e-178
	dbj D37937 D37937	Cucumis melo mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN	V.radiata mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769	Carica papaya 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814	Antirrhinum majus ACC synthase 1 (ACS1) mR...	605	e-172
55	emb AF178077 AF178077	Carica papaya 1-aminocyclopropane-1-carbox...	316	e-171
	emb AF239989 AF239989	Prunus persica ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523	Mangifera indica 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS	D.caryophyllus mRNA for 1-aminocyclopropane-1-...	396	e-168
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60	emb AF170705 AF170705	Mangifera indica 1-aminocyclopropane-1-car...	290	e-167
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 gb|L31347|MAUACCSYN *Malus domestica* 1-aminocyclopropane-1-carbox... 357 e-162  
 emb|AB015495|AB015495 *Passiflora edulis* PE-ACS2 mRNA for ACC synth... 368 e-162  
 5 emb|Z77854|PSPACS1 *Phalaenopsis* species mRNA for 1-aminocyclopro... 514 e-161  
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 emb|X87112|PCPCACS1G *P. communis* mRNA for 1-aminocyclopropane-1-c... 346 e-159  
 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclop... 336 e-159  
 gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 504 e-158  
 10 gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1... 343 e-157  
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 20 emb|Z27234|STACCAS2 *S. tuberosum* STACS2 gene for 1-Aminocycloprop... 234 e-146  
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 25 gb|U18055|LEU18055 *Lycopersicon esculentum* 1-aminocyclopropane-1... 236 e-143  
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 30 gb|L07883|DORAMICARB *Moth orchid* 1-aminocyclopropane-1-carboxyla... 243 e-139  
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40 Database: plantfungal  
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	emb X82273 BOACCS <i>B. oleracea</i> mRNA for ACC synthase.	944 0.0
	emb X72676 BJMACC <i>B. juncea</i> mRNA for 1-Aminocyclopropane-1-carbo...	833 0.0
50	emb AB034992 AB034992 <i>Malus domestica</i> MdACS-5A mRNA for 1-aminoc...	725 0.0
	emb AF057563 AF057563 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-...	729 0.0
	emb AJ005002 NTAJ5002 <i>Nicotiana tabacum</i> mRNA for 1-aminocyclopro...	726 0.0
	emb AB034993 AB034993 <i>Malus domestica</i> MdACS-5B mRNA for 1-aminoc...	723 0.0
	gb U72389 LEU72389 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1...	724 0.0
55	gb U72390 LEU72390 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1...	720 0.0
	gb U68216 CPU68216 <i>Carica papaya</i> ACC synthase mRNA, complete cds.	435 0.0
	emb AB033503 AB033503 <i>Populus euramericana</i> peacs-2 mRNA for 1-am...	713 0.0
	emb AF061605 AF061605 <i>Nicotiana glutinosa</i> ACC synthase mRNA, com...	712 0.0
	emb AJ012551 CSI012551 <i>Citrus sinensis</i> mRNA for ACC synthase.	420 0.0
60	emb AB033502 AB033502 <i>Populus euphratica</i> peacs-1 mRNA for 1-amin...	591 0.0
	emb AB013100 AB013100 <i>Lycopersicon esculentum</i> LE-ACS6 mRNA for 1...	706 0.0

	emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy...	704	0.0
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	emb Z11613 VRACCSYNM <i>V.radiata</i> mRNA for ACC synthase.	428	0.0
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5	emb X67100 GMCACCS1 <i>G.max</i> mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSI012696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY <i>P.hybrida</i> mRNA for 1-aminocyclopropane 1-ca...	424	0.0
	emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac...	424	0.0
	emb Z18952 DCAMCRBSY <i>D.caryophyllus</i> mRNA for 1-aminocyclopropane...	686	0.0
10	emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth...	423	0.0
	emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459 <i>Pisum sativum</i> 1-aminocyclopropane-1-carbox...	415	0.0
	dbj D30805 CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy...	678	0.0
	emb X65982 NTXACCSYN <i>N.tabacum</i> mRNA for 1-aminocyclopropane-1-ca...	417	0.0
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	emb AB021906 AB021906 <i>Musa acuminata</i> MA-ACS1 mRNA for ACC syntha...	671	0.0
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	gb M63490 TOMACCS Tomato 1-aminocyclopropane-1-carboxylate synth...	657	0.0
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35	gb U79999 MAU79999 <i>Musa acuminata</i> ACC synthase (acs3) mRNA, comp...	655	0.0
	emb AF178076 AF178076 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	395	0.0
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	gb U73815 MDU73815 <i>Malus domestica</i> ACC synthase (MdACS-2) mRNA, ...	623	e-178
45	dbj D37937 D37937 <i>Cucumis melo</i> mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN <i>V.radiata</i> mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814 <i>Antirrhinum majus</i> ACC synthase 1 (ACS1) mR...	605	e-172
	emb AF178077 AF178077 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	316	e-171
50	emb AF239989 AF239989 <i>Prunus persica</i> ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523 <i>Mangifera indica</i> 1-aminocyclopropane-carboxyl...	359	e-169
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	emb AF170705 AF170705 <i>Mangifera indica</i> 1-aminocyclopropane-1-car...	290	e-167
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60	emb Z77854 PSPACS1 <i>Phalaenopsis species</i> mRNA for 1-aminocyclopro...	514	e-161
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 emb|Z27234|STACCAS2 *S.tuberosum* STACS2 gene for 1-Aminocycloprop... 234 e-146  
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 25 emb|AB021908|AB021908 *Musa acuminata* MA-ACS3 mRNA for ACC syntha... 298 e-138

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35 Database: plantfungal  
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- emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24  
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30 Database: plantfungal  
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Database: plantfungal  
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25 Database: plantfungal  
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Searching.....done

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20 Database: plantfungal  
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Searching:.....done

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(528 letters)

20 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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25 Score E  
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

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			(bits) Value
20	Sequences producing significant alignments:		
	emb X62120 BNCRU1 B.napus cru1 gene for cruciferin subunit.	169	4e-48
	gb J05233 BNACRUCA B.napus cruciferin mRNA, 3' end.	169	9e-48
	emb X59808 RSCRUG R.sativus pgCruRsE5 gene for cruciferin.	168	4e-43
	emb X59802 RSCRUI R.sativus pAF7 mRNA for cruciferin.	165	1e-42
25	emb X59804 RSCRUI R.sativus pAC2 mRNA for cruciferin.	123	1e-41
	emb X57850 BNCRU4RN B.napus cru4 mRNA for cruciferin cru4 subunit.	138	2e-32
	emb X57848 BNCRU4RNA B.napus cru4 mRNA for cruciferin cru4 subunit.	137	6e-32
	gb M16860 BNACRUC Rapeseed cruciferin mRNA, complete cds.	132	1e-30
	emb X59294 BNC1G B.napus BnCl gene for cruciferin storage protein.	132	1e-30
30	emb X14555 BNCRUA Brassica napus cruA gene for cruciferin.	132	1e-30
	emb X57849 BNCRU23 B.napus cru2/3 mRNA for cruciferin cru2/3 sub...	132	1e-30
	emb X59807 RSCRUI R.sativus pAE10 mRNA for cruciferin.	131	3e-30
	emb X59806 RSCRUI R.sativus pBB6 mRNA for cruciferin.	131	3e-30
	emb X59295 BNC2G B.napus BnCl gene for cruciferin storage protein.	130	5e-30
35	emb X82121 AHGLOBLN A.hypochondriacus mRNA for globulin.	118	3e-26
	gb U38914 CSU38914 Citrus sinensis seed storage protein citrin m...	108	3e-23
	emb X59803 RSCRUI R.sativus pAG4 mRNA for cruciferin.	81	3e-22
	emb AF262998 AF262998 Ricinus communis legumin-like protein mRNA...	104	4e-22
	gb T14851 T14851 crs298 lambdaZAPST Ricinus communis cDNA clone ...	99	2e-20
40	emb X82464 MSLEGA2 M.salicifolia mRNA for legumin precursor (A2).	99	2e-20
	emb X78119 PABTPRU1 P.amygdalus, Batsch (Texas) pru1 mRNA.	99	2e-20
	gb T23274 T23274 crs1128 lambdaZAPST Ricinus communis cDNA clone...	98	3e-20
	emb AF262999 AF262999 Ricinus communis seed storage protein mRNA...	98	3e-20
	gb T15203 T15203 crs691 lambdaZAPST Ricinus communis cDNA clone ...	98	3e-20
45	gb T14921 T14921 crs404 lambdaZAPST Ricinus communis cDNA clone ...	98	3e-20
	gb T15096 T15096 crs739 lambdaZAPST Ricinus communis cDNA clone ...	98	4e-20
	emb X78120 PABTPRU2 P.amygdalus, Batsch (Texas) pru2 mRNA.	97	6e-20
	emb X82463 MSLEGA11 M.salicifolia mRNA for legumin precursor (A1...	97	8e-20
	gb T15159 T15159 crs641 lambdaZAPST Ricinus communis cDNA clone ...	95	4e-19
50	gb U64443 CAU64443 Coffea arabica 11S storage globulin mRNA, com...	94	5e-19
	gb T24329 T24329 crs1443 lambdaZAPST Ricinus communis cDNA clone...	93	1e-18
	gb U43727 GHU43727 Gossypium hirsutum legumin B (LegB-C134) gene...	92	2e-18
	gb M16936 COTSPB G.hirsutum (cotton) storage protein (beta-globu...	92	2e-18
	emb AF054895 AF054895 Coffea arabica 11S storage globulin mRNA, ...	92	2e-18
55	emb Y16976 CAR16976 Coffea arabica mRNA for 11S storage protein.	92	3e-18
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	emb AW036288 AW036288 EST278367 tomato seed, TAMU Lycopersicon e...	90	7e-18
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60	emb Y09116 SSPPLEGUM S.sagittifolia mRNA for pre-pro-legumin.	89	2e-17
	emb X82465 MSLEGB14 M.salicifolia mRNA for legumin precursor (B14).	89	2e-17

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5	emb AF152003 AF152003 Fagopyrum esculentum major allergenic stor...	87 6e-17
	emb AW036551 AW036551 EST283050 tomato seed, TAMU Lycopersicon e...	87 6e-17
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10	emb X68648 AS12S A.sativa pseudogene for 12S seed globulin.	86 1e-16
	gb M69188 COTDGALA Cotton legumin A D-genome alloallele gene, co...	86 1e-16
	gb M16905 COTSPD G.hirsutum (cotton) storage protein (beta-globu...	86 1e-16
	emb X74741 ASGLAV3G A.sativa GLAV 3 gene for 11S globulin.	86 1e-16
	emb AF091842 AF091842 Sesamum indicum strain Tainan 1 11S globul...	86 2e-16
15	gb J05485 ASTSSP12S A.sativa 12S globulin seed storage protein g...	85 2e-16
	emb X17637 AS12SSP Oat gene for 12S seed storage protein.	85 2e-16
	gb T24158 T24158 crs141 lambdaZAPST Ricinus communis cDNA clone ...	85 3e-16
	emb X15121 GMGY1 Soybean Gyl gene for glycinin subunit G1.	84 4e-16
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20	gb M36686 SOYGLYBSU Soybean glycinin A-1a-B-x subunit mRNA, comp...	84 4e-16
	emb AW318204 AW318204 sg62d03.y1 Gm-c1007 Glycine max cDNA clone...	84 4e-16
	emb AW397452 AW397452 sg79a12.y1 Gm-c1007 Glycine max cDNA clone...	84 4e-16
	gb T14825 T14825 crs267 lambdaZAPST Ricinus communis cDNA clone ...	84 4e-16
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25	emb AI748751 AI748751 sb61e06.y1 Gm-c1010 Glycine max cDNA clone...	84 4e-16
	emb X02985 GMGLY1A Soybean mRNA for glycinin A1aBx precursor.	84 4e-16
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	dbj E08573 E08573 cDNA encoding 12S globulin A2B of oats.	84 6e-16
	emb X76738 AS12SGLOB A.sativa (L) mRNA for 12S globulin (1685 bp).	84 6e-16
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	emb AW036283 AW036283 EST278362 tomato seed, TAMU Lycopersicon e...	83 1e-15
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	emb AF193433 AF193433 Elaeis guineensis glutelin (PKT9) mRNA, co...	81 4e-15
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55	gb M16868 ASTGLOB Oat storage protein 12S globulin mRNA, partial...	81 5e-15
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 (965 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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emb AB000408 AB000408 Populus kitakamiensis mRNA for caffeoyl-Co...	215	3e-73	
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emb AW624860 AW624860 EST313689 tomato radicle, 5 d post-imbibit...	139	2e-67	
emb AF022775 AF022775 Nicotiana tabacum caffeoyl-CoA 3-O-methylt...	138	2e-67	
emb Z54233 VCCCOAOMT V.vinifera mRNA for caffeoyl-CoA O-methyltr...	136	9e-67	
gb M69184 PUMCCOAMT Petroselinum crispum caffeoyl-CoA 3-O-methyl...	133	2e-66	
gb U27116 PTU27116 Populus tremuloides caffeoyl-CoA 3-O-methyltr...	135	3e-66	
emb AJ224894 PBT AJ4894 Populus balsamifera subsp. trichocarpa mR...	135	3e-66	
gb U13151 ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-...	136	4e-66	
emb AI489305 AI489305 EST247644 tomato ovary, TAMU Lycopersicon ...	139	4e-66	
emb AJ224895 PBT AJ4895 Populus balsamifera subsp. trichocarpa mR...	136	6e-66	
emb AJ224896 PBT AJ4896 Populus balsamifera subsp. trichocarpa mR...	136	6e-66	
emb AF168780 AF168780 Eucalyptus globulus caffeoyl-CoA O-methylt...	133	8e-66	
emb AF053553 AF053553 Mesembryanthemum crystallinum caffeoyl-CoA...	132	1e-65	
emb AF240466 AF240466 Populus tomentosa caffeoyl-CoA O-methyltra...	135	1e-65	
emb A22706 A22706 Caffeoyl-CoA-3-O-Methyltransferase gene.	129	3e-65	
gb U62734 NTU62734 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134	5e-65	
emb Z56282 NTCCOAOMT N.tabacum mRNA for caffeoyl-CoA O-methyltra...	132	5e-65	
gb U62736 NTU62736 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	136	5e-65	
gb U38612 NTU38612 Nicotiana tabacum caffeoyl-coenzymeA O-methyl...	136	5e-65	
emb Y12228 EG12228 E.gunnii mRNA for caffeoyl-CoA O-methyltransf...	133	7e-65	
gb L22203 SLASADEN Stellaria longipes S-adenosyl-L-methionine:tr...	124	8e-65	
emb AF046122 AF046122 Eucalyptus globulus caffeoyl-CoA 3-O-methy...	133	9e-65	
gb U62735 NTU62735 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134	3e-64	
emb AF036095 AF036095 Pinus taeda caffeoyl-CoA O-methyltransfera...	130	6e-64	
emb AF060180 AF060180 Nicotiana tabacum caffeoyl-coenzyme A trun...	90	9e-60	
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emb AW030736 AW030736 EST273991 tomato callus, TAMU Lycopersicon...	133	8e-53	
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	emb AW733300 AW733300 sk71f10.y1 Gm-c1016 Glycine max cDNA clone...	134	1e-52
	emb AW442463 AW442463 EST307393 tomato mixed elicitor, BTI Lycop...	133	1e-52
5	emb AW094365 AW094365 EST287545 tomato mixed elicitor, BTI Lycop...	133	1e-52
	gb BE021597 BE021597 sm60a04.y1 Gm-c1028 Glycine max cDNA clone ...	135	1e-52
	emb AW034347 AW034347 EST277918 tomato callus, TAMU Lycopersicon...	133	2e-52
	emb AI443130 AI443130 sa84g01.y1 Gm-c1004 Glycine max cDNA clone...	131	2e-51
	emb AI898952 AI898952 EST268395 tomato ovary, TAMU Lycopersicon ...	139	2e-51
10	emb AW424002 AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone...	115	2e-51
	emb AW707192 AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone...	132	3e-50
	emb AI899227 AI899227 EST268670 tomato ovary, TAMU Lycopersicon ...	139	3e-50
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	emb AW776435 AW776435 EST335500 DSIL Medicago truncatula cDNA cl...	142	5e-47
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	emb Z82982 NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran...	136	1e-39
55	emb AW218486 AW218486 EST303669 tomato radicle, 5 d post-imbibit...	136	1e-39

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(827 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

10

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 emb|AI490284|AI490284 EST248610 tomato ovary, TAMU Lycopersicon ... 103 2e-22  
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 emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17  
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 emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17  
 45 gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17  
 gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17  
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 50 emb|AW830090|AW830090 sm22a12.y1 Gm-c1028 Glycine max cDNA clone... 64 8e-17  
 emb|AW126204|AW126204 N100049e rootphos(-) Medicago truncatula c... 57 8e-17  
 emb|X52242|TTCALM T.thermophila mRNA for calmodulin. 73 1e-16  
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 55 gb|K02944|TRBCMRSG Trypanosoma brucei gambiense calmodulin genes... 73 2e-16  
 gb|M88307|BNACALM Brassica juncea calmodulin mRNA, complete cds. 73 2e-16  
 gb|U10150|BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,... 73 2e-16  
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 60 emb|AW101324|AW101324 sd77e09.y1 Gm-c1009 Glycine max cDNA clone... 59 2e-16  
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 5 emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16  
 emb|AL116760|CNS01DFK Botrytis cinerea strain T4 cDNA library un... 73 2e-16  
 emb|AW573768|AW573768 EST316359 GVN Medicago truncatula cDNA clo... 72 2e-16  
 emb|Y13784|MSCALMODU Mougeotia scalaris mRNA for calmodulin. 70 3e-16  
 emb|AI727960|AI727960 BNLGHi9833 Six-day Cotton fiber Gossypium ... 73 3e-16  
 emb|AA660367|AA660367 00239 MtRHE Medicago truncatula cDNA 5' si... 71 3e-16  
 10 emb|AW164628|AW164628 se74e01.y1 Gm-c1023 Glycine max cDNA clone... 60 3e-16  
 emb|AF150059|AF150059 Brassica napus calmodulin (CaM1) mRNA, com... 72 3e-16  
 emb|AW738989|AW738989 gb23c06.y1 Moss EST library PPN Physcomitr... 73 3e-16  
 gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16  
 gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16  
 15 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16  
 emb|AF064552|AF064552 Apium graveolens calmodulin mRNA, complete... 73 4e-16  
 gb|S81594|S81594 auxin-regulated calmodulin [Vigna radiata=mung ... 73 4e-16  
 gb|L20691|VIRCALMOD Vigna radiata calmodulin mRNA, complete cds. 73 4e-16  
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 20 gb|BE036340|BE036340 MO23E04 MO Mesembryanthemum crystallinum cD... 73 4e-16  
 emb|AF030032|AF030032 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16  
 gb|L01431|SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds. 73 4e-16  
 emb|Y09853|CACAM Cicer arietinum mRNA for CaM protein. 73 4e-16  
 gb|L01432|SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds. 73 4e-16  
 25 gb|U49104|TAU49104 Triticum aestivum calmodulin TaCaM3-3 mRNA, c... 73 4e-16  
 gb|U49105|TAU49105 Triticum aestivum calmodulin TaCaM4-1 mRNA, c... 73 4e-16  
 emb|AF030034|AF030034 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16  
 emb|AW728030|AW728030 GA\_\_Ea0029H21 Gossypium arboreum 7-10 dpa ... 73 4e-16  
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 30 gb|U48242|TAU48242 Triticum aestivum calmodulin TaCaM1-1 mRNA, c... 73 4e-16  
 gb|M80836|PETCAM81 Petunia hybrida CAM81 mRNA, 73 4e-16  
 gb|U49103|TAU49103 Triticum aestivum calmodulin TaCaM3-2 mRNA, c... 73 4e-16  
 emb|X52398|MSCAL1 Alfalfa call mRNA for calmodulin. 73 4e-16  
 gb|U48688|TAU48688 Triticum aestivum calmodulin TaCaM1-2 mRNA, c... 73 4e-16  
 35 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16  
 emb|AW927068|AW927068 HVSMEg0009G21 Hordeum vulgare pre-anthesis... 73 4e-16  
 gb|U48689|TAU48689 Triticum aestivum calmodulin TaCaM1-3 mRNA, c... 73 4e-16  
 gb|M80831|PETCALPRO Petunia hybrida CAM53 mRNA, complete cds. 73 4e-16  
 emb|AW348582|AW348582 GM210002B22C3R Gm-r1021 Glycine max cDNA 3... 73 4e-16  
 40 emb|X59751|DCCAM1G Carrot Ccam-1 gene for calmodulin. 73 4e-16  
 emb|AW775754|AW775754 EST334819 DSIL Medicago truncatula cDNA cl... 73 4e-16  
 gb|BE052400|BE052400 GA\_\_Ea0001L24f Gossypium arboreum 7-10 dpa ... 73 4e-16  
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 gb|U13882|PSU13882 Pisum sativum Alaska calmodulin mRNA, complet... 73 4e-16  
 45 gb|BE051931|BE051931 GA\_\_Ea0002G11f Gossypium arboreum 7-10 dpa ... 73 4e-16  
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 emb|AW108833|AW108833 gate0001L24f Gossypium arboreum 7-10 dpa f... 73 4e-16  
 emb|Z12839|LLCALMOD L.longiflorum mRNA encoding calmodulin. 73 4e-16  
 gb|L18912|LILCALMODU Lilium longiflorum calmodulin mRNA, complet... 73 4e-16  
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 thaliana] /blast\_score 1.00e-113 /ec\_number /family /chip nova  
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 (1408 letters)

55

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

60

Score E

Sequences producing significant alignments:

(bits) Value

	emb AB014483 AB014483 Nicotiana tabacum NtHSF1 mRNA for heat sho...	213	2e-62
	emb X55347 LPHSF24 Tomato mRNA for heat stress transcription fac...	210	2e-53
5	emb AI900223 AI900223 sc02f05.y1 Gm-c1012 Glycine max cDNA clone...	205	3e-53
	emb Z46953 GMHSF34 G.max mRNA for heat shock transcription facto...	203	6e-53
	emb AV408054 AV408054 AV408054 Lotus japonicus young plants (two...	203	3e-51
	emb AV415115 AV415115 AV415115 Lotus japonicus young plants (two...	197	2e-49
	emb AW774951 AW774951 EST334102 KV3 Medicago truncatula cDNA clo...	194	1e-48
10	emb AW689532 AW689532 NF021G10ST1F1000 Developing stem Medicago ...	194	1e-48
	emb AI728175 AI728175 BNLGHi10028 Six-day Cotton fiber Gossypium...	192	5e-48
	emb AI055366 AI055366 coau0003M17 Cotton Boll Abscission Zone cD...	191	1e-47
	emb AW703969 AW703969 skl4g08.y1 Gm-c1023 Glycine max cDNA clone...	191	1e-47
	emb AW428882 AW428882 Ljirmp25-001-b9 Ljirmp Lambda HybriZap ...	190	2e-47
15	emb AW931781 AW931781 EST357624 tomato fruit mature green, TAMU ...	189	3e-47
	emb AW686121 AW686121 NF033H01NR1F1000 Nodulated root Medicago t...	188	1e-46
	emb Z46956 GMHSF5 G.max mRNA for heat shock transcription factor 5.	185	6e-46
	emb AW109013 AW109013 gate0002O16f Gossypium arboreum 7-10 dpa f...	179	4e-44
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20	gb BE020791 BE020791 sm52h09.y1 Gm-c1028 Glycine max cDNA clone ...	178	1e-43
	emb AW696868 AW696868 NF111F05ST1F1046 Developing stem Medicago ...	166	3e-43
	emb AW686271 AW686271 NF039H06NR1F1000 Nodulated root Medicago t...	171	5e-42
	emb AW931176 AW931176 EST357019 tomato fruit mature green, TAMU ...	168	8e-41
	gb C95479 C95479 C95479 Citrus unshiu Miyagawa-wase maturation s...	166	5e-40
25	emb AW033421 AW033421 EST276992 tomato callus, TAMU Lycopersicon...	165	1e-39
	emb AW030725 AW030725 EST273980 tomato callus, TAMU Lycopersicon...	165	1e-39
	emb AW041695 AW041695 EST284559 tomato mixed elicitor, BTI Lycop...	165	1e-39
	emb AW217982 AW217982 EST296697 tomato flower buds, anthesis, Co...	165	1e-39
	emb X67600 LPHSF8 L.peruvianum Lp-hsf8 mRNA for heat stress tran...	161	1e-38
30	emb AW774397 AW774397 EST333548 KV3 Medicago truncatula cDNA clo...	160	2e-38
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	emb AW738023 AW738023 EST339450 tomato flower buds, anthesis, Co...	150	2e-35
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35	emb AI729182 AI729182 BNLGHi12855 Six-day Cotton fiber Gossypium...	149	5e-35
	emb AI489721 AI489721 EST248060 tomato ovary, TAMU Lycopersicon ...	149	5e-35
	emb AW034402 AW034402 EST277973 tomato callus, TAMU Lycopersicon...	148	7e-35
	emb X67601 LPHSF30 L.peruvianum Lp-hsf30 mRNA for heat stress tr...	148	9e-35
	emb AW906822 AW906822 EST342945 potato stolon, Cornell Universit...	147	2e-34
40	emb AW164509 AW164509 se74f12.y1 Gm-c1023 Glycine max cDNA clone...	147	2e-34
	emb AW034874 AW034874 EST279103 tomato callus, TAMU Lycopersicon...	147	2e-34
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	emb Z46952 GMHSF21 G.max mRNA for heat shock transcription facto...	145	8e-34
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45	emb AW222011 AW222011 EST298822 tomato fruit red ripe, TAMU Lyco...	144	2e-33
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	emb AB014484 AB014484 Nicotiana tabacum NtHSF2 mRNA for heat sho...	140	3e-32
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50	emb AW738534 AW738534 EST339961 tomato flower buds, anthesis, Co...	139	5e-32
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	emb AW874988 AW874988 00109 leafy spurge Lambda HybriZAP 2.1 two...	138	1e-31
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	emb AV415736 AV415736 AV415736 Lotus japonicus young plants (two...	138	1e-31
55	emb AW979619 AW979619 EST341218 tomato root deficiency, Cornell ...	137	2e-31
	emb AW932142 AW932142 EST357985 tomato fruit mature green, TAMU ...	136	3e-31
	emb Z46954 GMHSF33 G.max mRNA for heat shock transcription facto...	135	9e-31
	emb AW569138 AW569138 si63g09.y1 Gm-r1030 Glycine max cDNA clone...	134	1e-30
	emb AW569256 AW569256 si64g09.y1 Gm-r1030 Glycine max cDNA clone...	134	1e-30
60	emb AW203851 AW203851 sf38h11.y1 Gm-c1028 Glycine max cDNA clone...	133	3e-30
	emb AW220758 AW220758 EST297227 tomato fruit mature green, TAMU ...	132	6e-30



- emb|AI728806|AI728806 BNLGH11701 Six-day Cotton fiber Gossypium... 108 2e-28  
 emb|AW736596|AW736596 EST333088 KV3 Medicago truncatula cDNA clo... 103 3e-28  
 emb|AI895934|AI895934 EST265377 tomato callus, TAMU Lycopersicon... 123 2e-27  
 5 emb|Z46951|GMHSF29 G.max mRNA for heat shock transcription facto... 120 2e-26  
 gb|BE019974|BE019974 sm38b12.y1 Gm-cl028 Glycine max cDNA clone ... 119 6e-26  
 emb|Z46955|GMHSF31 G.max mRNA for heat shock transcription facto... 115 8e-25  
 emb|X67599|LEHSF8 L.esculentum Le-hsf8 gene for heat stress tran... 114 2e-24  
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 emb|AW775388|AW775388 EST334453 DSIL Medicago truncatula cDNA cl... 66 1e-23  
 10 emb|AW931892|AW931892 EST357735 tomato fruit mature green, TAMU ... 104 2e-21  
 emb|AQ579623|AQ579623 T135087b shotgun sub-library of BAC clone ... 103 4e-21  
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 15 emb|AV413314|AV413314 AV413314 Lotus japonicus young plants (two... 102 8e-21  
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 emb|AI895294|AI895294 EST264737 tomato callus, TAMU Lycopersicon... 101 1e-20  
 emb|AJ010644|PSA010643 Pisum sativum hsfA gene, exons 1 to 2, pa... 99 7e-20  
 emb|AW924303|AW924303 WS1\_52\_H11.b1\_A002 Water-stressed 1 (WS1) ... 99 7e-20  
 20 emb|AI895834|AI895834 EST265277 tomato callus, TAMU Lycopersicon... 95 9e-19  
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 25 emb|AW933448|AW933448 EST359387 tomato fruit mature green, TAMU ... 89 8e-17  
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 emb|AZ045432|AZ045432 T234030b shotgun sub-library of BAC clone ... 84 2e-15  
 emb|X83031|SCPOS9 S.cerevisiae POS9 gene. 83 5e-15  
 gb|U00485|YSCSKN7 Saccharomyces cerevisiae putative transcriptio... 83 5e-15  
 30 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 83 5e-15  
 emb|Z69726|SPAC2E12 S.pombe chromosome I cosmid c2E12. 83 6e-15  
 gb|M22040|YSCHSF1A S.cerevisiae heat shock transcription factor ... 81 2e-14  
 emb|Z72596|SCYGL074C S.cerevisiae chromosome VII reading frame O... 81 2e-14  
 gb|J03139|YSCHSF S.cerevisiae heat shock factor gene (HSF), comp... 81 2e-14  
 35 emb|AI212342|AI212342 x3c12a1.rl Aspergillus nidulans 24hr asexu... 73 8e-14  
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 emb|AZ048458|AZ048458 PSB119 Barley PstI genomic clones Hordeum ... 78 2e-13  
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 emb|AW933529|AW933529 EST359288 tomato fruit mature green, TAMU ... 72 1e-11  
 40 emb|AW307441|AW307441 sf57a06.y1 Gm-cl009 Glycine max cDNA clone... 70 5e-11  
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 /gb\_link http://www3.ncbi.nlm.nih.gov/htbin-  
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 http://www.ncgr.org/cgi-bin/ff?hsp176a  
 50 (613 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

55 Searching.....done

Score E  
 Sequences producing significant alignments: (bits) Value

- 60 gb|M33901|PEAHSP177A Pisum sativum 17.7 kDa heat shock protein (... 126 3e-44  
 gb|M99429|PHNSHSPA Ipomoea nil small heat shock protein, complet... 171 4e-42

- emb|X98617|MSSH17KD M.sativa mRNA for 17kD heat shock protein. 171 6e-42  
emb|AF159562|AF159562 Prunus dulcis cytosolic class II low molec... 105 7e-42  
gb|L47740|PIAEMB29R Picea glauca class II cytoplasmic small mole... 169 2e-41  
emb|AW569703|AW569703 si79c12.y1 Gm-c1031 Glycine max cDNA clone... 107 6e-41  
5 emb|X99346|PASHSP P.abies mRNA for small heat shock protein. 166 1e-40  
emb|AW667877|AW667877 GA\_\_Ea0011C02 Gossypium arboreum 7-10 dpa ... 110 2e-40  
emb|AW725392|AW725392 GA\_\_Ea0017J18 Gossypium arboreum 7-10 dpa ... 110 2e-40  
emb|AW569553|AW569553 si88e08.y1 Gm-c1031 Glycine max cDNA clone... 107 1e-39  
emb|AW620261|AW620261 si93g10.y1 Gm-c1031 Glycine max cDNA clone... 107 1e-39  
10 gb|BE053976|BE053976 GA\_\_Ea0002N06f Gossypium arboreum 7-10 dpa ... 110 3e-39  
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15 emb|AW569546|AW569546 si88e01.y1 Gm-c1031 Glycine max cDNA clone... 103 2e-38  
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emb|AW570000|AW570000 si85d08.y1 Gm-c1031 Glycine max cDNA clone... 104 1e-37  
emb|AW730881|AW730881 GA\_\_Ea0029C17 Gossypium arboreum 7-10 dpa ... 103 3e-37  
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20 emb|AI812703|AI812703 18B10 Pine Lambda Zap Xylem library Pinus ... 145 3e-34  
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emb|AB027500|AB027500 Daucus carota Dchsp-1 mRNA, complete cds. 98 2e-26  
25 emb|AJ225049|LPAJ5049 Lycopersicon peruvianum mRNA for Hsp20.2 p... 105 8e-26  
emb|AF090115|AF090115 Lycopersicon esculentum cytosolic class II... 106 3e-25  
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30 emb|AW569456|AW569456 si87d04.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW569687|AW569687 si79b06.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW568954|AW568954 si73e12.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW569158|AW569158 si75b01.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW568867|AW568867 si73c04.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
35 emb|AW569632|AW569632 si89d12.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW569640|AW569640 si89e09.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW568707|AW568707 si72b01.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW569586|AW569586 si88h09.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
emb|AW620228|AW620228 si93d08.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24  
40 gb|L47717|PIAEMB27R Picea glauca heat shock protein 17.0 (EMB27)... 110 1e-23  
emb|AW570013|AW570013 si85f01.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23  
emb|AW185394|AW185394 se90h07.y1 Gm-c1027 Glycine max cDNA clone... 108 3e-23  
emb|AW620212|AW620212 si93c03.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23  
emb|AI900116|AI900116 sc01a11.y1 Gm-c1012 Glycine max cDNA clone... 108 3e-23  
45 emb|AW569816|AW569816 si81h07.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23  
emb|AW569179|AW569179 si75e02.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23  
emb|AW289617|AW289617 NXNV003E01F Nsf Xylem Normal wood Vertical... 108 5e-23  
emb|Z29554|HA179HSP H.annuus (Sunweed) mRNA for 17.9 kDa heat-sh... 105 3e-22  
emb|X92983|PMLMWHSPA P.menziesii mRNA for low molecular weight h... 104 6e-22  
50 emb|AW569996|AW569996 si85c11.y1 Gm-c1031 Glycine max cDNA clone... 104 6e-22  
emb|X92984|PMLMWHSPB P.menziesii mRNA for low molecular weight h... 104 6e-22  
dbj|D21816|LILLIM10 Lily mRNA for small heat shock protein, part... 68 1e-21  
emb|X58279|TAHSP173 T.aestivum mRNA for heat shock protein 17.3: 102 1e-21  
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55 gb|M33899|PEAHSP181A Pisum sativum 18.1 kDa heat shock protein (... 65 5e-21  
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gb|U63631|FXU63631 Fragaria x ananassa LMW heat shock protein mR... 63 2e-20  
gb|U46545|HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 63 2e-20  
emb|X13431|TAHSPLW Wheat mRNA for putative low molecular weight ... 65 2e-20  
60 emb|AF123255|AF123255 Lycopersicon esculentum 17.7 kD class I sm... 61 3e-20  
emb|X58711|MSHSP182 M.sativa mRNA for heat shock protein (clone ... 61 3e-20



emb|AW929084|AW929084 EST337788 tomato flower buds 8 mm to pre-a... 61 3e-20  
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 5 emb|AW289567|AW289567 NXNV002G05F Nsf Xylem Normal wood Vertical... 98 5e-20  
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 emb|AF022217|AF022217 Brassica rapa low molecular weight heat-sh... 63 8e-20  
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 emb|AF161179|AF161179 Malus domestica low molecular weight heat ... 60 1e-19  
 10 emb|AW597262|AW597262 si91d02.y1 Gm-c1031 Glycine max cDNA clone... 61 1e-19  
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 15 emb|AF123256|AF123256 Lycopersicon esculentum 17.8 kD class I sm... 61 2e-19  
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 20 emb|AW221905|AW221905 EST298716 tomato fruit red ripe, TAMU Lyco... 62 4e-19  
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 25 emb|AJ225046|LPAJ5046 Lycopersicon peruvianum mRNA for Hsp20.1 p... 59 5e-19  
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 30 emb|AW569644|AW569644 si89f04.y1 Gm-c1031 Glycine max cDNA clone... 59 7e-19  
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 35 emb|AF089845|AF089845 Funaria hygrometrica cytosolic II small he... 94 1e-18  
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 Sequences producing significant alignments: (bits) Value  
  
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 55 gb|U55859|TAU55859 Triticum aestivum heat shock protein 80 mRNA,... 575 0.0  
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 60 emb|AF042329|AF042329 Eimeria tenella heat shock protein 90 (hsp... 514 0.0  
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10	gb U92465 AFU92465 Aspergillus fumigatus heat shock protein (Hsp...	458	e-165
	emb AF212996 AF212996 Neurospora crassa heat shock protein 80 ge...	473	e-165
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15	emb Z67751 SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb).	448	e-159
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40	emb AW931002 AW931002 EST356845 tomato fruit mature green, TAMU ...	436	e-121
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	emb AW011081 AW011081 ST16E03 Pine TriplEx shoot tip library Pin...	421	e-116
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 10 emb|AW738535|AW738535 EST339962 tomato flower buds, anthesis, Co... 242 e-109  
 emb|AW649397|AW649397 EST327851 tomato germinating seedlings, TA... 394 e-108  
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 15 emb|AI781620|AI781620 EST262499 tomato susceptible, Cornell Lyco... 389 e-107  
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 20 emb|AW651194|AW651194 EST329648 tomato germinating seedlings, TA... 266 e-106  
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 25 gb|L34028|PFAHSP86B Plasmodium falciparum (clone HB3) heat shock... 382 e-105  
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Database: plantfungal  
 40 661,018 sequences; 426,114,510 total letters

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50	emb A92828 A92828 Sequence 2 from Patent WO9804586.	261	e-116
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60	emb AV426381 AV426381 AV426381 Lotus japonicus young plants (two...	145	3e-43
	emb AI729043 AI729043 BNLGHi12416 Six-day Cotton fiber Gossypium...	142	6e-42



	emb Y14573 HVCH4H Hordeum vulgare DNA for chromosome 4H.	107 7e-41
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5	emb AI166945 AI166945 xylem.est.727 Poplar xylem Lambda ZAPII li...	149 4e-35
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10	emb AI778500 AI778500 EST259379 tomato susceptible, Cornell Lyco...	76 3e-30
	emb AW299018 AW299018 EST305692 KV2 Medicago truncatula cDNA clo...	125 1e-27
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50	emb X05498 SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA.	35 1.8
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 emb|AA003500|AA003500 T3189 MVAT4 bloodstream form of serodeme W... 33 6.5  
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35 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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45	emb AI856734 AI856734 sb41e04.y1 <i>Gm-c1014</i> Glycine max cDNA clone...	110	1e-23
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	emb AW437881 AW437881 ST73F03 Pine TriplEx shoot tip library Pin...	84	1e-15
	emb AW760009 AW760009 sl56h04.y1 <i>Gm-c1027</i> Glycine max cDNA clone...	83	3e-15
50	emb AW397963 AW397963 sg70e07.y1 <i>Gm-c1007</i> Glycine max cDNA clone...	53	2e-06
	emb AI440799 AI440799 sa48g03.y1 <i>Gm-c1004</i> Glycine max cDNA clone...	47	1e-04
	emb AI563168 AI563168 EST00292 watermelon lambda zap library Cit...	47	1e-04
	emb AI491014 AI491014 EST241723 tomato shoot, Cornell Lycopersic...	44	0.001
	emb AW034769 AW034769 EST278805 tomato callus, TAMU Lycopersicon...	44	0.001
55	emb AI777269 AI777269 EST258234 tomato resistant, Cornell Lycope...	44	0.001
	emb AQ653339 AQ653339 Sheared DNA-6G13.TF Sheared DNA Trypanosom...	34	1.5
	dbj D50838 CREACTINA <i>Chlamydomonas reinhardtii</i> DNA for actin, co...	33	2.0
	emb AL109815 PFMAL13PA <i>Plasmodium falciparum</i> chromosome 13 strai...	33	2.0
	emb AW257048 AW257048 EST305185 KV2 <i>Medicago truncatula</i> cDNA clo...	32	3.8
60	gb U52151 APU52151 <i>Aspergillus parasiticus</i> polyketide synthase P...	32	3.8
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emb|AB009881|AB009881 Nicotiana tabacum mRNA for myo-inositol 1-... 32 3.8  
 emb|AQ643140|AQ643140 RPCI93-EcoRI-6J20.TJ RPCI93-EcoRI Trypanos... 32 3.8  
 emb|X56441|GL35 G. lemaneiformis plasmid GL3.5 DNA starting at Ec... 28 5.1  
 gb|M60208|YSPHSP70 S.pombe mitochondrial heat shock protein (HSP... 32 5.2  
 5 emb|AF083468|AF083468 Emericella nidulans putative zinc finger p... 32 5.2  
 emb|AU011047|AU011047 AU011047 Schizosaccharomyces pombe late lo... 32 5.2  
 emb|AL136235|SPAC664 S.pombe chromosome I cosmid c664. 32 5.2  
 emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 31 7.1  
 emb|X70810|CLEGCGA Euglena gracilis chloroplast complete genome. 31 7.1  
 10 emb|AW923451|AW923451 DG1\_52\_H09.b1\_A002 Dark Grown 1 (DG1) Sorg... 31 7.1  
 emb|AQ845394|AQ845394 LMAJFV1\_lm24h05.y1 Leishmania major FV1 ra... 31 7.1  
 emb|AQ908191|AQ908191 GSSTc08820 Trypanosome cruzi random genomi... 31 7.1  
 emb|AV410934|AV410934 AV410934 Lotus japonicus young plants (two... 31 7.1  
 emb|Z11874|CHEGZ Euglena gracilis Z Chloroplast DNA. 31 7.1  
 15 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 31 9.8  
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 emb|AF245210|AF245210 Thuja plicata clone Tp6 microsatellite seq... 31 9.8  
 emb|AC006281|AC006281 Plasmodium falciparum chromosome 12 clone ... 31 9.8  
 25 emb|AI897641|AI897641 EST267084 tomato ovary, TAMU Lycopersicon ... 31 9.8  
 emb|AF163675|AF163675 Sclerotium cepivorum strain SQ-48 anonymou... 31 9.8  
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

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	emb AL031744 PFMAL1P1 Plasmodium falciparum chromosome 1 strain ...	33	2.0
	emb AW033792 AW033792 EST277363 tomato callus, TAMU Lycopersicon...	33	2.5
50	emb Z49705 SC8520X S.cerevisiae chromosome XIII cosmid 8520.	32	3.8
	emb AB001684 AB001684 Chlorella vulgaris C-27 chloroplast DNA, c...	32	3.8
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	emb AW101318 AW101318 sd77e03.y1 Gm-c1009 Glycine max cDNA clone...	32	3.8
	emb AQ909718 AQ909718 GSSTc09185 Trypanosome cruzi random genomi...	31	5.3
55	emb AW991095 AW991095 SsS0129 Suaeda salsa ZAP cDNA library Suae...	28	5.9
	emb AJ273065 AJ273065 AJ273065 Metarhizium anisopliae ARSEF 2575...	31	6.5
	emb AF057379 AF057379 Nicotiana tabacum clone G8-1 unknown mRNA.	31	6.5
	emb AB005455 AB005455 Antirrhinum majus DNA, genomic survey sequ...	31	7.3
	gb BE036743 BE036743 MP04G02 MP Mesembryanthemum crystallinum cD...	31	7.3
60	emb AI460510 AI460510 sa80h11.y1 Gm-c1004 Glycine max cDNA clone...	31	7.3
	emb AI026500 AI026500 TENU0712 T. cruzi epimastigote normalized ...	31	7.3

emb|AW651081|AW651081 EST329535 tomato germinating seedlings, TA... 30 10.0  
 emb|Z50113|SPAC31A2 S.pombe chromosome I cosmid c31A2. 30 10.0  
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 5 gb|L38011|L38011 BNAF0228E Mustard flower buds Brassica rapa cDN... 30 10.0

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Database: plantfungal  
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	emb AV428133 AV428133 AV428133 Lotus japonicus young plants (two...	53	9e-07	
	emb AV412192 AV412192 AV412192 Lotus japonicus young plants (two...	53	9e-07	
	emb AW350135 AW350135 GM210007B10E8R Gm-r1021 Glycine max cDNA 3...	51	2e-06	
25	emb AW349971 AW349971 GM210006B10B12R Gm-r1021 Glycine max cDNA ...	51	2e-06	
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	emb AW030108 AW030108 EST273363 tomato callus, TAMU Lycopersicon...	51	2e-06	
	emb AI895822 AI895822 EST265265 tomato callus, TAMU Lycopersicon...	51	2e-06	
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	emb AW625260 AW625260 EST319263 tomato radicle, 5 d post-imbibit...	51	2e-06	
	emb AW441936 AW441936 EST311332 tomato fruit red ripe, TAMU Lyco...	51	2e-06	
	emb AI441970 AI441970 sa82e02.y1 Gm-cl004 Glycine max cDNA clone...	51	2e-06	
	emb AW705827 AW705827 sk63d05.y1 Gm-cl016 Glycine max cDNA clone...	51	3e-06	
35	emb AV428923 AV428923 AV428923 Lotus japonicus young plants (two...	51	3e-06	
	gb BE124339 BE124339 EST393374 GVN Medicago truncatula cDNA clon...	48	2e-05	
	emb AW442099 AW442099 EST311495 tomato fruit red ripe, TAMU Lyco...	48	3e-05	
	emb AW625258 AW625258 EST319261 tomato radicle, 5 d post-imbibit...	47	4e-05	
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40	emb AW775746 AW775746 EST334811 DSIL Medicago truncatula cDNA cl...	46	1e-04	
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	emb AW278224 AW278224 sf41c11.y1 Gm-cl009 Glycine max cDNA clone...	45	3e-04	
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	emb AW152886 AW152886 se32c07.y1 Gm-cl015 Glycine max cDNA clone...	38	0.024	
	emb AW661378 AW661378 833004H08.y1 C. reinhardtii CC-125 -S, Lam...	38	0.033	
	emb AW625785 AW625785 EST319692 tomato radicle, 5 d post-imbibit...	37	0.045	
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55	emb X02873 DCEXTG Carrot gene for extensin.	37	0.062	
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	emb X55682 LEEXTEN2 Tomato extensin mRNA (clone wY).	35	0.16	
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	gb M34311 YSCTSDNAB S.cerevisiae telomeric sequence DNA, clone Y...	27	0.25
10	emb AF163953 AF163953 Saccharomyces cerevisiae isolate wt-2 telo...	29	0.26
	emb X59720 SCCHRIII S.cerevisiae chromosome III complete DNA seq...	28	0.30
	gb M15317 PFAHRPA P.lophurae histidine-rich protein mRNA, 3' end.	35	0.30
	emb AV408422 AV408422 AV408422 Lotus japonicus young plants (two...	35	0.30
	emb AF163955 AF163955 Saccharomyces cerevisiae isolate wt-8 telo...	33	0.34
15	emb AL116033 CNS01CVD Botrytis cinerea strain T4 cDNA library un...	27	0.38
	gb BE034443 BE034443 MH05A01 MH Mesembryanthemum crystallinum cD...	34	0.42
	gb M12922 YSCARSX Yeast (S.cerevisiae) chromosome III L terminal...	28	0.44
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25	emb AF163957 AF163957 Saccharomyces cerevisiae isolate wt-11 tel...	30	0.60
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	emb Y15372 MTY15372 Medicago truncatula mRNA for MtN4 gene, part...	33	0.79
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30	emb AL117324 LMFL2719 Leishmania major Friedlin chromosome 23 co...	33	0.79
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	emb AW712341 AW712341 glb02ne.fl Neurospora crassa evening cDNA ...	33	0.79
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	gb L07282 CREPETE Chlamydomonas reinhardtii plastocyanin (petE) ...	33	1.1
	emb AW471567 AW471567 si12b01.y1 Gm-c1029 Glycine max cDNA clone...	33	1.1
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45	emb AW725658 AW725658 GA_Ea0019C15 Gossypium arboreum 7-10 dpa ...	27	1.5
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	emb AJ245479 BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,...	260	e-121
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	emb AF179222 AF179222 Brassica rapa subsp. pekinensis floral nec...	43	2e-08
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	emb AW650581 AW650581 EST329035 tomato germinating seedlings, TA...	49	6e-06
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	emb AW033701 AW033701 EST277272 tomato callus, TAMU Lycopersicon...	47	2e-04
25	emb AW738253 AW738253 EST339680 tomato flower buds, anthesis, Co...	46	5e-04
	emb AW285102 AW285102 LG1_300_F04.g1_A002 Light Grown 1 (LG1) So...	40	6e-04
	emb AI896626 AI896626 EST266069 tomato callus, TAMU Lycopersicon...	46	6e-04
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30	emb AF133053 AF133053 Clarkia breweri S-adenosyl-L-methionine:sa...	42	0.006
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	emb X79107 STLOX1 S.tuberosum (Desiree) mRNA for lipoxxygenase.	33	4.6
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60	emb X95516 STLIPOT13 S.tuberosum mRNA for lipoxxygenase (clone T13).	33	4.6
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	gb U60201 STU60201 Solanum tuberosum lipoxxygenase (POTLX-2) mRNA...	33	4.6
	emb AW759238 AW759238 sl38f10.y1 Gm-c1027 Glycine max cDNA clone...	33	4.6
	emb AQ399938 AQ399938 mgxb0012004f CUGI Rice Blast BAC Library P...	33	4.6
5	emb AF019613 AF019613 Solanum tuberosum lipoxxygenase (plox1) mRN...	33	4.6
	emb X95512 STLIPOXT6 S.tuberosum mRNA for lipoxxygenase (clone T6).	33	4.6
	emb AW278834 AW278834 sf99c02.y1 Gm-c1019 Glycine max cDNA clone...	32	6.3
	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom...	32	6.3
	emb AB005555 AB005555 Triticum aestivum mRNA for wga20, complete...	32	6.3
10	emb AA786508 AA786508 m3a04a1.r1 Aspergillus nidulans 24hr asexu...	32	6.3
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	emb Y14007 TAY14007 Triticum aestivum mRNA for gibberellin 20-ox...	32	6.3
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	emb AC004710 AC004710 Plasmodium falciparum chromosome 12, *** S...	32	8.6
15	emb AA273033 AA273033 T4296 MVAT4 bloodstream form of serodeme W...	32	8.6
	emb AZ215931 AZ215931 Sheared DNA-116D3.TR Sheared DNA Trypanoso...	32	8.6
	emb AA495648 AA495648 c078 Zhou and Ragan 1993 Gracilaria gracil...	32	8.6
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai...	32	8.6
	emb X56775 HVGLB1 H.vulgare Glb 1 gene for 1-3,1-4-beta-D-glucan...	32	8.6
20	emb Z72916 SCYGR131W S.cerevisiae chromosome VII reading frame O...	32	8.6
	emb Z72915 SCYGR130C S.cerevisiae chromosome VII reading frame O...	32	8.6
	gb U10083 TGU10083 Toxoplasma gondii RH hypoxanthine-guanine pho...	32	8.6
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	gb U09219 TGU09219 Toxoplasma gondii RH hypoxanthine-guanine pho...	32	8.6
25	gb U10247 TGU10247 Toxoplasma gondii RH hypoxanthine-xanthine-gu...	32	8.6
	emb AB012774 AB012774 AB012774 Toxoplasma gondii mRNA (T.Koyama)...	32	8.6
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30	emb X56260 HVGLUEND Barley DNA for (1,3;1,4)-beta-glucanase.(EC ...	32	8.6
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40 Database: plantfungal  
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	emb X87143 HACYTB5RN H.annuus mRNA for extraplastidial fusion pr...	34	0.49
	emb X74782 BNSACPD1 B.napus gene for stearyl-acyl carrier prote...	32	1.3
	emb AW560462 AW560462 EST315510 DSIR Medicago truncatula cDNA cl...	32	1.3
50	emb AW687516 AW687516 NF010D12RT1F1101 Developing root Medicago ...	32	1.3
	emb AW256825 AW256825 EST304962 KV2 Medicago truncatula cDNA clo...	32	1.3
	emb X07644 NTALSURA Tobacco acetolactate synthase gene, ALS SuRA...	32	1.7
	emb AA451568 AA451568 AOB213F Onion seedling leaf cDNA library A...	31	2.4
	emb AW067623 AW067623 SBcD89 Sugar beet leaf cDNA library Beta v...	31	3.3
55	emb AF030694 AF030694 Plasmodium falciparum strain Dd2 heat shoc...	31	3.3
	emb X12493 SCADR6 Yeast ADR6 gene for transcription factor.	30	4.5
	gb U14726 SCU14726 Saccharomyces cerevisiae Syg1p (SYG1) gene, c...	30	4.5
	emb Z46861 SC9905 S.cerevisiae chromosome IX cosmid 9905 and lam...	30	4.5
	gb L29456 TOBHIC12X Nicotiana tabacum histone H1 (H1C12) mRNA, c...	30	4.5
60	gb U33335 U33335 Saccharomyces cerevisiae chromosome XVI, left a...	30	4.5
	emb AJ290663 PAB290663 Picea abies copia like retroelement parti...	30	6.2



emb|AL115708|CNS01CMC Botrytis cinerea strain T4 cDNA library un... 30 6.2  
 emb|Z71630|SCYNR015W S.cerevisiae chromosome XIV reading frame O... 29 8.5  
 emb|Z71629|SCYNR014W S.cerevisiae chromosome XIV reading frame O... 29 8.5  
 emb|AQ875584|AQ875584 V127B11 mTn-3xHA/lacZ Insertion Library, s... 29 8.5  
 5 gb|L16451|YSAAPRP Candida albicans acid proteinase-related prote... 29 8.5  
 emb|AW981797|AW981797 PC18H02 Pine TriplEx pollen cone library P... 29 8.5  
 emb|AQ644958|AQ644958 RPCI93-DpnII-30N9.TJ RPCI93-DpnII Trypanos... 29 8.5  
 emb|AW672524|AW672524 LG1\_360\_D10.b1\_A002 Light Grown 1 (LG1) So... 29 8.5  
 emb|AW564851|AW564851 LG1\_310\_D10.b1\_A002 Light Grown 1 (LG1) So... 29 8.5  
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Database: plantfungal  
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	dbj D26015 D26015 Nicotiana tabacum mRNA for CND41, chloroplast ...	148	9e-56
	emb AI487587 AI487587 EST245909 tomato ovary, TAMU Lycopersicon ...	152	4e-54
	emb AI489151 AI489151 EST247490 tomato ovary, TAMU Lycopersicon ...	152	4e-54
30	emb AI483907 AI483907 EST249778 tomato ovary, TAMU Lycopersicon ...	152	1e-52
	emb AW931514 AW931514 EST357357 tomato fruit mature green, TAMU ...	145	4e-52
	emb AI771546 AI771546 EST252646 tomato ovary, TAMU Lycopersicon ...	144	2e-49
	emb AW736637 AW736637 EST333129 KV3 Medicago truncatula cDNA clo...	142	6e-48
	emb AI166286 AI166286 xylem.est.133 Poplar xylem Lambda ZAPII li...	151	6e-40
35	emb AW693272 AW693272 NF064A05ST1F1000 Developing stem Medicago ...	143	3e-39
	emb AW736636 AW736636 EST333128 KV3 Medicago truncatula cDNA clo...	145	5e-39
	emb AW559446 AW559446 EST314494 DSIR Medicago truncatula cDNA cl...	143	1e-38
	emb AW730900 AW730900 GA__Ea0029G11 Gossypium arboreum 7-10 dpa ...	146	2e-37
	emb AW692307 AW692307 NF049H04ST1F1043 Developing stem Medicago ...	143	1e-36
40	emb AW737187 AW737187 EST338614 tomato flower buds, anthesis, Co...	149	3e-36
	emb AW688595 AW688595 NF009D06ST1F1000 Developing stem Medicago ...	137	8e-35
	emb AI974844 AI974844 T113327e KV2 Medicago truncatula cDNA clon...	143	3e-33
	emb AW773698 AW773698 EST332684 KV3 Medicago truncatula cDNA clo...	129	1e-32
	emb AV408654 AV408654 AV408654 Lotus japonicus young plants (two...	135	6e-32
45	emb AW688941 AW688941 NF013E03ST1F1000 Developing stem Medicago ...	121	4e-30
	emb AI725786 AI725786 BNLGHi12992 Six-day Cotton fiber Gossypium...	66	7e-29
	emb AW677148 AW677148 DG1_5_C02.b1_A002 Dark Grown 1 (DG1) Sorgh...	92	4e-27
	emb AW932074 AW932074 EST357917 tomato fruit mature green, TAMU ...	116	3e-26
	emb AI731300 AI731300 BNLGHi9147 Six-day Cotton fiber Gossypium ...	50	9e-25
50	emb AW933383 AW933383 EST359322 tomato fruit mature green, TAMU ...	57	5e-23
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	emb AW221352 AW221352 EST297821 tomato fruit mature green, TAMU ...	63	2e-21
	emb AW307535 AW307535 sf58b08.y1 Gm-c1009 Glycine max cDNA clone...	63	2e-21
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55	emb AI772366 AI772366 EST253466 tomato resistant, Cornell Lycope...	63	7e-21
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	emb AW219354 AW219354 EST301836 tomato root during/after fruit s...	64	1e-19
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	emb AW690628 AW690628 NF036F05ST1F1000 Developing stem Medicago ...	60	1e-18
5	emb AW398635 AW398635 EST309135 L. pennellii trichome, Cornell U...	48	1e-18
	gb BE033948 BE033948 MG02E01 MG Mesembryanthemum crystallinum cD...	68	2e-18
	emb AW980831 AW980831 EST391984 GVN Medicago truncatula cDNA clo...	48	2e-17
	emb AW266728 AW266728 L48-63T3 Ice plant Lambda Uni-Zap XR expre...	89	4e-17
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	emb AW693054 AW693054 NF059C10ST1F1081 Developing stem Medicago ...	63	1e-16
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15	emb AW686542 AW686542 NF039C04NR1F1000 Nodulated root Medicago t...	60	4e-16
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40	emb AW697024 AW697024 NF111E05ST1F1038 Developing stem Medicago ...	43	1e-10
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55	emb AW647996 AW647996 EST326450 tomato germinating seedlings, TA...	64	2e-09
	emb AW218271 AW218271 EST303452 tomato radicle, 5 d post-imbibit...	64	2e-09
	emb AI776062 AI776062 EST257162 tomato resistant, Cornell Lycope...	64	2e-09
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	emb AW650814 AW650814 EST329268 tomato germinating seedlings, TA...	64	2e-09
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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 gb|BE036389|BE036389 MO24B03 MO Mesembryanthemum crystallinum cD... 44 2e-06  
 25 gb|BE034652|BE034652 ML01E04 ML Mesembryanthemum crystallinum cD... 35 0.57  
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 emb|AA739646|AA739646 411 PtIFG2 Pinus taeda cDNA clone 8694M 3'... 30 9.9  
 emb|AL034353|SPBC1271 S.pombe chromosome II cosmid c1271. 30 9.9  
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments: (bits) Value

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 emb|AI938454|AI938454 sc45e10.y1 Gm-cl015 Glycine max cDNA clone... 44 0.001  
 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 36 0.38  
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 emb|AI210373|AI210373 i0e05a1.r1 Aspergillus nidulans 24hr asexu... 34 1.8  
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 20 emb|AW651276|AW651276 EST329730 tomato germinating seedlings, TA... 33 3.5  
 emb|AI392128|AI392128 NCSM1B1T7 Subtracted Mycelial Neurospora c... 32 4.8  
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 emb|AL160716|P406R Leishmania major Friedlin PAC P406 right end-... 31 9.0  
 emb|AQ851400|AQ851400 LMAJFV1\_lm40b04.y1 Leishmania major FV1 ra... 31 9.0  
 emb|AF061068|AF061068 Phleum pratense clone 10029 major allergen... 31 9.0  
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 emb|AW309665|AW309665 sf22g06.x1 Gm-cl028 Glycine max cDNA clone... 26 9.5  
 emb|AW310247|AW310247 sf33d01.x1 Gm-cl028 Glycine max cDNA clone... 26 9.5  
 emb|AW508196|AW508196 si50d10.y1 Gm-r1030 Glycine max cDNA clone... 27 9.6  
 45 emb|AW102012|AW102012 sd81h10.y1 Gm-cl009 Glycine max cDNA clone... 26 9.8  
 emb|AW309166|AW309166 sg05b01.y1 Gm-cl019 Glycine max cDNA clone... 26 9.8  
 emb|AW598779|AW598779 sj46h06.y1 Gm-cl033 Glycine max cDNA clone... 26 9.8  
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/description no hits found less than or equal to 1e-15. /blast\_score

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(430 letters)

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

60

Score E



Sequences producing significant alignments: (bits) Value

emb|AQ952678|AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso... 35 0.32  
 5 emb|AW698685|AW698685 R125 non-glandular-haired subtracted cDNA ... 32 1.4  
 emb|AF061282|AF061282 Sorghum bicolor 22 kDa kafirin cluster. 31 5.6  
 emb|AL031854|SPBC337 S.pombe chromosome II cosmid c337. 31 5.6  
 emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, \*\*\* S... 31 5.6  
 emb|AC006280|AC006280 Plasmodium falciparum chromosome 12 clone ... 31 5.6  
 10 gb|M74062|YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl... 31 5.6  
 emb|AQ947500|AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso... 31 5.6  
 gb|M83307|YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl... 31 5.6  
 emb|AL031856|SPBC1734 S.pombe chromosome II cosmid c1734. 31 5.6  
 emb|AC073246|AC073246 Trypanosoma brucei chromosome II clone RPC... 30 7.7  
 emb|AL031535|SPCC16C4 S.pombe chromosome III cosmid c16C4. 30 7.7  
 15 emb|AC012647|AC012647 Trypanosoma brucei chromosome II clone RPC... 30 7.7  
 gb|L28038|TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc... 30 7.7  
 emb|AB004322|AB004322 Nicotiana sylvestris NsPMT1 gene for putre... 30 7.7  
 emb|AQ941496|AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso... 30 7.7  
 emb|AQ946940|AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom... 30 7.7  
 20 emb|AQ942433|AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom... 30 7.7  
 emb|AF133529|AF133529 Candida albicans mRNA cap methyltransferas... 30 7.7

25 Query= Novartis73\_RC\_at 14202\_at /id\_source  
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30 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

35 Score E  
 Sequences producing significant alignments: (bits) Value

emb|AQ952678|AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso... 35 0.32  
 emb|AW698685|AW698685 R125 non-glandular-haired subtracted cDNA ... 32 1.4  
 emb|AF061282|AF061282 Sorghum bicolor 22 kDa kafirin cluster. 31 5.6  
 40 emb|AL031854|SPBC337 S.pombe chromosome II cosmid c337. 31 5.6  
 emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, \*\*\* S... 31 5.6  
 emb|AC006280|AC006280 Plasmodium falciparum chromosome 12 clone ... 31 5.6  
 gb|M74062|YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl... 31 5.6  
 emb|AQ947500|AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso... 31 5.6  
 45 gb|M83307|YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl... 31 5.6  
 emb|AL031856|SPBC1734 S.pombe chromosome II cosmid c1734. 31 5.6  
 emb|AC073246|AC073246 Trypanosoma brucei chromosome II clone RPC... 30 7.7  
 emb|AL031535|SPCC16C4 S.pombe chromosome III cosmid c16C4. 30 7.7  
 emb|AC012647|AC012647 Trypanosoma brucei chromosome II clone RPC... 30 7.7  
 50 gb|L28038|TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc... 30 7.7  
 emb|AB004322|AB004322 Nicotiana sylvestris NsPMT1 gene for putre... 30 7.7  
 emb|AQ941496|AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso... 30 7.7  
 emb|AQ946940|AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom... 30 7.7  
 emb|AQ942433|AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom... 30 7.7  
 55 emb|AF133529|AF133529 Candida albicans mRNA cap methyltransferas... 30 7.7

60 Query= Novartis9\_at 14223\_at /id\_source  
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 (1761 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

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	gb BE023215 BE023215 sm70a04.y1 Gm-cl028 Glycine max cDNA clone ...	236	5e-61
	emb AW399343 AW399343 EST309843 L. pennellii trichome, Cornell U...	234	2e-60
	emb AW618318 AW618318 EST320304 L. pennellii trichome, Cornell U...	177	1e-53
	emb AW310982 AW310982 sg31b02.x1 Gm-cl024 Glycine max cDNA clone...	97	1e-51
15	emb AI442277 AI442277 sa66a04.y1 Gm-cl004 Glycine max cDNA clone...	200	2e-50
	emb AW687759 AW687759 NF013B05RT1F1044 Developing root Medicago ...	160	1e-46
	emb AW684122 AW684122 NF012F06NR1F1000 Nodulated root Medicago t...	83	2e-44
	emb AW309867 AW309867 sf25g10.x1 Gm-cl028 Glycine max cDNA clone...	89	5e-43
	gb BE020423 BE020423 sm40e08.y1 Gm-cl028 Glycine max cDNA clone ...	88	2e-39
20	emb AW691118 AW691118 NF041D08ST1F1000 Developing stem Medicago ...	78	2e-35
	emb AW160235 AW160235 EST290093 L. pennellii trichome, Cornell U...	120	6e-32
	emb AI960862 AI960862 sc91f07.y1 Gm-cl019 Glycine max cDNA clone...	74	5e-30
	emb AW349633 AW349633 GM210006A11B3R Gm-r1021 Glycine max cDNA 3...	89	8e-29
	emb AW775076 AW775076 EST334227 KV3 Medicago truncatula cDNA clo...	81	6e-26
25	gb BE020331 BE020331 sm40d08.y1 Gm-cl028 Glycine max cDNA clone ...	69	4e-23
	emb AW746031 AW746031 WS1_39_A03.b1_A002 Water-stressed I (WS1) ...	74	8e-23
	emb AW621546 AW621546 EST312344 tomato root during/after fruit s...	64	1e-13
	emb AW622846 AW622846 EST306916 tomato flower buds 3-8 mm, Corne...	54	2e-12
	gb L43984 BLYBD Hordeum vulgare (clone ABG377) chromosome 3H STS...	69	8e-11
30	emb AW774216 AW774216 EST333367 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW774324 AW774324 EST333475 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW686169 AW686169 NF038H07NR1F1000 Nodulated root Medicago t...	68	2e-10
	emb AW160234 AW160234 EST290092 L. pennellii trichome, Cornell U...	46	2e-08
	emb AW685496 AW685496 NF030G02NR1F1000 Nodulated root Medicago t...	45	2e-07
35	emb AW684082 AW684082 NF011H08NR1F1000 Nodulated root Medicago t...	55	2e-06
	emb AW693839 AW693839 NF069F08ST1F1074 Developing stem Medicago ...	53	6e-06
	emb AI163659 AI163659 A046p04u Hybrid aspen plasmid library Popu...	53	6e-06
	emb AW033404 AW033404 EST276975 tomato callus, TAMU Lycopersicon...	49	1e-04
	emb AI054662 AI054662 coau0001K11 Cotton Boll Abscission Zone cD...	37	2e-04
40	emb AW758414 AW758414 874008A01.y1 C. reinhardtii CC-1690, Lambd...	41	0.022
	emb AW746188 AW746188 WS1_39_A03.g1_A002 Water-stressed I (WS1) ...	41	0.022
	emb Z99126 SPAC26H5 S.pombe chromosome I cosmid c26H5.	41	0.022
	emb AJ225805 EDKCHALPH Egeria densa mRNA for inward potassium ch...	39	0.14
	emb AI488725 AI488725 EST247064 tomato ovary, TAMU Lycopersicon ...	38	0.20
45	emb Z69731 SPAC6C3 S.pombe chromosome I cosmid c6C3.	36	0.71
	emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168.	36	0.71
	emb AW925349 AW925349 HVSMEg0001B12 Hordeum vulgare pre-anthesis...	36	0.71
	emb AW671585 AW671585 LG1_348_H11.b1_A002 Light Grown I (LG1) So...	36	0.97
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50	emb AW216501 AW216501 EST295215 tomato callus, TAMU Lycopersicon...	36	0.97
	emb AW680841 AW680841 WS1_7_E11.g1_A002 Water-stressed I (WS1) S...	35	1.3
	emb AQ911629 AQ911629 LMAJFV1_lm96c04.y1 Leishmania major FV1 ra...	35	1.3
	emb AW100578 AW100578 sd57b08.y1 Gm-cl008 Glycine max cDNA clone...	35	1.3
	emb AW010724 AW010724 ST11E02 Pine TriplEx shoot tip library Pin...	35	1.8
55	emb AL138854 SPAC23G3 S.pombe chromosome I cosmid c23G3.	35	2.5
	emb AW934681 AW934681 EST353573 tomato flower buds 0-3 mm, Corne...	34	3.5
	emb Z98975 SPAC19E9 S.pombe chromosome I cosmid c19E9.	34	3.5
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	emb Z50142 SPAC2F7 S.pombe chromosome I cosmid c2F7.	34	3.5
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	emb AI779448 AI779448 EST260327 tomato susceptible, Cornell Lyco...	34	4.8

emb|AQ639314|AQ639314 927P1-2A10.TV 927P1 Trypanosoma brucei gen... 34 4.8  
emb|AW725460|AW725460 GA\_\_Ea0018B02 Gossypium arboreum 7-10 dpa ... 34 4.8  
emb|AW256577|AW256577 EST304714 KV2 Medicago truncatula cDNA clo... 34 4.8  
emb|AW234006|AW234006 sE3a07.y1 Gm-cl028 Glycine max cDNA clone... 34 4.8  
5 emb|AW727061|AW727061 GA\_\_Ea0011B08 Gossypium arboreum 7-10 dpa ... 34 4.8  
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emb|AA898817|AA898817 NCP3G4T7 Perithecial Neurospora crassa cDN... 34 4.8  
emb|AI329539|AI329539 b6b04ne.fl Neurospora crassa evening cDNA ... 33 6.6  
10 emb|AW754602|AW754602 PC04B10 Pine TriplEx pollen cone library P... 33 6.6  
emb|AL049181|PFMAL13P4 Plasmodium falciparum chromosome 13 strai... 33 6.6  
emb|AW756307|AW756307 sl19a02.y1 Gm-cl036 Glycine max cDNA clone... 33 6.6  
emb|AC004145|AC004145 Leishmania major chromosome 3 clone L5801 ... 33 6.6  
emb|AI778201|AI778201 EST259080 tomato susceptible, Cornell Lyco... 33 9.0  
15 emb|AZ215585|AZ215585 Sheared DNA-74E7.TR Sheared DNA Trypanosom... 33 9.0  
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emb|AI896488|AI896488 EST265931 tomato callus, TAMU Lycopersicon... 33 9.0  
emb|AW670919|AW670919 LG1\_266\_B11.bl\_A002 Light Grown 1 (LG1) So... 33 9.0  
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20 emb|AW982007|AW982007 PC23H10 Pine TriplEx pollen cone library P... 33 9.0  
gb|U51030|YSCD9954 Saccharomyces cerevisiae chromosome IV cosmid... 33 9.0  
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emb|AQ023613|AQ023613 CpGR0073A Cryptosporidium parvum genomic r... 33 9.0  
25 gb|BE024936|BE024936 894007A03.y1 C. reinhardtii CC-1690, normal... 33 9.0  
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emb|AQ648055|AQ648055 RPCI93-DpnII-30G1.TJ RPCI93-DpnII Trypanos... 33 9.0  
emb|AQ641411|AQ641411 RPCI93-DpnII-28C15.TJ RPCI93-DpnII Trypano... 33 9.0  
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Database: plantfungal

40 661,018 sequences; 426,114,510 total letters

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emb|AV423458|AV423458 AV423458 Lotus japonicus young plants (two... 28 0.005  
50 emb|AV422547|AV422547 AV422547 Lotus japonicus young plants (two... 28 0.006  
emb|AW706554|AW706554 sj58h12.y1 Gm-cl033 Glycine max cDNA clone... 28 0.010  
emb|AW508852|AW508852 si41b07.y1 Gm-r1030 Glycine max cDNA clone... 28 0.015  
emb|AW432586|AW432586 sh76d11.y1 Gm-cl015 Glycine max cDNA clone... 28 0.016  
emb|AI965714|AI965714 sc77f01.y1 Gm-cl018 Glycine max cDNA clone... 28 0.021  
55 emb|AI930916|AI930916 sb44d12.y1 Gm-cl015 Glycine max cDNA clone... 28 0.031  
emb|AW100187|AW100187 sd26g01.y1 Gm-cl012 Glycine max cDNA clone... 26 0.031  
emb|AW153030|AW153030 se34a10.y1 Gm-cl015 Glycine max cDNA clone... 30 0.13  
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gb|U91857|SHU91857 Stylosanthes hamata ethylene-responsive eleme... 28 0.29  
60 emb|AW329270|AW329270 N200490e rootphos(-) Medicago truncatula c... 29 0.33  
emb|X02873|DCEXTG Carrot gene for extensin. 35 0.34



	gb M11221 DAREXTA Carrot (D.carota) extensin mRNA, partial cds.	35	0.47
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5	emb AV411578 AV411578 AV411578 Lotus japonicus young plants (two...	26	0.68
	emb AW618112 AW618112 EST314162 L. pennellii trichome, Cornell U...	28	0.72
	emb AW164515 AW164515 se74g06.y1 Gm-cl023 Glycine max cDNA clone...	27	0.74
	emb AI900852 AI900852 sb95c05.y1 Gm-cl012 Glycine max cDNA clone...	27	0.75
	emb AW328989 AW328989 N200181e rootphos(-) Medicago truncatula c...	27	0.81
10	emb AV425804 AV425804 AV425804 Lotus japonicus young plants (two...	34	0.89
	emb AV427232 AV427232 AV427232 Lotus japonicus young plants (two...	34	0.89
	emb AI775562 AI775562 EST256662 tomato resistant, Cornell Lycopersicon...	28	1.2
	emb AW647824 AW647824 EST326278 tomato germinating seedlings, TA...	28	1.2
	emb AI486798 AI486798 EST245120 tomato ovary, TAMU Lycopersicon ...	28	1.3
15	emb AW568194 AW568194 si57g03.y1 Gm-r1030 Glycine max cDNA clone...	29	1.3
	emb AW031184 AW031184 EST274722 tomato callus, TAMU Lycopersicon...	28	1.3
	emb AW622531 AW622531 EST313331 tomato root during/after fruit s...	28	1.3
	dbj D38124 TOBBY4B Tobacco mRNA for EREBP-3, complete cds.	28	1.4
	emb AW695699 AW695699 NF097F03ST1F1029 Developing stem Medicago ...	31	1.4
20	emb AW186005 AW186005 se62d09.y1 Gm-cl019 Glycine max cDNA clone...	29	1.5
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	dbj D86853 D86853 Catharanthus roseus cycl5 mRNA for extensin, c...	33	1.7
	emb AW650803 AW650803 EST329257 tomato germinating seedlings, TA...	33	1.7
	emb X63339 SRENOD2 S.rostrata Enod2 gene for nodulin.	32	2.3
25	gb C95684 C95684 C95684 Marchantia polymorpha immature sex organ...	32	2.3
	gb M12865 YSCRSCATC Yeast (S.cerevisiae) CAT repetitive element,...	27	2.7
	emb AW040234 AW040234 EST282740 tomato mixed elicitor, BTI Lycopersicon...	28	3.0
	emb AW720424 AW720424 LjNEST22g2r Lotus japonicus nodule library...	32	3.2
	emb AW686730 AW686730 NF041H01NR1F1000 Nodulated root Medicago t...	32	3.2
30	emb AV412432 AV412432 AV412432 Lotus japonicus young plants (two...	26	3.2
	emb AV407890 AV407890 AV407890 Lotus japonicus young plants (two...	26	3.4
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	emb AV413265 AV413265 AV413265 Lotus japonicus young plants (two...	26	3.6
	gb U10398 YSCH9315 Saccharomyces cerevisiae chromosome VIII cosm...	27	3.6
35	emb AV412856 AV412856 AV412856 Lotus japonicus young plants (two...	26	3.7
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	emb AV413154 AV413154 AV413154 Lotus japonicus young plants (two...	28	4.3
	emb AQ944381 AQ944381 Sheared DNA-53H12.TF Sheared DNA Trypanoso...	31	4.3
	emb AI166472 AI166472 xylem.est.300 Poplar xylem Lambda ZAPII li...	31	4.3
	emb AI495395 AI495395 sa97d11.y1 Gm-cl004 Glycine max cDNA clone...	25	4.9
45	emb AW278410 AW278410 sf43g05.y1 Gm-cl009 Glycine max cDNA clone...	25	5.0
	emb AV425829 AV425829 AV425829 Lotus japonicus young plants (two...	28	5.2
	emb AV414990 AV414990 AV414990 Lotus japonicus young plants (two...	28	5.2
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50	emb AW724180 AW724180 f4c08nm.r1 Neurospora crassa morning cDNA ...	31	6.0
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	emb AV395215 AV395215 AV395215 Chlamydomonas reinhardtii C9 Chla...	31	6.0
	emb AW720526 AW720526 LjNEST18f4r Lotus japonicus nodule library...	31	6.0
55	emb AW717057 AW717057 h6e06nm.r1 Neurospora crassa morning cDNA ...	31	6.0
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	emb AW234792 AW234792 sf19c08.y1 Gm-cl028 Glycine max cDNA clone...	31	6.0
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60	emb AI487770 AI487770 EST246092 tomato ovary, TAMU Lycopersicon ...	28	6.6
	emb AA840807 AA840807 CFB53 Floral bud cDNA library of Hot peppe...	23	6.8



emb|AF056182|AF056182 Emericella nidulans G-protein beta subunit... 30 8.2  
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 emb|AC010851|AC010851 Leishmania major chromosome 22 clone L4134... 30 8.2  
 emb|AW707173|AW707173 sk10f12.y1 Gm-c1023 Glycine max cDNA clone... 30 8.2  
 5 emb|AW686992|AW686992 NF004G07RT1F1055 Developing root Medicago ... 30 8.2  
 emb|AW618891|AW618891 EST320877 L. pennellii trichome, Cornell U... 30 8.2  
 emb|AW507786|AW507786 si45a10.y1 Gm-r1030 Glycine max cDNA clone... 30 8.2  
 emb|AQ910557|AQ910557 GSSTc05793 Trypanosome cruzi random genomi... 28 8.5  
 emb|AW032140|AW032140 EST275594 tomato callus, TAMU Lycopersicon... 26 8.7  
 10 emb|AW932239|AW932239 EST358082 tomato fruit mature green, TAMU ... 26 8.7  
 emb|AW933044|AW933044 EST358887 tomato fruit mature green, TAMU ... 26 8.7  
 emb|AW030545|AW030545 EST273800 tomato callus, TAMU Lycopersicon... 26 8.8  
 emb|AW932961|AW932961 EST358804 tomato fruit mature green, TAMU ... 26 8.8  
  
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 20 gb|t76255, gb|t20906 and gb|ai100027 come from this gene."  
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 25 (1635 letters)  
  
 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters  
  
 30 Searching.....done  
  

	Score	E
Sequences producing significant alignments:	(bits)	Value
35 emb AF029858 AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C...	220	e-104
gb M32885 AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ...	173	3e-89
gb BE054146 BE054146 GA_Ea0034H12f Gossypium arboreum 7-10 dpa ...	167	7e-50
gb L24438 THLCYP450A Thlaspi arvense germline cytochrome P450 mR...	144	2e-48
emb Z22545 PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA.	77	9e-47
40 dbj D14588 PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h...	77	9e-47
emb Z22544 PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA.	71	2e-44
dbj D85184 D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd...	85	8e-44
emb AW234222 AW234222 sf22f08.y1 Gm-c1028 Glycine max cDNA clone...	147	5e-43
emb Y09423 NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C...	126	8e-40
45 emb AF122821 AF122821 Capsicum annuum cytochrome P450 (PepCYP) m...	127	2e-39
gb U48435 SCU48435 Solanum chacoense putative cytochrome P450 ge...	136	3e-39
emb AJ238612 CRO238612 Catharanthus roseus mRNA for cytochrome P...	135	3e-39
emb AF124815 AF124815 Mentha spicata cytochrome p450 mRNA, compl...	134	4e-39
emb AW053855 AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp...	130	9e-39
50 gb U48434 SCU48434 Solanum chacoense cytochrome P450 mRNA, compl...	124	2e-38
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emb AF022460 AF022460 Glycine max cytochrome P450 monooxygenase ...	116	3e-37
emb AW349428 AW349428 GM210007A20E11R Gm-r1021 Glycine max cDNA ...	69	8e-37
55 emb X71658 SMCYPEG8 S.melongena CYP76A1 mRNA.	130	2e-36
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- emb|AF166332|AF166332 *Nicotiana tabacum* cytochrome P450 gene, co... 127 2e-33
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- emb|AF150881|AF150881 *Lycopersicon esculentum* x *Lycopersicon per...* 78 3e-31
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- 25 emb|AW569661|AW569661 si89h01.y1 *Gm-c1031* Glycine max cDNA clone... 137 3e-31
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- emb|AW677294|AW677294 DG1\_5\_H08.g1\_A002 Dark Grown 1 (DG1) Sorgh... 136 4e-31
- emb|AW623139|AW623139 EST321084 tomato flower buds 3-8 mm, Come... 117 5e-31
- 30 emb|AW256491|AW256491 EST304628 KV2 *Medicago truncatula* cDNA clo... 136 6e-31
- dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 66 6e-31
- emb|AW922446|AW922446 DG1\_19\_F10.g1\_A002 Dark Grown 1 (DG1) Sorg... 135 1e-30
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- emb|AW031613|AW031613 EST275067 tomato callus, TAMU Lycopersicon... 73 2e-30
- 35 emb|Y10490|GMC450CP3 *G.max* mRNA for putative cytochrome P450, cl... 133 3e-30
- emb|AF156976|AF156976 *Gerbera hybrida* flavone synthase II (CYP93... 63 3e-30
- emb|AW218579|AW218579 EST303762 tomato radicle, 5 d post-imbibit... 133 4e-30
- emb|AB028152|AB028152 *Torenia hybrida* TFNS5 mRNA for cytochrome ... 64 4e-30
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- emb|AW458764|AW458764 sh82d02.y1 *Gm-c1016* Glycine max cDNA clone... 130 3e-29
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- 45 emb|AF014800|AF014800 *Eschscholzia californica* (S)-N-methylcocla... 105 5e-29
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- emb|AW728587|AW728587 GA\_Ea0017C12 *Gossypium arboreum* 7-10 dpa ... 101 1e-28
- 50 emb|AW922486|AW922486 DG1\_19\_B12.g1\_A002 Dark Grown 1 (DG1) Sorg... 128 1e-28
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- emb|AW255421|AW255421 ML442 peppermint glandular trichome *Mentha*... 125 8e-28
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- 60 dbj|E05111|E05111 cDNA encoding solanum flavonoid 3',5'-hydroxyg... 72 1e-27
- emb|AB006790|AB006790 *Petunia x hybrida* IMT-2 mRNA for cytochrom... 75 1e-27

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Database: plantfungal  
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emb|AV423915|AV423915 AV423915 Lotus japonicus young plants (two... 98 6e-20  
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40 emb|AW559251|AW559251 EST306087 DSIR Medicago truncatula cDNA cl... 97 4e-19  
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 (1732 letters)

Database: plantfungal  
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 emb|AW349142|AW349142 GM210003B22H5R *Gm-r1021* *Glycine max* cDNA 3... 57 3e-09  
 emb|AW065112|AW065112 ST39G09 Pine TriplEx shoot tip library Pin... 62 1e-08  
 60 emb|AW736866|AW736866 NXNV\_083\_H05\_F Nsf Xylem Normal wood Verti... 52 2e-08  
 emb|AW685287|AW685287 NF027B11NR1F1000 *Nodulated root* *Medicago t...* 46 4e-08

	emb AW031593 AW031593 EST275047 tomato callus, TAMU Lycopersicon...	35	2e-07
	emb AW560074 AW560074 EST315122 DSIR Medicago truncatula cDNA cl...	48	5e-07
	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo...	51	5e-07
	emb AW704685 AW704685 sk39c02.y1 Gm-c1028 Glycine max cDNA clone...	39	5e-07
5	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic...	53	1e-06
	emb AW349364 AW349364 GM210004B12G1R Gm-r1021 Glycine max cDNA 3...	56	1e-06
	emb AW560073 AW560073 EST315121 DSIR Medicago truncatula cDNA cl...	46	1e-06
	emb AW432244 AW432244 sh71a11.y1 Gm-c1015 Glycine max cDNA clone...	52	2e-06
	emb AW773847 AW773847 EST332833 KV3 Medicago truncatula cDNA clo...	39	4e-06
10	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago ...	37	8e-06
	emb AW687653 AW687653 NF011G04RT1F1035 Developing root Medicago ...	49	1e-04
	emb AI416889 AI416889 sa19d09.x1 Gm-c1005 Glycine max cDNA clone...	49	1e-04
	emb AW438038 AW438038 ST83G07 Pine TriplEx shoot tip library Pin...	49	1e-04
	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco...	34	4e-04
15	emb AW985058 AW985058 NXNV_130_D03_F Nsf Xylem Normal wood Verti...	31	7e-04
	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso...	46	9e-04
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso...	46	0.001
	emb AW933515 AW933515 EST359274 tomato fruit mature green, TAMU ...	32	0.003
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso...	36	0.003
20	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un...	35	0.004
	emb AW870252 AW870252 NXNV_128_C06_F Nsf Xylem Normal wood Verti...	44	0.004
	emb AW687535 AW687535 NF010F08RT1F1074 Developing root Medicago ...	43	0.006
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic...	31	0.006
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U...	33	0.009
25	emb AW317531 AW317531 sg51e11.y1 Gm-c1025 Glycine max cDNA clone...	41	0.013
	emb AW686129 AW686129 NF033H12NR1F1000 Nodulated root Medicago t...	32	0.023
	emb AV417662 AV417662 AV417662 Lotus japonicus young plants (two...	30	0.025
	emb AW010126 AW010126 ST02C06 Pine TriplEx shoot tip library Pin...	41	0.029
	emb AW686977 AW686977 NF004F04RT1F1042 Developing root Medicago ...	33	0.031
30	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c...	40	0.075
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	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus ...	39	0.14
	emb AW774485 AW774485 EST333636 KV3 Medicago truncatula cDNA clo...	39	0.14
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	emb AW705444 AW705444 sk49b08.y1 Gm-c1019 Glycine max cDNA clone...	39	0.14
	emb AW695353 AW695353 NF094C07ST1F1053 Developing stem Medicago ...	39	0.14
	emb AW257266 AW257266 EST305403 KV2 Medicago truncatula cDNA clo...	39	0.14
40	emb AW934555 AW934555 EST353447 tomato flower buds 0-3 mm, Corne...	38	0.27
	emb AW307176 AW307176 sf53g04.y1 Gm-c1009 Glycine max cDNA clone...	31	0.36
	emb AL031525 SPCC1682 S.pombe chromosome III cosmid c1682.	37	0.51
	emb AW698283 AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti...	28	0.66
	emb AW698011 AW698011 NXNV_079_E11_F Nsf Xylem Normal wood Verti...	29	0.88
45	emb AW693913 AW693913 NF070E02ST1F1017 Developing stem Medicago ...	36	0.96
	emb AW686305 AW686305 NF036D07NR1F1000 Nodulated root Medicago t...	36	0.96
	emb AW685079 AW685079 NF024H05NR1F1000 Nodulated root Medicago t...	36	0.96
	emb AW043221 AW043221 ST30G04 Pine TriplEx shoot tip library Pin...	36	0.96
	emb AF127256 AF127256 Laureliopsis philippiana rpl16 gene, chlor...	35	1.8
50	emb AF127255 AF127255 Laurelia sempervirens rpl16 gene, chloropl...	35	1.8
	emb AF127257 AF127257 Nemuaron vieillardii rpl16 gene, chloropla...	35	1.8
	emb AW508953 AW508953 si38d01.y1 Gm-r1030 Glycine max cDNA clone...	28	2.1
	emb AW719424 AW719424 LjNEST4d11r Lotus japonicus nodule library...	28	2.1
	emb AW032864 AW032864 EST276423 tomato callus, TAMU Lycopersicon...	29	2.1
55	emb AW306559 AW306559 se52d10.y1 Gm-c1017 Glycine max cDNA clone...	35	2.5
	emb AI399344 AI399344 NCW01D11T7 Westergaards Neurospora crassa ...	35	2.5
	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon ...	34	3.4
	emb Z49212 SC9952X S.cerevisiae chromosome XIII cosmid 9952.	34	3.4
	emb AA741585 AA741585 LmLv39p3/132B Leishmania major promastigot...	34	3.4
60	emb X81715 SCMDYGENE S.cerevisiae partial MDY gene.	34	3.4
	emb X73956 TBMAP292 T.brucei Tb-292 mRNA for membrane associated...	34	3.4

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 emb|X82612|SCATM1 S.cerevisiae ATM1 gene. 34 3.4  
 emb|AC005139|AC005139 Plasmodium falciparum chromosome 12, \*\*\* S... 34 4.7  
 emb|AA649446|AA649446 T4369 MVAT4 bloodstream form of serodeme W... 34 4.7

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 gb|aad18156.2| (ac006260) phenylalanine ammonia lyase (pal1)  
 [arabidopsis /blast\_score 1.00e-134 /ec\_number /family /chip nova  
 /gb\_link /ncgi  
 (848 letters)

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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E  
 Sequences producing significant alignments: (bits) Value

20

emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 419 e-115  
 emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 412 e-113  
 dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 411 e-113  
 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 408 e-112  
 25 emb|Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 331 e-112  
 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 407 e-112  
 gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 407 e-112  
 emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 328 e-111  
 gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 403 e-111  
 30 dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 403 e-111  
 emb|X58180|MSPAL M.sativa PAL-mRNA for phenylalanine ammonia-lyase. 398 e-109  
 gb|L11747|POPPALGA Populus tricarpha X Populus deltoides (hybri... 318 e-109  
 gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 396 e-109  
 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 395 e-108  
 35 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 319 e-108  
 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 312 e-106  
 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 312 e-105  
 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 373 e-102  
 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 174 e-102  
 40 emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 173 e-101  
 emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 214 2e-95  
 emb|AW667320|AW667320 GA\_\_Ea0008P06 Gossypium arboreum 7-10 dpa ... 349 8e-95  
 dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 347 3e-94  
 dbj|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 347 3e-94  
 45 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 291 3e-94  
 emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 314 3e-91  
 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 326 6e-88  
 emb|AW725857|AW725857 GA\_\_Ea0019O22 Gossypium arboreum 7-10 dpa ... 319 9e-86  
 emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 319 1e-85  
 50 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 220 2e-85  
 emb|Z49147|HVPAL7RM H.vulgare partial PAL-mRNA for phenylalanine... 154 5e-85  
 gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 296 9e-81  
 emb|AW774460|AW774460 EST333611 KV3 Medicago truncatula cDNA clo... 302 1e-80  
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 55 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 292 8e-78  
 emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 292 1e-77  
 emb|AI899906|AI899906 sb96a02.y1 Gm-cl012 Glycine max cDNA clone... 287 3e-76  
 emb|AW691458|AW691458 NF045B11ST1F1000 Developing stem Medicago ... 286 6e-76  
 emb|AW696215|AW696215 NF103G12ST1F1099 Developing stem Medicago ... 283 7e-76  
 60 emb|AW688208|AW688208 NF004F12ST1F1000 Developing stem Medicago ... 278 1e-73  
 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 275 9e-73



- emb|AF218454|AF218454 *Coffea arabica* clone 430.4 phenylalanine a... 275 2e-72  
emb|AW560722|AW560722 EST315770 *DSIR Medicago truncatula* cDNA cl... 269 7e-71  
emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 262 1e-68  
5 emb|AV407891|AV407891 AV407891 *Lotus japonicus* young plants (two... 260 3e-68  
emb|AI729040|AI729040 BNLGH12413 Six-day Cotton fiber *Gossypium*... 258 1e-67  
emb|AI780119|AI780119 EST260998 tomato susceptible, Cornell Lyco... 237 3e-66  
emb|X99705|TAPALGEN1 *T.aestivum* PAL gene. 156 2e-65  
emb|AW694081|AW694081 NF072E06ST1F1050 Developing stem *Medicago* ... 225 8e-65  
emb|AW688761|AW688761 NF011C12ST1F1000 Developing stem *Medicago* ... 246 7e-64  
10 emb|AW684895|AW684895 NF022G07NR1F1000 Nodulated root *Medicago* t... 237 3e-63  
emb|AW267882|AW267882 EST306160 *DSIR Medicago truncatula* cDNA cl... 240 4e-62  
emb|AW685144|AW685144 NF025D11NR1F1000 Nodulated root *Medicago* t... 232 5e-61  
emb|AW686498|AW686498 NF042A10NR1F1000 Nodulated root *Medicago* t... 168 2e-60  
gb|U39792|PTU39792 *Pinus taeda* phenylalanine ammonia-lyase (lpPA... 129 5e-60  
15 dbj|D10002|PEAPAL1 *P.sativum* gene for phenylalanine ammonia-lyas... 231 2e-59  
emb|AW720528|AW720528 LjNEST18f8r *Lotus japonicus* nodule library... 146 7e-58  
emb|AI563248|AI563248 EST00372 watermelon lambda zap library Cit... 222 7e-57  
emb|AJ289609|BPE289609 *Betula pendula* partial pal gene for pheny... 133 3e-56  
emb|AW685192|AW685192 NF027D11NR1F1000 Nodulated root *Medicago* t... 219 6e-56  
20 emb|AJ278116|BPE278116 *Betula pendula* partial pall gene for phen... 131 9e-56  
emb|AW033848|AW033848 EST277419 tomato callus, TAMU *Lycopersicon*... 218 1e-55  
emb|AW039368|AW039368 EST281625 tomato mixed elicitor, BTI *Lycop*... 218 1e-55  
emb|AB015871|AB015871 *Vitis vinifera* gene for phenylalanine ammo... 215 8e-55  
emb|AW031670|AW031670 EST275124 tomato callus, TAMU *Lycopersicon*... 215 8e-55  
25 emb|AW650661|AW650661 EST329115 tomato germinating seedlings, TA... 213 4e-54  
emb|AB015870|AB015870 *Vitis vinifera* gene for phenylalanine ammo... 213 4e-54  
emb|X52953|DMPAL1 *Glycine max* PAL1 gene for phenylalanine ammoni... 213 5e-54  
emb|AW219754|AW219754 EST302236 tomato root during/after fruit s... 211 2e-53  
emb|AW690758|AW690758 NF033B06ST1F1000 Developing stem *Medicago* ... 210 3e-53  
30 dbj|D30656|POPPALA *Populus kitakamiensis* gene for phenylalanine ... 208 1e-52  
dbj|D43802|POPPALG2BA *Populus kitakamiensis* gene for phenylalani... 208 2e-52  
emb|AW689402|AW689402 NF018G12ST1F1000 Developing stem *Medicago* ... 207 2e-52  
gb|M91192|TFRPAL1X *Trifolium subterraneum* phenylalanine ammonia-... 197 3e-52  
emb|AW034358|AW034358 EST277929 tomato callus, TAMU *Lycopersicon*... 190 1e-51  
35 emb|AB008200|AB008200 *Nicotiana tabacum* palB gene for phenylalan... 204 2e-51  
gb|M84466|TOBTPA1A Tobacco phenylalanine ammonialyase (tpal) gen... 204 2e-51  
gb|M90692|TOMPAL5A *Lycopersicon esculentum* phenylalanine ammonia... 203 5e-51  
emb|Y07654|PCPAL1 *P.crispum* pal1 gene. 173 6e-51  
dbj|D43803|POPPALG4B *Populus kitakamiensis* gene for phenylalanin... 201 2e-50  
40 emb|AI495627|AI495627 sb11c09.y1 Gm-c1004 *Glycine max* cDNA clone... 140 4e-50  
gb|M83314|TOMPHEAMLY *Lycopersicon esculentum* phenylalanine ammon... 199 7e-50  
dbj|D85850|D85850 *Daucus carota* gDcPAL1 gene for phenylalanine a... 198 1e-49  
emb|AW034782|AW034782 EST278818 tomato callus, TAMU *Lycopersicon*... 141 1e-49  
emb|AW689099|AW689099 NF015D05ST1F1000 Developing stem *Medicago* ... 197 3e-49  
45 emb|AB008199|AB008199 *Nicotiana tabacum* palA gene for phenylalan... 195 6e-49  
emb|X15473|PCPAL1GN *P.crispum* PAL-1 gene for phenylalanine ammon... 120 6e-49  
emb|X63104|STPAL2 *S.tuberosum* PAL-2 gene for phenylalanine ammon... 193 5e-48  
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50 emb|AF019965|AF019965 *Pinus monticola* phenylalanine ammonia lyas... 130 4e-45  
emb|AI778115|AI778115 EST258994 tomato susceptible, Cornell Lyco... 166 1e-44  
emb|AW031859|AW031859 EST275313 tomato callus, TAMU *Lycopersicon*... 165 4e-44  
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emb|AW757191|AW757191 sl30c12.y1 Gm-c1027 *Glycine max* cDNA clone... 174 2e-42  
55 emb|AI484637|AI484637 EST242898 tomato ovary, TAMU *Lycopersicon* ... 174 2e-42  
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emb|AI495119|AI495119 sb03f10.y1 Gm-c1004 *Glycine max* cDNA clone... 169 7e-41  
emb|AW922611|AW922611 DG1\_46\_C11.b1\_A002 Dark Grown 1 (DG1) *Sorg*... 102 1e-40  
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 5 (3115 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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	Sequences producing significant alignments:		(bits) Value
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	dbj D10001 PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase...	232	9e-60
	dbj D10002 PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas...	231	2e-59
	emb AW774460 AW774460 EST333611 KV3 Medicago truncatula cDNA clo...	228	2e-58
	emb AW688761 AW688761 NF011C12ST1F1000 Developing stem Medicago ...	226	5e-58
20	emb AW694081 AW694081 NF072E06ST1F1050 Developing stem Medicago ...	225	1e-57
	emb AW684895 AW684895 NF022G07NR1F1000 Nodulated root Medicago t...	222	9e-57
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	emb AF036948 AF036948 Prunus avium phenylalanine ammonia-lyase (...)	220	6e-56
	emb AF237955 AF237955 Rubus idaeus phenylalanine ammonia-lyase 2...	220	6e-56
25	dbj D10003 PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas...	219	9e-56
	emb X58180 MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase.	219	9e-56
	emb AB015871 AB015871 Vitis vinifera gene for phenylalanine ammo...	215	1e-54
	dbj D26596 CMEPAL Camellia sinensis mRNA for phenylalanine ammon...	215	2e-54
	emb AJ002221 DLJ002221 Digitalis lanata mRNA for phenylalanine a...	214	4e-54
30	emb AW667320 AW667320 GA_Ea0008P06 Gossypium arboreum 7-10 dpa ...	214	4e-54
	emb AB015870 AB015870 Vitis vinifera gene for phenylalanine ammo...	213	5e-54
	emb AW725857 AW725857 GA_Ea0019O22 Gossypium arboreum 7-10 dpa ...	212	1e-53
	emb AW696215 AW696215 NF103G12ST1F1099 Developing stem Medicago ...	211	2e-53
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	dbj D43802 POPPALG2BA Populus kitakamiensis gene for phenylalani...	207	3e-52
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50	emb AB042520 AB042520 Catharanthus roseus mRNA for phenylalanine...	207	5e-52
	gb M90692 TOMPAL5A Lycopersicon esculentum phenylalanine ammonia...	207	5e-52
	emb AI729040 AI729040 BNLGHi12413 Six-day Cotton fiber Gossypium...	206	6e-52
	emb AW686498 AW686498 NF042A10NR1F1000 Nodulated root Medicago t...	153	9e-52
	gb L11747 POPPALGA Populus tricarpha X Populus deltoides (hybri...	205	2e-51
55	emb AB008200 AB008200 Nicotiana tabacum palB gene for phenylalan...	204	2e-51
	gb M84466 TOBTPA1A Tobacco phenylalanine ammonia-lyase (tpal) gen...	204	2e-51
	gb U43338 CLU43338 Citrus limon phenylalanine ammonia-lyase (pal...	204	3e-51
	emb AW033848 AW033848 EST277419 tomato callus, TAMU Lycopersicon...	203	8e-51
	emb AW650661 AW650661 EST329115 tomato germinating seedlings, TA...	203	8e-51
60	emb AW219754 AW219754 EST302236 tomato root during/after fruit s...	203	8e-51
	emb AW220322 AW220322 EST302805 tomato root during/after fruit s...	203	8e-51

- emb|AW039368|AW039368 EST281625 tomato mixed elicitor, BTI Lycop... 203 8e-51  
 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 202 1e-50  
 emb|AI563248|AI563248 EST00372 watermelon lambda zap library Cit... 202 2e-50  
 emb|AW031670|AW031670 EST275124 tomato callus, TAMU Lycopersicon... 202 2e-50  
 5 emb|Y07654|PCPAL1 P.crispum pal1 gene. 173 2e-50  
 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 201 3e-50  
 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 174 4e-50  
 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 199 4e-50  
 emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 173 7e-50  
 10 emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 199 7e-50  
 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 195 1e-49  
 gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 199 1e-49  
 emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 199 1e-49  
 dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 198 2e-49  
 15 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 195 3e-49  
 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 197 4e-49  
 emb|AW720528|AW720528 LjNEST18f8r Lotus japonicus nodule library... 116 5e-49  
 emb|AW689099|AW689099 NF015D05ST1F1000 Developing stem Medicago ... 197 5e-49  
 emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 197 5e-49  
 20 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 196 7e-49  
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	gb BE035432 BE035432 MO05D07 MO Mesembryanthemum crystallinum cD...	111	1e-23
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25	emb AQ874893 AQ874893 V118C3 mTn-3xHA/lacZ Insertion Library, st...	49	1e-07
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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40	emb A26875 A26875 R.sativus AFP1 gene.	160	5e-39
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	gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl...	127	6e-37
	gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot...	138	1e-35
	emb X97318 RSAFP4 R.sativus mRNA for antifungal protein 4.	145	3e-34
45	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3.	127	2e-31
	emb A26963 A26963 D.merkii AMP1 sequence.	76	2e-13
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emb|AW032139|AW032139 EST275593 tomato callus, TAMU Lycopersicon... 145 6e-58  
emb|AW034330|AW034330 EST277901 tomato callus, TAMU Lycopersicon... 144 2e-57  
emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 149 2e-57  
5 emb|AI352771|AI352771 MB58-5G PZ204.BNlib Brassica napus cDNA cl... 220 2e-57  
emb|AW032749|AW032749 EST276308 tomato callus, TAMU Lycopersicon... 149 3e-57  
emb|AI894391|AI894391 EST263846 tomato callus, TAMU Lycopersicon... 142 4e-57  
emb|AI896249|AI896249 EST265692 tomato callus, TAMU Lycopersicon... 142 5e-57  
emb|AI782621|AI782621 EST263500 tomato susceptible, Cornell Lyco... 144 7e-57  
10 emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 160 3e-56  
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emb|AW033687|AW033687 EST277258 tomato callus, TAMU Lycopersicon... 149 2e-55  
emb|AI352783|AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c... 198 3e-55  
emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 140 4e-55  
15 emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 135 6e-55  
emb|AW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 147 1e-53  
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gb|BE034214|BE034214 MH01C07 MH Mesembryanthemum crystallinum cD... 112 4e-52  
emb|AW053720|AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-52  
20 emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 81 4e-52  
emb|AI352801|AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl... 194 1e-51  
emb|X17681|NTPR1CA Tobacco gene for pathogenesis-related protein... 111 2e-51  
emb|X05454|NTPR1CR Nicotiana tabacum mRNA for PR-1c protein. 111 2e-51  
emb|X12487|NTPR1C Tobacco mRNA fragment for pathogenesis-related... 111 2e-51  
25 emb|AJ011520|LES011520 Lycopersicon esculentum pr1a (P4) gene. 98 1e-50  
gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50  
emb|A22634|LEPI4GENE L.esculentum P14 gene. 98 1e-50  
emb|AJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 99 2e-50  
emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50  
30 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50  
emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 116 3e-50  
emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 116 3e-50  
dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 104 3e-50  
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35 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50  
emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50  
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emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50  
40 emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50  
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45 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49  
emb|AW034167|AW034167 EST277738 tomato callus, TAMU Lycopersicon... 94 2e-49  
emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 103 3e-49  
emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 103 3e-49  
dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 103 3e-49  
50 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 6e-49  
gb|M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 92 6e-49  
emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(pl... 92 6e-49  
emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 92 6e-49  
emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 92 6e-49  
55 emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 92 6e-49  
emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 92 6e-49  
emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco... 92 6e-49  
emb|AI782822|AI782822 EST263701 tomato susceptible, Cornell Lyco... 92 6e-49  
emb|AI778686|AI778686 EST259565 tomato susceptible, Cornell Lyco... 92 6e-49  
60 emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 92 6e-49  
emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 92 6e-49



emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 92 6e-49  
 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycope... 92 6e-49  
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 5 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 92 6e-49  
 emb|AW032026|AW032026 EST275480 tomato callus, TAMU Lycopersicon... 92 6e-49  
 emb|AI782288|AI782288 EST263167 tomato susceptible, Cornell Lyco... 92 6e-49  
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 emb|AI781431|AI781431 EST262298 tomato susceptible, Cornell Lyco... 92 6e-49  
 10 emb|AI780973|AI780973 EST261852 tomato susceptible, Cornell Lyco... 92 6e-49  
 emb|AI895236|AI895236 EST264679 tomato callus, TAMU Lycopersicon... 92 6e-49

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 /blast\_score 0 /ec\_number /family /chip nova /gb\_link /ncgi  
 (1236 letters)

20 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
	Sequences producing significant alignments:			(bits) Value
	gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge...	744	0.0	
	emb A00741 A00741 A.rusticana synthetic gene (reverse complement...	692	0.0	
	emb A00740 A00740 A.rusticana synthetic gene for peroxidase.	692	0.0	
30	dbj E01651 E01651 cDNA encoding horseradish peroxidase.	692	0.0	
	gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge...	371	e-133	
	emb X97349 PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P...	473	e-132	
	emb X97350 PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P...	469	e-131	
	dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds.	468	e-131	
35	gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge...	363	e-130	
	emb X97348 PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P...	463	e-129	
	dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part...	441	e-123	
	emb X97351 PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P...	383	e-120	
	dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part...	356	e-112	
40	emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor ...	227	e-107	
	gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple...	229	e-107	
	emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1)...	229	e-106	
	gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA...	381	e-105	
	emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A.	211	e-105	
45	dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i...	296	e-103	
	emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod ...	138	2e-97	
	emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor ...	142	4e-97	
	emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B.	231	1e-95	
	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C.	226	7e-94	
50	gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA.	210	2e-89	
	emb AI959837 AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone...	228	6e-89	
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	emb AW559660 AW559660 EST314772 DSIR Medicago truncatula cDNA cl...	236	1e-87	
	emb AW774581 AW774581 EST333732 KV3 Medicago truncatula cDNA clo...	236	7e-87	
55	emb AF155124 AF155124 Gossypium hirsutum bacterial-induced perox...	215	2e-86	
	emb AW981426 AW981426 EST392579 DSIL Medicago truncatula cDNA cl...	236	2e-85	
	emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per...	209	2e-85	
	emb AF244923 AF244923 Spinacia oleracea peroxidase prx14 precurs...	205	9e-85	
	emb AJ250121 PAB250121 Picea abies mRNA for SPI2 protein (spi2 g...	253	1e-83	
60	emb AW775762 AW775762 EST334827 DSIL Medicago truncatula cDNA cl...	236	6e-83	
	emb Y10466 SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18.	218	3e-82	



- emb|AW775425|AW775425 EST334490 DSIL Medicago truncatula cDNA cl... 208 1e-81  
emb|AW685437|AW685437 NF029D09NR1F1000 Nodulated root Medicago t... 230 9e-80  
emb|AB024439|AB024439 Scutellaria baicalensis mRNA for peroxidase... 209 2e-79  
5 emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 212 3e-79  
emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 115 6e-78  
emb|AW776273|AW776273 EST335338 DSIL Medicago truncatula cDNA cl... 222 1e-77  
emb|AW267813|AW267813 EST305941 DSIR Medicago truncatula cDNA cl... 200 1e-76  
emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 196 5e-76  
10 emb|AF049881|AF049881 Linum usitatissimum peroxidase FLXPER4 (PE... 207 7e-76  
emb|AW256487|AW256487 EST304624 KV2 Medicago truncatula cDNA clo... 200 9e-76  
emb|AW775890|AW775890 EST334955 DSIL Medicago truncatula cDNA cl... 200 3e-74  
emb|AW257195|AW257195 EST305332 KV2 Medicago truncatula cDNA clo... 214 5e-74  
gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 86 2e-73  
gb|U41657|GMU41657 Glycine max seed coat peroxidase isozyme (SPO... 159 3e-73  
15 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 197 5e-73  
gb|L36110|SSNPEROXIA Stylosanthes humilis peroxidase mRNA. 199 5e-73  
gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 204 7e-73  
emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root Medicago t... 236 9e-73  
emb|AW278775|AW278775 sf97d02.y1 Gm-c1019 Glycine max cDNA clone... 155 1e-72  
20 emb|X71593|LECEV11A L.esculentum CEVI-1 mRNA. 99 2e-72  
gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 100 2e-72  
emb|AW559945|AW559945 EST314993 DSIR Medicago truncatula cDNA cl... 233 2e-72  
emb|AW980744|AW980744 EST391897 GVN Medicago truncatula cDNA clo... 235 5e-70  
emb|Y10467|SOPR XR6 S.oleracea mRNA for peroxidase, clone PC23. 105 1e-69  
25 dbj|D83225|POPP02 Populus nigra peroxidase gene, complete cds. 196 2e-69  
gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 205 6e-69  
emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 211 1e-68  
gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68  
emb|AW574244|AW574244 EST316835 GVN Medicago truncatula cDNA clo... 202 1e-67  
30 emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 98 3e-67  
emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root Medicago t... 236 5e-67  
emb|AW561032|AW561032 EST316080 DSIR Medicago truncatula cDNA cl... 203 7e-67  
emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66  
emb|AW185769|AW185769 se59d08.y1 Gm-c1019 Glycine max cDNA clone... 219 4e-65  
35 emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 96 2e-64  
gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64  
emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidase... 205 7e-64  
gb|M91374|CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 76 2e-63  
gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 167 2e-63  
40 gb|M91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 134 2e-63  
emb|AF043235|AF043235 Striga asiatica ferriprotein porphyrin-con... 199 3e-63  
emb|AW288002|AW288002 N100846e rootphos(-) Medicago truncatula c... 182 7e-63  
emb|AW126121|AW126121 N100318e rootphos(-) Medicago truncatula c... 216 1e-62  
gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62  
45 emb|AW687443|AW687443 NF009F07RT1F1062 Developing root Medicago ... 235 1e-61  
emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem Medicago ... 236 3e-61  
emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidase... 163 3e-61  
emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 133 5e-61  
emb|AI496388|AI496388 sb04a11.y1 Gm-c1004 Glycine max cDNA clone... 224 6e-61  
50 emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root Medicago t... 222 8e-61  
dbj|D38050|POPP1 Aspen prxA3a gene for peroxidase, complete cds. 121 9e-61  
emb|AW704659|AW704659 sk54h10.y1 Gm-c1019 Glycine max cDNA clone... 149 9e-61  
emb|Y10464|SOPR XR3 S.oleracea mRNA for peroxidase, clone PC42. 80 3e-60  
emb|AW705730|AW705730 sk51b02.y1 Gm-c1019 Glycine max cDNA clone... 149 8e-60  
55 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60  
gb|U12314|CCU12314 Cenchrus ciliaris clone PX7 peroxidase mRNA, ... 105 9e-60  
emb|AI938533|AI938533 sb46h09.y1 Gm-c1015 Glycine max cDNA clone... 145 1e-59  
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60 emb|AF149278|AF149278 Phaseolus vulgaris peroxidase 3 precursor ... 90 3e-59  
gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59

emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59  
 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59  
 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58  
 emb|AW705946|AW705946 sk52h07.y1 Gm-c1019 Glycine max cDNA clone... 224 6e-58

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 (939 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20

emb|AW730233|AW730233 GA\_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98  
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83  
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77  
 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75  
 25 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72  
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70  
 emb|Z21642|CHASTRNA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67  
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59  
 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58  
 30 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56  
 emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53  
 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49  
 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49  
 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49  
 35 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47  
 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46  
 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46  
 dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45  
 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43  
 40 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42  
 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42  
 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38  
 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38  
 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32  
 45 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycopers... 138 5e-32  
 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30  
 emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26  
 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21  
 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19  
 50 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17  
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 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10  
 emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10  
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 emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09  
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 60 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08  
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	emb AW693052 AW693052 NF059C08ST1F1065 Developing stem Medicago ...	51	1e-05
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	emb AW616467 AW616467 EST322878 L. hirsutum trichome, Cornell Un...	48	7e-05
	emb AL354022 P761R Leishmania major Friedlin PAC P761 right end-...	44	0.002
5	gb M91656 CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1...	43	0.005
	emb AQ903789 AQ903789 GSSTc04230 Trypanosome cruzi random genom...	35	0.24
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10	emb AL139794 LMFP1105 Leishmania major Friedlin chromosome 4 PAC...	35	0.87
	emb AW926438 AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis...	34	1.2
	emb AA965348 AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	gb U12630 ENU12630 Emericella nidulans R153 core histone H3 (H3)...	34	1.3
	emb AI007494 AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
15	emb AA787433 AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	emb X55548 ANH3GENE A.nidulans gene for core histone for H3.	34	1.3
	emb AQ396426 AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P...	34	1.6
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	gb M19025 CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c...	34	1.6
20	emb AF084888 AF084888 Neurospora crassa 656-2A mutant tryptophan...	31	1.7
	emb AF084887 AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta...	31	1.7
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	emb AQ500614 AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc...	33	2.5
25	emb AW187498 AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187530 AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW694072 AW694072 NF072B12ST1F1096 Developing stem Medicago ...	33	3.1
	emb AW186883 AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187537 AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ...	33	3.1
30	emb AW187474 AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33	3.5
	emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two...	33	4.3
	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33	4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33	4.7
35	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32	5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom...	32	5.9
	emb AW728623 AW728623 GA__Ea0017G06 Gossypium arboreum 7-10 dpa ...	32	5.9
	gb BE027723 BE027723 EtESTea86c08.y1 Eimeria M5-6 Merozoite stag...	32	5.9
40	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st...	32	5.9
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	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone...	32	5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32	5.9
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45	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32	6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32	6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien...	28	7.3
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50	emb AW703740 AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AW703739 AW703739 sk23g08.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
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	emb AV420652 AV420652 AV420652 Lotus japonicus young plants (two...	32	8.1
55	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two...	32	8.1
	emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two...	32	8.1
	emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two...	32	8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library...	32	8.1
60	emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron.	32	8.1



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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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15	emb AF042320 AF042320 <i>Camptotheca acuminata</i> tryptophan synthase ...	858	0.0
	emb AF047024 AF047024 <i>Chlamydomonas reinhardtii</i> tryptophan synth...	712	0.0
	gb J04594 NEUTRP3A <i>N.crassa</i> tryptophan synthetase (trp3) alpha-2...	473	e-140
	emb Z98974 SPAC19A8 <i>S.pombe</i> chromosome I cosmid c19A8.	462	e-135
	emb AW031813 AW031813 EST275267 tomato callus, TAMU <i>Lycopersicon</i> ...	429	e-119
20	emb AF121272 AF121272 <i>Gracilaria gracilis</i> putative NAD-myo-inosi...	426	e-118
	dbj D89113 D89113 <i>Schizosaccharomyces pombe</i> mRNA, partial cds, c...	310	e-114
	emb AI055312 AI055312 coau0003K07 Cotton Boll Abscission Zone cD...	404	e-112
	emb AF042321 AF042321 <i>Camptotheca acuminata</i> tryptophan synthase ...	346	e-109
	gb BE126222 BE126222 DG1_68_D09.b1_A002 Dark Grown 1 (DG1) Sorgh...	379	e-104
25	emb AW650635 AW650635 EST329089 tomato germinating seedlings, TA...	372	e-102
	emb AI487343 AI487343 EST245665 tomato ovary, TAMU <i>Lycopersicon</i> ...	354	8e-97
	emb AI488733 AI488733 EST247072 tomato ovary, TAMU <i>Lycopersicon</i> ...	353	2e-96
	emb AA495663 AA495663 c313 Zhou and Ragan 1993 <i>Gracilaria gracil</i> ...	350	1e-95
	emb AW160221 AW160221 EST290079 <i>L. pennellii</i> trichome, Cornell U...	327	1e-88
30	emb V01342 SCTRP5A Yeast gene (trp5) for tryptophan synthetase.	270	6e-88
	emb Z72548 SCYGL026C <i>S.cerevisiae</i> chromosome VII reading frame O...	270	6e-88
	emb AI485149 AI485149 EST243453 tomato ovary, TAMU <i>Lycopersicon</i> ...	319	3e-86
	emb AI966766 AI966766 sc57f10.y1 Gm-cl016 Glycine max cDNA clone...	306	3e-82
	gb M91659 CCITRP08 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	302	4e-81
35	gb BE058277 BE058277 sn13h12.y1 Gm-cl016 Glycine max cDNA clone ...	259	6e-68
	emb AI488512 AI488512 EST246851 tomato ovary, TAMU <i>Lycopersicon</i> ...	237	2e-63
	emb AI487792 AI487792 EST246114 tomato ovary, TAMU <i>Lycopersicon</i> ...	232	8e-62
	emb AW696637 AW696637 NF109C11ST1F1085 Developing stem <i>Medicago</i> ...	213	2e-59
	emb AI898827 AI898827 EST268270 tomato ovary, TAMU <i>Lycopersicon</i> ...	228	7e-59
40	emb AQ450225 AQ450225 500009D01.x1 CpIOWAM13mp18gDNA1 <i>Cryptospor</i> ...	175	3e-58
	emb AW160220 AW160220 EST290078 <i>L. pennellii</i> trichome, Cornell U...	223	3e-57
	emb AF084902 AF084902 <i>Neurospora crassa</i> TD2(4A-4A)2A mutant tryp...	214	2e-54
	emb AF084903 AF084903 <i>Neurospora crassa</i> TD71-19A mutant tryptoph...	213	3e-54
45	emb AF084904 AF084904 <i>Neurospora crassa</i> TD54-6A mutant tryptoph...	210	3e-53
	emb AI779245 AI779245 EST260124 tomato susceptible, Cornell Lyco...	208	8e-53
	emb AI487088 AI487088 EST245410 tomato ovary, TAMU <i>Lycopersicon</i> ...	149	3e-51
	emb AQ876415 AQ876415 V99F5 mTn-3xHA/lacZ Insertion Library, str...	183	4e-50
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	emb AF084892 AF084892 <i>Neurospora crassa</i> 314-567-9A mutant trypto...	132	1e-37
	emb AF084891 AF084891 <i>Neurospora crassa</i> 314-616-2A mutant trypto...	132	1e-37
	emb AF084895 AF084895 <i>Neurospora crassa</i> TD10-8A mutant tryptoph...	130	1e-37
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	emb AF084901 AF084901 <i>Neurospora crassa</i> TD72-1-25A mutant trypto...	129	1e-37
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	emb AF084898 AF084898 <i>Neurospora crassa</i> TD6(1-8A)22A mutant tryp...	129	1e-37
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	emb AF084897 AF084897 <i>Neurospora crassa</i> TD3-32-16A mutant trypto...	128	3e-37
	emb AI399300 AI399300 NCW07F11T3 Westergaards <i>Neurospora crassa</i> ...	145	3e-37
	emb AF084906 AF084906 <i>Neurospora crassa</i> NG40-5A mutant tryptopha...	152	8e-36
	emb AF084905 AF084905 <i>Neurospora crassa</i> NG25-4A mutant tryptopha...	152	8e-36
5	gb BE024522 BE024522 894003E01.y1 <i>C. reinhardtii</i> CC-1690, normal...	142	6e-33
	emb AJ229567 KLAJ9567 <i>Kluyveromyces lactis</i> DNA fragment for sequ...	137	3e-31
	emb AQ449630 AQ449630 500002F12.x2 CplOWAM13mp18gDNA1 <i>Cryptospor...</i>	116	1e-27
	emb AW695848 AW695848 NF099D01ST1F1012 Developing stem <i>Medicago</i> ...	116	9e-27
10	emb AW098758 AW098758 ga01a03.y1 Moss EST library CPU <i>Ceratodon</i> ...	118	1e-25
	gb M91658 CCITRP07 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	115	8e-25
	emb AW086510 AW086510 ga01a03.x1 Moss EST library CPU <i>Ceratodon</i> ...	103	4e-21
	emb AW221168 AW221168 EST297637 tomato fruit mature green, TAMU ...	96	5e-19
	emb AW650217 AW650217 EST328671 tomato germinating seedlings, TA...	95	1e-18
15	emb AV408265 AV408265 AV408265 <i>Lotus japonicus</i> young plants (two...	77	4e-13
	emb AW688230 AW688230 NF005A01ST1F1000 Developing stem <i>Medicago</i> ...	72	1e-11
	emb AI488384 AI488384 EST246706 tomato ovary, TAMU <i>Lycopersicon</i> ...	70	4e-11
	emb AW032971 AW032971 EST276530 tomato callus, TAMU <i>Lycopersicon</i> ...	60	6e-08
	emb AW755317 AW755317 sl01e06.y1 Gm-cl036 <i>Glycine max</i> cDNA clone...	57	4e-07
20	emb AW153250 AW153250 se37h08.y1 Gm-cl015 <i>Glycine max</i> cDNA clone...	56	1e-06
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	emb AW625162 AW625162 EST319069 tomato radicle, 5 d post-imbibit...	45	0.001
	gb M91656 CCITRP05 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	45	0.002
	emb AW926725 AW926725 HVSMEg0007P16 <i>Hordeum vulgare</i> pre-anthesis...	42	0.013
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35	emb AW185330 AW185330 se90b04.y1 Gm-cl027 <i>Glycine max</i> cDNA clone...	37	0.32
	emb Z38061 SC9168 <i>S.cerevisiae</i> chromosome IX cosmid 9168.	37	0.32
	emb AF160799 AF160799 <i>Sporidiobolus salmonicolor</i> aldehyde reduct...	37	0.44
	emb AC016161 AC016161 <i>Leishmania major</i> chromosome 35 clone L8149...	37	0.44
	emb AW185636 AW185636 se80e06.y1 Gm-cl023 <i>Glycine max</i> cDNA clone...	37	0.44
40	emb AB030490 AB030490 <i>Glycine max</i> SG-05 gene for thiamin biosynt...	36	0.60
	emb AW278827 AW278827 sf99b01.y1 Gm-cl019 <i>Glycine max</i> cDNA clone...	36	0.60
	emb Z93048 SLZ93048 <i>S.latifolia</i> mRNA, clone CCLS 37.1.	30	0.72
	emb AV393412 AV393412 AV393412 <i>Chlamydomonas reinhardtii</i> C9 Chla...	36	0.83
	emb AL035581 SPBC1677 <i>S.pombe</i> chromosome II cosmid c1677.	36	0.83
45	emb AV425767 AV425767 AV425767 <i>Lotus japonicus</i> young plants (two...	36	0.83
	emb AI727538 AI727538 BNLGHi8343 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	gb BE053957 BE053957 GA_Ea0033K12f <i>Gossypium arboreum</i> 7-10 dpa ...	35	1.1
	emb AI731384 AI731384 BNLGHi8894 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AW596016 AW596016 si96g09.y1 Gm-cl032 <i>Glycine max</i> cDNA clone...	35	1.1
50	emb AI730998 AI730998 BNLGHi8370 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AJ276509 TAE276509 <i>Triticum aestivum</i> grpl gene for glycine-r...	28	1.3
	gb B13527 B13527 jd421 Trypanosome Shotgun M13 genomic Trypanoso...	29	1.4
	gb U56698 CPU56698 <i>Ceratodon purpureus</i> phytochrome photoreceptor...	35	2.2
	emb AF079252 AF079252 <i>Dichanthium aristatum</i> granule-bound starch...	35	2.2
55	emb AJ133604 TAE133604 <i>Triticum aestivum</i> mRNA for alpha-gliadin ...	34	4.1

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	emb AW171733 AW171733 N100627e rootphos(-) Medicago truncatula c...	36	0.099
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35	emb AI777176 AI777176 EST258141 tomato resistant, Cornell Lycopen...	35	0.26
	gb C22084 C22084 C22084 Miyagawa-wase satsuma mandarin orange (M...	35	0.26
	emb AW755041 AW755041 PC10A02 Pine TriplEx pollen cone library P...	35	0.26
	emb AW218263 AW218263 EST303444 tomato radicle, 5 d post-imbibit...	35	0.26
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40	emb AA557085 AA557085 927 Loblolly pine N Pinus taeda cDNA clone...	35	0.26
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	emb AW982079 AW982079 PC23E11 Pine TriplEx pollen cone library P...	35	0.35
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45	emb AI812646 AI812646 17D5 Pine Lambda Zap Xylem library Pinus t...	35	0.35
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	gb BE034004 BE034004 MG03C08 MG Mesembryanthemum crystallinum cD...	33	1.3

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5 emb|AW216739|AW216739 EST295453 tomato callus, TAMU Lycopersicon... 33 1.3  
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10 emb|AW255347|AW255347 ML358 peppermint glandular trichome Menth... 32 2.4  
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25 emb|AI938315|AI938315 sc42h10.y1 Gm-c1014 Glycine max cDNA clone... 31 4.5  
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35 emb|AW683985|AW683985 NF004G11NR1F1000 Nodulated root Medicago t... 30 8.5  
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45 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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50 Score E  
Sequences producing significant alignments: (bits) Value

emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 105 1e-22  
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55 emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 105 1e-22  
emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 105 1e-22  
emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 105 1e-22  
emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 105 1e-22  
emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 105 1e-22  
60 emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 105 1e-22  
emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 104 2e-22



	emb AW399412 AW399412 EST309912 <i>L. pennellii</i> trichome, Cornell U...	104	2e-22
	emb AI773854 AI773854 EST254954 tomato resistant, Cornell Lycopersicon...	104	3e-22
	gb BE125244 BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh...	99	9e-21
	emb AI736542 AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone...	64	5e-17
5	emb AI938176 AI938176 sc40e07.y1 Gm-c1014 Glycine max cDNA clone...	84	2e-16
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	emb AW133238 AW133238 sel6b04.y1 Gm-c1013 Glycine max cDNA clone...	84	3e-16
	emb AW568464 AW568464 si59b03.y1 Gm-r1030 Glycine max cDNA clone...	84	3e-16
	emb AW832123 AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone...	84	5e-16
10	emb AI899328 AI899328 EST268771 tomato ovary, TAMU Lycopersicon...	82	2e-15
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	emb AI443600 AI443600 sa42b08.y1 Gm-c1004 Glycine max cDNA clone...	72	1e-12
	gb BE057559 BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone...	70	5e-12
	emb AI896759 AI896759 EST266202 tomato callus, TAMU Lycopersicon...	61	3e-09
15	gb BE123900 BE123900 EST394025 <i>DSIL Medicago truncatula</i> cDNA clo...	58	2e-08
	emb AW030966 AW030966 EST274273 tomato callus, TAMU Lycopersicon...	34	8e-05
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	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone...	40	0.004
20	emb AW217201 AW217201 EST295915 tomato callus, TAMU Lycopersicon...	29	0.010
	emb AI487153 AI487153 EST245475 tomato ovary, TAMU Lycopersicon...	35	0.14
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	emb AW395281 AW395281 sh46b07.y1 Gm-c1017 Glycine max cDNA clone...	32	1.8
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35	emb AW034791 AW034791 EST278827 tomato callus, TAMU Lycopersicon...	31	2.4
	emb AI780125 AI780125 EST261004 tomato susceptible, Cornell Lyco...	31	2.4
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40	emb AW623982 AW623982 EST321927 tomato flower buds 3-8 mm, Corne...	29	2.5
	emb AW719534 AW719534 LjNEST5c5rW <i>Lotus japonicus</i> nodule library...	31	3.3
	emb AW926699 AW926699 HVSMEg0007O14 <i>Hordeum vulgare</i> pre-anthesis...	31	3.3
	emb AL035264 LMFL8032 <i>Leishmania major</i> Friedlin chromosome 4 cos...	30	4.5
	emb AF015462 AF015462 <i>Plasmodium falciparum</i> microsatellite 14D s...	30	4.5
45	emb AQ989347 AQ989347 Gm_ISb001_080_I14R ISU Soybean BAC Library...	30	4.5
	emb AL354553 LMFL232 <i>Leishmania major</i> Friedlin chromosome 14 cos...	30	6.2
	emb AL049498 SPCC645 <i>S.pombe</i> chromosome III cosmid c645.	30	6.2
	emb AI352775 AI352775 MB58-8A PZ204.BNlib <i>Brassica napus</i> cDNA cl...	30	6.2
	emb AZ216688 AZ216688 Sheared DNA-84G11.TF Sheared DNA Trypanoso...	30	6.2
50	emb AQ160113 AQ160113 mgxb0003K19r CUGI Rice Blast BAC Library P...	30	6.2
	emb AF105143 AF105143 <i>Brassica napus</i> chromosome N3 disease resis...	29	8.6
	emb AV394954 AV394954 AV394954 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AF162071 AF162071 <i>Mortierella verticillata</i> beta-tubulin 1 (b...	29	8.6
	emb AV395268 AV395268 AV395268 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
55	emb AI960376 AI960376 sc82g12.y1 Gm-c1018 Glycine max cDNA clone...	29	8.6
	emb AV393824 AV393824 AV393824 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
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	emb AV396392 AV396392 AV396392 <i>Chlamydomonas reinhardtii</i> C9 Chla...	29	8.6
	emb AQ659750 AQ659750 Sheared DNA-16J7.TF Sheared DNA Trypanosom...	29	8.6
60	emb AL163505 LMFL3640 <i>Leishmania major</i> Friedlin chromosome 21 co...	29	8.6



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5 http://www3.ncbi.nlm.nih.gov/htbin-  
post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt788|/ncgi  
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10 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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	emb AI210929 AI210929 m0d12a1.r1 Aspergillus nidulans 24hr asexu...	34	0.81	
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25	emb AF093253 AF093253 Selaginella deflexa ribulose biphosphate ...	34	1.1	
	emb AW692476 AW692476 NF052A03ST1F1000 Developing stem Medicago ...	33	1.5	
	emb AW756661 AW756661 sl25e12.y1 Gm-c1027 Glycine max cDNA clone...	33	1.5	
	emb AW278522 AW278522 sf45e07.y1 Gm-c1009 Glycine max cDNA clone...	33	1.5	
	emb AW424313 AW424313 sh63h04.y1 Gm-c1015 Glycine max cDNA clone...	33	1.5	
30	emb AW696170 AW696170 NF103B07ST1F1060 Developing stem Medicago ...	33	1.5	
	emb AW569414 AW569414 si86g10.y1 Gm-c1031 Glycine max cDNA clone...	33	1.5	
	emb AW830833 AW830833 sm36c08.y1 Gm-c1028 Glycine max cDNA clone...	33	1.5	
	emb AW831982 AW831982 sm18e08.y1 Gm-c1027 Glycine max cDNA clone...	33	1.5	
	emb AW734341 AW734341 sk81h11.y1 Gm-c1016 Glycine max cDNA clone...	33	1.5	
35	emb Y07940 SSY07940 S.selaginoides chloroplast rbcL gene.	33	2.1	
	emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi...	32	4.0	
	emb AQ946352 AQ946352 Sheared DNA-45B22.TF Sheared DNA Trypanoso...	31	5.5	
	emb AW180477 AW180477 MgA0600f MgA Library Mycosphaerella gramin...	31	5.5	
	emb AQ651798 AQ651798 Sheared DNA-20J13.TR Sheared DNA Trypanoso...	31	5.5	

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45 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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	emb AF133302 AF133302 Brassica rapa subsp. pekinensis type 2 per...	331	2e-90	
55	emb AW667697 AW667697 GA__Ea0010E14 Gossypium arboreum 7-10 dpa ...	287	6e-77	
	emb AI778230 AI778230 EST259109 tomato susceptible, Cornell Lyco...	287	6e-77	
	emb AW218621 AW218621 EST303804 tomato radicle, 5 d post-imbibit...	287	6e-77	
	emb AW668548 AW668548 GA__Ea0014I16 Gossypium arboreum 7-10 dpa ...	287	6e-77	
	emb AW668413 AW668413 GA__Ea0013N18 Gossypium arboreum 7-10 dpa ...	287	6e-77	
60	emb AI782495 AI782495 EST263374 tomato susceptible, Cornell Lyco...	285	3e-76	
	emb AI779421 AI779421 EST260300 tomato susceptible, Cornell Lyco...	285	3e-76	

- emb|AI775630|AI775630 EST256730 tomato resistant, Cornell Lycopersicon... 285 3e-76  
gb|BE055389|BE055389 GA\_\_Ea0026N20f Gossypium arboreum 7-10 dpa ... 284 5e-76  
emb|AI779420|AI779420 EST260299 tomato susceptible, Cornell Lycopersicon... 282 2e-75  
5 emb|AW349482|AW349482 GM210007A20G5R Gm-r1021 Glycine max cDNA 3... 282 2e-75
- emb|AW041006|AW041006 EST283870 tomato mixed elicitor, BTI Lycopersicon... 279 2e-74  
emb|AW597183|AW597183 sj74f03.y1 Gm-c1034 Glycine max cDNA clone... 278 3e-74  
gb|BE055703|BE055703 GA\_\_Ea0033C16f Gossypium arboreum 7-10 dpa ... 275 2e-73  
10 emb|AW567736|AW567736 si54c02.y1 Gm-r1030 Glycine max cDNA clone... 275 2e-73  
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emb|AW472050|AW472050 si19d05.y1 Gm-c1029 Glycine max cDNA clone... 273 8e-73  
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emb|AW568074|AW568074 si68b05.y1 Gm-r1030 Glycine max cDNA clone... 272 1e-72  
15 emb|AW733947|AW733947 sk85e02.y1 Gm-c1035 Glycine max cDNA clone... 271 4e-72  
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emb|AW573705|AW573705 EST316296 GVN Medicago truncatula cDNA clone... 271 4e-72  
emb|AW508326|AW508326 si52e11.y1 Gm-r1030 Glycine max cDNA clone... 270 7e-72  
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20 emb|AI930835|AI930835 sc47h06.y1 Gm-c1015 Glycine max cDNA clone... 269 1e-71  
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25 emb|AW559683|AW559683 EST314795 DSIR Medicago truncatula cDNA clone... 260 6e-69  
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- 30 emb|AW094638|AW094638 EST287806 tomato mixed elicitor, BTI Lycopersicon... 255 3e-67  
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- emb|AW666097|AW666097 sk32b07.y1 Gm-c1028 Glycine max cDNA clone... 248 4e-65  
35 emb|AW756544|AW756544 sl23d11.y1 Gm-c1036 Glycine max cDNA clone... 247 6e-65  
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40 emb|AI162549|AI162549 A019P27U Hybrid aspen plasmid library Populus... 236 2e-61  
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emb|AW065021|AW065021 ST38F08 Pine TriplEx shoot tip library Pinus... 236 2e-61  
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emb|AW043308|AW043308 ST31G09 Pine TriplEx shoot tip library Pinus... 230 1e-59  
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45 emb|AI774108|AI774108 EST255208 tomato resistant, Cornell Lycopersicon... 227 7e-59  
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- 55 emb|AW747461|AW747461 WS1\_68\_B01.g1\_A002 Water-stressed 1 (WS1) ... 181 1e-51  
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60 emb|AI164569|AI164569 A065P13U Hybrid aspen plasmid library Populus... 180 2e-48  
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emb|AI855650|AI855650 sc32c06.y1 Gm-cl014 Glycine max cDNA clone... 127 3e-45  
 emb|AI777234|AI777234 EST258199 tomato resistant, Cornell Lycopen... 148 1e-44  
 emb|AI165310|AI165310 A081P03U Hybrid aspen plasmid library Popu... 152 7e-44  
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 5 emb|AI484178|AI484178 EST249331 tomato resistant, Cornell Lycopen... 144 2e-43  
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 15 emb|AI484189|AI484189 EST249342 tomato resistant, Cornell Lycopen... 157 9e-38  
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 25 emb|AI165031|AI165031 A073p61u Hybrid aspen plasmid library Popu... 131 6e-32  
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Database: plantfungal  
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 emb|AW933092|AW933092 EST358935 tomato fruit mature green, TAMU ... 287 4e-76  
 emb|AW442160|AW442160 EST311556 tomato fruit red ripe, TAMU Lyco... 220 8e-74  
 emb|AW681014|AW681014 WS1\_8\_B05.b1\_A002 Water-stressed 1 (WS1) S... 275 1e-72  
 60 emb|AW933411|AW933411 EST359350 tomato fruit mature green, TAMU ... 272 1e-71  
 emb|AW931846|AW931846 EST357689 tomato fruit mature green, TAMU ... 264 3e-69



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	emb AW035300 AW035300 EST280663 tomato callus, TAMU Lycopersicon...	241	3e-62
	emb AW934545 AW934545 EST353353 tomato flower buds 0-3 mm, Corne...	230	4e-59
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5	emb AL022244 SPBC3B8 S.pombe chromosome II cosmid c3B8.	181	2e-56
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	emb AW035261 AW035261 EST280523 tomato callus, TAMU Lycopersicon...	142	4e-52
	emb AI896768 AI896768 EST266211 tomato callus, TAMU Lycopersicon...	192	2e-47
10	emb Z71665 SCYNR050C S.cerevisiae chromosome XIV reading frame O...	155	5e-47
	emb X77363 SCLYS9 S.cerevisiae LYS9 gene.	155	5e-47
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	emb AW441656 AW441656 EST311052 tomato fruit red ripe, TAMU Lyco...	110	2e-38
	emb AI486762 AI486762 EST245084 tomato ovary, TAMU Lycopersicon ...	161	3e-38
20	emb AI488387 AI488387 EST246709 tomato ovary, TAMU Lycopersicon ...	160	6e-38
	emb AW093830 AW093830 EST287010 tomato mixed elicitor, BTI Lycop...	98	4e-33
	emb AV427683 AV427683 AV427683 Lotus japonicus young plants (two...	142	2e-32
	emb AI782310 AI782310 EST263189 tomato susceptible, Cornell Lyco...	139	1e-31
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25	emb AL111972 CNS019QK Botrytis cinerea strain T4 cDNA library un...	136	1e-30
	emb AU012735 AU012735 AU012735 Schizosaccharomyces pombe late lo...	125	5e-30
	emb AI771382 AI771382 EST252482 tomato ovary, TAMU Lycopersicon ...	132	1e-29
	emb AW681093 AW681093 WS1_8_B05.g1_A002 Water-stressed 1 (WS1) S...	127	7e-28
	emb AU010645 AU010645 AU010645 Schizosaccharomyces pombe late lo...	118	2e-25
30	emb AW038858 AW038858 EST280814 tomato mixed elicitor, BTI Lycop...	114	5e-24
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	emb AI487518 AI487518 EST245840 tomato ovary, TAMU Lycopersicon ...	110	6e-23
	emb AI486763 AI486763 EST245085 tomato ovary, TAMU Lycopersicon ...	110	6e-23
	emb AI399018 AI399018 NCW10A5T3 Westergaards Neurospora crassa c...	63	1e-21
35	emb AW031018 AW031018 EST274325 tomato callus, TAMU Lycopersicon...	101	4e-20
	emb AW932183 AW932183 EST358026 tomato fruit mature green, TAMU ...	72	9e-13
	emb AW096237 AW096237 EST289417 tomato mixed elicitor, BTI Lycop...	67	8e-10
	emb AA577639 AA577639 EST213 Sugarcane leaf roll Saccharum sp. c...	65	3e-09
	emb AW224318 AW224318 EST301045 tomato fruit red ripe, TAMU Lyco...	51	5e-05
40	emb AI900022 AI900022 sb97g03.y1 Gm-c1012 Glycine max cDNA clone...	50	1e-04
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	emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168.	45	0.004
	emb X77362 SCLYS1 S.cerevisiae LYS1 gene.	45	0.004
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45	gb U13233 CAU13233 Candida albicans saccharopine dehydrogenase (...)	40	0.078
	emb AL110979 CNS018Z0 Botrytis cinerea strain T4 cDNA library un...	35	0.079
	emb AL133156 SPAC227 S.pombe chromosome I cosmid c227.	40	0.15
	emb AF178855 AF178855 Candida albicans Crm1p (CRM1) gene, comple...	37	0.99
	emb AI667978 AI667978 TENG0800 T. Cruzi epimastigote normalised ...	36	1.4
50	emb AW310192 AW310192 sf32e10.x1 Gm-c1028 Glycine max cDNA clone...	36	1.4
	emb AW705872 AW705872 sk52a01.y1 Gm-c1019 Glycine max cDNA clone...	35	2.6
	emb AL355930 NCB208 Neurospora crassa DNA linkage group II BAC c...	35	3.5
	gb N82089 N82089 TgESTzy41f01.r1 TgRH Tachyzoite cDNA Toxoplasma...	35	3.5
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	emb AA451583 AA451583 AJK252 Onion seedling leaf cDNA library Al...	35	4.8
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60	emb X99000 CS39KBCIV S.cerevisiae 39kb DNA segment of chromosome...	34	6.7
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5	emb AV420631 AV420631 AV420631 Lotus japonicus young plants (two...	34	6.7
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15	emb AF106954 AF106954 Brassica napus galactinol synthase (GS) mR...	34	9.2
	emb AW164589 AW164589 se73h03.y1 Gm-cl023 Glycine max cDNA clone...	34	9.2
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	emb AI897690 AI897690 EST267133 tomato ovary, TAMU Lycopersicon ...	205	7e-54
45	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	162	1e-53
	emb AI486547 AI486547 EST244868 tomato ovary, TAMU Lycopersicon ...	150	1e-53
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	165	1e-53
	emb AI489882 AI489882 EST248221 tomato ovary, TAMU Lycopersicon ...	205	3e-53
	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	168	5e-53
50	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	163	9e-53
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	170	8e-52
	emb AI485022 AI485022 EST243302 tomato ovary, TAMU Lycopersicon ...	205	1e-51
	emb AI484547 AI484547 EST242777 tomato ovary, TAMU Lycopersicon ...	205	1e-51
	emb AI484020 AI484020 EST249891 tomato ovary, TAMU Lycopersicon ...	205	1e-51
55	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	160	2e-51
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	emb AW616916 AW616916 EST323327 L. hirsutum trichome, Cornell Un...	145	3e-51
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60	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	154	7e-50
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	164	7e-50

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5 emb|AW266297|AW266297 L30-3030T3 Ice plant Lambda Uni-Zap XR exp... 169 3e-48  
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15 emb|Y18260|BOY18260 *Brassica oleracea* mRNA for SRK15 protein, pa... 150 1e-46  
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25 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 145 2e-45  
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30 emb|AF220603|AF220603 *Lycopersicon esculentum* VFNT Cherry Pto lo... 96 2e-44  
emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber *Gossypium* ... 132 3e-44  
emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 151 4e-44  
emb|AI489009|AI489009 EST247348 tomato ovary, TAMU *Lycopersicon* ... 117 7e-44  
emb|AI483732|AI483732 EST249603 tomato ovary, TAMU *Lycopersicon* ... 177 4e-43  
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35 gb|U59315|LPU59315 *Lycopersicon pimpinellifolium* serine/threonin... 88 1e-42  
gb|U02271|LEU02271 *Lycopersicon pimpinellifolium* Rio Grande-PtoR... 88 1e-42  
emb|AJ245479|BNA245479 *Brassica napus* Sll3, slk, srk, CePP, Fmt,... 80 2e-42  
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45 gb|U59316|LEU59316 *Lycopersicon esculentum* serine/threonine prot... 87 1e-41  
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60 gb|U59318|LEU59318 *Lycopersicon esculentum* serine/threonine prot... 92 6e-40  
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emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 129 1e-39.  
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 5 emb|AW284352|AW284352 LG1\_275\_D12.g1\_A002 Light Grown 1 (LG1) So... 165 2e-39  
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Database: plantfungal  
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	emb AW666282 AW666282 sk34f11.y1 Gm-cl028 Glycine max cDNA clone...	360	2e-98
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	emb AW737130 AW737130 EST338557 tomato flower buds, anthesis, Co...	325	1e-87
	emb AW689358 AW689358 NF018C09ST1F1000 Developing stem Medicago ...	281	3e-85
40	emb AW650696 AW650696 EST329150 tomato germinating seedlings, TA...	179	2e-84
	emb AW625020 AW625020 EST313849 tomato radicle, 5 d post-imbibit...	301	1e-80
	emb AI813214 AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta...	297	2e-80
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	gb BE052354 BE052354 GA_Ea0034P16f Gossypium arboreum 7-10 dpa ...	282	5e-75
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 10 emb|AA660997|AA660997 00894 MtRHE Medicago truncatula cDNA 5' si... 72 2e-34  
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 20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 5e-27  
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 emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 80 2e-22  
 25 emb|AW689996|AW689996 NF026G01ST1F1000 Developing stem Medicago ... 91 7e-20  
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 35 emb|AI486949|AI486949 EST245271 tomato ovary, TAMU Lycopersicon ... 83 1e-14  
 emb|Z71550|SCYNL274C S.cerevisiae chromosome XIV reading frame O... 83 1e-14  
 emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco... 83 1e-14  
 emb|AW030822|AW030822 EST274077 tomato callus, TAMU Lycopersicon... 83 1e-14  
 emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 83 1e-14  
 40 emb|AW442123|AW442123 EST311519 tomato fruit red ripe, TAMU Lyco... 83 1e-14  
 emb|AW651324|AW651324 EST329778 tomato germinating seedlings, TA... 83 1e-14  
 emb|AW647711|AW647711 EST307192 tomato germinating seedlings, TA... 83 1e-14  
 emb|Z21493|MISTFDHD S.tuberosum mRNA for formate dehydrogenase. 83 1e-14  
 emb|AI822999|AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr... 82 1e-14  
 45 emb|AW693443|AW693443 NF065D03ST1F1000 Developing stem Medicago ... 71 2e-14  
 emb|AI488120|AI488120 EST246442 tomato ovary, TAMU Lycopersicon ... 80 5e-14  
 emb|AT000538|AT000538 AT000538 Brassica rapa guard cell Brassica... 80 7e-14  
 emb|AI490350|AI490350 EST248676 tomato ovary, TAMU Lycopersicon ... 79 9e-14  
 emb|AQ874261|AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st... 79 1e-13  
 50 emb|AI490396|AI490396 EST248734 tomato ovary, TAMU Lycopersicon ... 78 2e-13  
 dbj|D88272|D88272 Hordeum vulgare mRNA for formate dehydrogenase... 78 3e-13  
 emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 75 2e-12  
 emb|AW266848|AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr... 74 3e-12  
 emb|AI897727|AI897727 EST267170 tomato ovary, TAMU Lycopersicon ... 74 4e-12  
 55 emb|AI898003|AI898003 EST267446 tomato ovary, TAMU Lycopersicon ... 74 4e-12  
 emb|AI898454|AI898454 EST267897 tomato ovary, TAMU Lycopersicon ... 74 4e-12  
 emb|AI898267|AI898267 EST267710 tomato ovary, TAMU Lycopersicon ... 74 4e-12  
 emb|AW278707|AW278707 sf96b06.yl Gm-cl019 Glycine max cDNA clone... 73 6e-12  
 emb|AI483926|AI483926 EST249797 tomato ovary, TAMU Lycopersicon ... 73 8e-12  
 60 emb|AW930862|AW930862 EST356705 tomato fruit mature green, TAMU ... 73 1e-11  
 emb|AI899038|AI899038 EST268481 tomato ovary, TAMU Lycopersicon ... 73 1e-11



	gb BE055276 BE055276 GA__Ea0034L16f Gossypium arboreum 7-10 dpa ...	57	2e-11
	emb AI488243 AI488243 EST246565 tomato ovary, TAMU Lycopersicon ...	72	2e-11
	emb AW153099 AW153099 se34h11.y1 Gm-c1015 Glycine max cDNA clone...	71	4e-11
	emb AI940852 AI940852 sb80b11.y1 Gm-c1010 Glycine max cDNA clone...	71	4e-11
5	emb AW100275 AW100275 sd22a06.y2 Gm-c1012 Glycine max cDNA clone...	71	4e-11
	emb AW164250 AW164250 se23h05.y1 Gm-c1015 Glycine max cDNA clone...	70	5e-11
	emb AW981354 AW981354 EST392507 DSIL Medicago truncatula cDNA cl...	69	1e-10
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15	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
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	emb AI898446 AI898446 EST267889 tomato ovary, TAMU Lycopersicon ...	209	e-108
	emb AW217248 AW217248 EST295962 tomato callus, TAMU Lycopersicon...	245	3e-89
25	emb AI485780 AI485780 EST244101 tomato ovary, TAMU Lycopersicon ...	242	2e-86
	emb AI485695 AI485695 EST244016 tomato ovary, TAMU Lycopersicon ...	261	5e-86
	emb AI899197 AI899197 EST268640 tomato ovary, TAMU Lycopersicon ...	161	2e-78
	emb AI485239 AI485239 EST243543 tomato ovary, TAMU Lycopersicon ...	291	1e-77
	emb AW034573 AW034573 EST278257 tomato callus, TAMU Lycopersicon...	272	9e-72
30	emb AI488812 AI488812 EST247151 tomato ovary, TAMU Lycopersicon ...	251	1e-65
	emb AW687082 AW687082 NF005G09RT1F1071 Developing root Medicago ...	182	7e-65
	emb AI898248 AI898248 EST267691 tomato ovary, TAMU Lycopersicon ...	206	2e-64
	emb AI483614 AI483614 EST249464 tomato ovary, TAMU Lycopersicon ...	238	1e-61
	emb AI897089 AI897089 EST266532 tomato ovary, TAMU Lycopersicon ...	226	8e-58
35	emb AW774994 AW774994 EST334145 KV3 Medicago truncatula cDNA clo...	182	3e-56
	emb AW559604 AW559604 EST314652 DSIR Medicago truncatula cDNA cl...	177	4e-53
	emb AI485284 AI485284 EST243588 tomato ovary, TAMU Lycopersicon ...	206	5e-52
	emb AI485664 AI485664 EST243985 tomato ovary, TAMU Lycopersicon ...	198	2e-49
	emb AW774741 AW774741 EST333892 KV3 Medicago truncatula cDNA clo...	90	2e-48
40	emb AI487608 AI487608 EST245930 tomato ovary, TAMU Lycopersicon ...	187	3e-46
	emb AI483438 AI483438 EST249259 tomato ovary, TAMU Lycopersicon ...	169	7e-41
	emb AI485008 AI485008 EST243271 tomato ovary, TAMU Lycopersicon ...	157	3e-37
	emb AI938737 AI938737 sb58c06.y1 Gm-c1018 Glycine max cDNA clone...	151	2e-35
	emb AI967736 AI967736 Ljimpest11-837-a7 Ljimp Lambda HybriZap ...	147	4e-34
45	emb AW775688 AW775688 EST334753 DSIL Medicago truncatula cDNA cl...	108	8e-34
	emb Z50161 SCC14ORFS S.cerevisiae orfs and LEU4, MET4, POL1, RAS...	60	1e-33
	emb Z71382 SCYNL106C S.cerevisiae chromosome XIV reading frame O...	60	1e-33
	emb AI973618 AI973618 sd07d04.y1 Gm-c1020 Glycine max cDNA clone...	141	3e-32
	emb AI485392 AI485392 EST243713 tomato ovary, TAMU Lycopersicon ...	138	2e-31
50	emb X94335 SC130KBXV S.cerevisiae 130kb DNA fragment from chromo...	51	1e-29
	emb Z75017 SCYOR109W S.cerevisiae chromosome XV reading frame OR...	51	1e-29
	emb AL022103 SPBC2G2 S.pombe chromosome II cosmid c2G2.	78	3e-27
	emb X79743 SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes.	72	3e-27
	emb Z38062 SC9687 S.cerevisiae chromosome IX cosmid 9687.	72	3e-27
55	emb AI488810 AI488810 EST247149 tomato ovary, TAMU Lycopersicon ...	121	3e-26
	gb BE020060 BE020060 sm38e06.y1 Gm-c1028 Glycine max cDNA clone ...	118	2e-25
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	emb AW257207 AW257207 EST305344 KV2 Medicago truncatula cDNA clo...	75	2e-24
	emb AV406995 AV406995 AV406995 Lotus japonicus young plants (two...	67	2e-23
60	emb AW034093 AW034093 EST277588 tomato callus, TAMU Lycopersicon...	111	3e-23
	emb Z98763 SPAC9G1 S.pombe chromosome I cosmid c9G1.	59	9e-23

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	emb AI897134 AI897134 EST266577 tomato ovary, TAMU Lycopersicon ...	107	4e-22
	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	4e-21
	emb AW731056 AW731056 GA_Ea0008D13 Gossypium arboreum 7-10 dpa ...	100	5e-20
5	emb AV413397 AV413397 AV413397 Lotus japonicus young plants (two...	100	9e-20
	emb AW616540 AW616540 EST322951 L. hirsutum trichome, Cornell Un...	98	2e-19
	emb AL110506 SPBC577 S.pombe chromosome II cosmid c577.	74	2e-18
	emb AW126841 AW126841 ga16f04.y1 Moss EST library PPU Physcomitr...	94	4e-18
	emb AI780067 AI780067 EST260946 tomato susceptible, Cornell Lyco...	94	6e-18
10	emb AW687035 AW687035 NF005C05RT1F1037 Developing root Medicago ...	73	2e-17
	emb AW685930 AW685930 NF036F03NR1F1000 Nodulated root Medicago t...	73	2e-17
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	emb AW220291 AW220291 EST302774 tomato root during/after fruit s...	68	1e-14
15	emb AQ644913 AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso...	53	2e-13
	emb AA495505 AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil...	49	5e-13
	emb AW830613 AW830613 sm04c07.y1 Gm-c1027 Glycine max cDNA clone...	77	5e-13
	emb AW666237 AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone...	77	5e-13
	emb AW285758 AW285758 LG1_223_C03.b1_A002 Light Grown 1 (LG1) So...	74	5e-12
20	emb AQ658256 AQ658256 Sheared DNA-13C5.TR Sheared DNA Trypanosom...	73	1e-11
	emb AW704333 AW704333 sk18a03.y1 Gm-c1028 Glycine max cDNA clone...	71	5e-11
	emb AV390446 AV390446 AV390446 Chlamydomonas reinhardtii C9 Chla...	70	6e-11
	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom...	64	8e-11
	emb AW695904 AW695904 NF099H04ST1F1043 Developing stem Medicago ...	49	2e-10
25	emb AZ048449 AZ048449 PSB67 Barley PstI genomic clones Hordeum v...	67	8e-10
	emb AW760518 AW760518 sl51d02.y1 Gm-c1027 Glycine max cDNA clone...	66	1e-09
	emb AW332143 AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car...	36	1e-09
	emb AW687790 AW687790 NF013E04RT1F1034 Developing root Medicago ...	65	3e-09
	emb AI486692 AI486692 EST245014 tomato ovary, TAMU Lycopersicon ...	54	3e-09
30	emb AW333870 AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c...	36	5e-09
	emb AQ850639 AQ850639 LMAJFV1_lm41a04.x1 Leishmania major FV1 ra...	44	6e-09
	emb AW127178 AW127178 M110117 GVN Medicago truncatula cDNA clone...	63	1e-08
	emb AW616547 AW616547 EST322958 L. hirsutum trichome, Cornell Un...	62	2e-08
	emb AW399291 AW399291 EST309791 L. pennellii trichome, Cornell U...	62	2e-08
35	emb AW693686 AW693686 NF068A05ST1F1036 Developing stem Medicago ...	62	3e-08
	emb AW208046 AW208046 M111077e DSIR Medicago truncatula cDNA clo...	61	5e-08
	emb AQ642482 AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos...	53	7e-08
	emb AW686583 AW686583 NF039G02NR1F1000 Nodulated root Medicago t...	45	5e-07
	emb AQ849089 AQ849089 LMAJFV1_lm41a04.y1 Leishmania major FV1 ra...	44	6e-06
40	emb AI781410 AI781410 EST262277 tomato susceptible, Cornell Lyco...	52	2e-05
	emb AW617564 AW617564 EST323975 L. hirsutum trichome, Cornell Un...	49	2e-04
	emb AQ946427 AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom...	47	5e-04
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45	emb AQ655271 AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso...	38	0.004
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	emb AW437996 AW437996 ST83C09 Pine TriplEx shoot tip library Pin...	42	0.016
	emb AI440709 AI440709 sa62e11.y1 Gm-c1004 Glycine max cDNA clone...	31	0.045
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50	emb AF263282 AF263282 Filobasidiella neoformans var. neoformans ...	34	0.64
	emb AW702543 AW702543 TgESTzz85a12.y1 TgRH*-Tachyzoite cDNA Toxo...	32	0.69
	emb AZ214873 AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso...	37	0.74
	emb AQ939979 AQ939979 Sheared DNA-42A15.TF Sheared DNA Trypanoso...	37	0.74
	emb AQ651205 AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso...	37	0.74
55	emb AQ945454 AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso...	37	0.74
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	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai...	35	2.6
	gb M28064 PFAHRKP Plasmodium brasilianum DNA homologous to the h...	35	2.6
60	emb AI482770 AI482770 EST242093 tomato shoot, Cornell Lycopersic...	35	2.6
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 5 factor [arabidopsis thaliana] /blast\_score 3.00e-94  
 (938 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

10

Searching.....done

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			(bits) Value
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	gb U68763 GMU68763	Glycine max putative transcription factor SCO...	71 1e-35
	emb Y18788 MSY18788	Medicago sativa mRNA for putative TFIIIA (or...	71 3e-35
	emb AF053077 AF053077	Nicotiana tabacum osmotic stress-induced z...	70 3e-33
	emb AW729218 AW729218	GA_Ea0024G18 Gossypium arboreum 7-10 dpa ...	71 5e-33
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	dbj D26086 PETZFP4	Petunia zinc-finger protein gene.	68 3e-30
	emb AW560934 AW560934	EST315982 DSIR Medicago truncatula cDNA cl...	68 8e-30
	emb AW775559 AW775559	EST334624 DSIL Medicago truncatula cDNA cl...	70 1e-29
	gb BE123920 BE123920	EST394045 DSIL Medicago truncatula cDNA clp...	70 1e-29
25	emb AI988657 AI988657	sd06b03.y1 Gm-c1020 Glycine max cDNA clone...	70 9e-29
	emb AW102472 AW102472	sd88f02.y1 Gm-c1009 Glycine max cDNA clone...	64 1e-28
	dbj D26084 PETZFDB2	Petunia mRNA for zinc-finger DNA binding pro...	69 1e-28
	dbj D26083 PETZFDB1	Petunia hybrida gene for zinc-finger DNA bin...	68 4e-28
	emb AI988290 AI988290	sc98f10.y1 Gm-c1020 Glycine max cDNA clone...	64 3e-27
30	emb AW706944 AW706944	sk08e10.y1 Gm-c1023 Glycine max cDNA clone...	69 2e-26
	emb AW153229 AW153229	se37f05.y1 Gm-c1015 Glycine max cDNA clone...	69 3e-26
	emb AW616587 AW616587	EST322998 L. hirsutum trichome, Cornell Un...	68 5e-26
	gb BE095284 BE095284	00345 leafy spurge Lambda HybriZAP 2.1 two...	69 5e-26
	emb AW278572 AW278572	sf46c03.y1 Gm-c1009 Glycine max cDNA clone...	65 8e-26
35	emb AI487287 AI487287	EST245609 tomato ovary, TAMU Lycopersicon ...	68 9e-26
	dbj D26085 PETZFDB3	Petunia zinc-finger DNA binding protein gene.	60 1e-25
	emb AI778714 AI778714	EST259593 tomato susceptible, Cornell Lyco...	68 1e-25
	emb AW279005 AW279005	sg04d04.y1 Gm-c1019 Glycine max cDNA clone...	67 2e-25
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40	emb AF119050 AF119050	Datisca glomerata zinc-finger protein 1 (z...	71 2e-25
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	gb U76555 BRU76555	Brassica rapa zinc-finger protein BcZFP1 (BcA...	62 3e-24
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	emb AI488218 AI488218	EST246540 tomato ovary, TAMU Lycopersicon ...	62 9e-24
	emb AW037956 AW037956	EST279600 tomato mixed elicitor, BTI Lycop...	59 4e-23
	emb Y16131 Y16131	Y16131 young root nodules Medicago sativa subs...	67 8e-23
	emb AW030858 AW030858	EST274148 tomato callus, TAMU Lycopersicon...	66 9e-23
50	emb AW032112 AW032112	EST275566 tomato callus, TAMU Lycopersicon...	68 5e-22
	emb AW625323 AW625323	EST319146 tomato radicle, 5 d post-imbibit...	59 8e-21
	emb AW033257 AW033257	EST276828 tomato callus, TAMU Lycopersicon...	66 2e-20
	emb AI485651 AI485651	EST243972 tomato ovary, TAMU Lycopersicon ...	62 2e-20
	emb AW033574 AW033574	EST277145 tomato callus, TAMU Lycopersicon...	66 2e-20
55	emb AI896031 AI896031	EST265474 tomato callus, TAMU Lycopersicon...	66 3e-20
	emb AI771191 AI771191	EST252387 tomato ovary, TAMU Lycopersicon ...	66 3e-20
	emb AW032357 AW032357	EST275811 tomato callus, TAMU Lycopersicon...	66 3e-20
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	emb AW219517 AW219517	EST301915 tomato root during/after fruit s...	59 2e-19
60	emb AW706014 AW706014	sk64g01.y1 Gm-c1016 Glycine max cDNA clone...	69 1e-18
	emb AV426673 AV426673	AV426673 Lotus japonicus young plants (two...	60 5e-18



	emb AV423639 AV423639 AV423639 Lotus japonicus young plants (two...	66 7e-18
	gb BE021759 BE021759 sm62a09.yl Gm-cl028 Glycine max cDNA clone ...	71 3e-17
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	55 4e-17
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar...	64 6e-17
5	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	59 9e-17
	emb AB000455 AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com...	60 1e-16
	gb BE058334 BE058334 sn14g01.yl Gm-cl016 Glycine max cDNA clone ...	62 1e-16
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon...	55 2e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two...	66 3e-16
10	emb AW277333 AW277333 sf80a11.yl Gm-cl019 Glycine max cDNA clone...	64 4e-16
	emb AI900061 AI900061 sb98d02.yl Gm-cl012 Glycine max cDNA clone...	64 5e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	63 6e-16
	emb AI960244 AI960244 sc80g07.yl Gm-cl018 Glycine max cDNA clone...	64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	62 1e-15
15	emb AI736394 AI736394 sb28a06.yl Gm-cl009 Glycine max cDNA clone...	67 5e-15
	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon...	68 9e-15
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	68 9e-15
	emb AW755973 AW755973 sl11h06.yl Gm-cl036 Glycine max cDNA clone...	64 4e-14
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20	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge...	52 1e-13
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet...	52 1e-13
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge...	50 4e-13
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple...	50 4e-13
	emb AB006606 AB006606 Petunia x hybrida mRNA for ZPT4-4, complet...	51 8e-13
25	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root Medicago t...	54 8e-13
	emb AW776204 AW776204 EST335269 DSIL Medicago truncatula cDNA cl...	65 1e-12
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45	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds.	56 1e-11
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50	emb AI775063 AI775063 EST256163 tomato resistant, Cornell Lycop...	59 2e-11
	emb AI484099 AI484099 EST249970 tomato ovary, TAMU Lycopersicon ...	59 2e-11
	emb AW738399 AW738399 EST339826 tomato flower buds, anthesis, Co...	59 2e-11
	emb AB006602 AB006602 Petunia x hybrida mRNA for ZPT2-7, complet...	49 2e-11
55	emb AI959966 AI959966 sc35g05.xl Gm-cl014 Glycine max cDNA clone...	50 2e-11

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gb|aab97145.1| (af000977) mek1 [arabidopsis thaliana] thaliana]  
/blast\_score 0 /ec\_number /family /chip nova /gb\_link /ncgi  
(1352 letters)



Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments:

(bits) Value

	emb AJ000728 LEAJ728 Lycopersicon esculentum mRNA for MAP kinase...	555	e-157
10	emb AF165186 AF165186 Nicotiana tabacum MAP kinase kinase mRNA, ...	540	e-153
	emb AW945105 AW945105 EST337156 tomato flower buds 3-8 mm, Corne...	318	6e-86
	emb AW756736 AW756736 sl26f02.y1 Gm-c1027 Glycine max cDNA clone...	174	9e-75
	dbj D31964 TOBNPK2 Tobacco mRNA for protein kinase (NPK2), compl...	183	8e-65
	gb BE054500 BE054500 GA__Ea0031F11f Gossypium arboreum 7-10 dpa ...	165	1e-59
15	emb AW220008 AW220008 EST302491 tomato root during/after fruit s...	228	6e-59
	emb AW624623 AW624623 EST322568 tomato flower buds 3-8 mm, Corne...	215	9e-55
	emb AI438023 AI438023 sa34h10.y1 Gm-c1004 Glycine max cDNA clone...	208	7e-53
	emb AW617901 AW617901 EST296829 L. hirsutum trichome, Cornell Un...	203	2e-51
	emb AJ007393 YLI7393 Yarrowia lipolytica ste7 gene.	92	4e-49
20	emb AW931392 AW931392 EST357235 tomato fruit mature green, TAMU ...	189	3e-47
	emb AW039087 AW039087 EST281060 tomato mixed elicitor, BTI Lycop...	183	2e-45
	emb Z99259 SPAC2C4 S.pombe chromosome I cosmid c2C4.	85	6e-43
	emb AW032808 AW032808 EST276367 tomato callus, TAMU Lycopersicon...	175	9e-43
	gb U07801 UMU07801 Ustilago maydis serine/threonine/tyrosine kin...	121	2e-42
25	emb AJ009609 BNA9609 Brassica napus mRNA for MAP4K alpha2 protein.	87	1e-41
	dbj D13001 YSCSSP32 Yeast Mkk1/SSP32 gene for Mkk1 protein kinas...	72	3e-41
	emb Z75139 SCYOR231W S.cerevisiae chromosome XV reading frame OR...	72	3e-41
	emb AF169644 AF169644 Glomerella cingulata MAP kinase kinase (EM...	82	7e-41
	emb AJ009608 BNA9608 Brassica napus mRNA for MAP4K alpha 1 protein.	82	8e-41
30	emb AW127406 AW127406 M110589 DSIL Medicago truncatula cDNA clon...	94	2e-39
	emb AJ225532 AJ225532 AJ225532 Absciscic acid-treated protonemata...	162	5e-39
	emb AZ215495 AZ215495 Sheared DNA-56D6.TR Sheared DNA Trypanosom...	113	3e-38
	dbj D13785 YSCMKK2 S.cerevisiae gene for Mkk2 protein kinase, co...	68	1e-37
	gb U72980 CAU72980 Candida albicans Map kinase kinase (STE7) gen...	128	2e-37
35	gb L19195 YSASTKIN Candida albicans (clone pKB66) serine/threoni...	128	2e-37
	emb AL109822 SPBC409 S.pombe chromosome II cosmid c409.	68	2e-37
	gb U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi...	68	2e-37
	emb X62631 SPWIS1 S.pombe wis1 gene for protein kinase.	68	3e-37
	emb AW625928 AW625928 EST319823 tomato radicle, 5 d post-imbibit...	90	8e-37
40	emb AW348493 AW348493 GM210002B12A8R Gm-r1021 Glycine max cDNA 3...	154	1e-36
	emb AZ213240 AZ213240 Sheared DNA-102E10.TF Sheared DNA Trypanos...	140	3e-36
	emb AW497308 AW497308 ga57h06.y1 Moss EST library PPU Physcomitr...	150	2e-35
	emb Z49403 SCYJL128C S.cerevisiae chromosome X reading frame ORF...	78	5e-35
45	gb U12237 SCU12237 Saccharomyces cerevisiae suppressor of fluori...	78	5e-35
	gb J02946 YSCPBS2 Saccharomyces cerevisiae putative protein kina...	78	5e-35
	emb AJ243184 LIN243184 Leishmania infantum mkk gene for putative...	78	2e-34
	emb AW032663 AW032663 EST276222 tomato callus, TAMU Lycopersicon...	82	2e-34
	emb AJ243118 LME243118 Leishmania mexicana mkk gene for putative...	78	3e-34
50	emb AJ243187 LTR243187 Leishmania tropica mkk gene for putative ...	78	3e-34
	emb AJ243188 LMA243188 Leishmania major mkk gene for putative mi...	78	3e-34
	emb AJ243183 LAM243183 Leishmania amazonensis mkk gene for putat...	78	3e-34
	emb AJ243186 LAE243186 Leishmania aethiopica mkk gene for putati...	78	3e-34
	emb AW185502 AW185502 se80e12.y1 Gm-c1023 Glycine max cDNA clone...	85	6e-34
55	gb U16029 U16029 Leishmania donovani protein kinase (lpk) mRNA, ...	78	1e-33
	emb AJ243185 LDO243185 Leishmania donovani mkk gene for putative...	78	1e-33
	emb AI781759 AI781759 EST262638 tomato susceptible, Cornell Lyco...	97	3e-33
	gb BE059041 BE059041 sn24d08.y1 Gm-c1016 Glycine max cDNA clone ...	143	3e-33
	emb AW929787 AW929787 EST354057 tomato flower buds 8 mm to pre-a...	102	9e-32
60	emb AW981083 AW981083 EST392236 GVN Medicago truncatula cDNA clo...	88	3e-31
	gb BE036317 BE036317 MO23C02 MO Mesembryanthemum crystallinum cD...	82	1e-30

- emb|AF069777|AF069777 *Cryphonectria parasitica* mitogen-activated... 66 2e-30  
 emb|AW099876|AW099876 sd17g06.y2 *Gm-c1012* Glycine max cDNA clone... 80 3e-30  
 emb|AF249887|AF249887 *Pneumocystis carinii* map kinase kinase (mk... 72 6e-30  
 emb|AW622016|AW622016 EST312814 tomato root during/after fruit s... 97 7e-29  
 5 emb|Z69239|SPAC1D4 *S.pombe* chromosome I cosmid c1D4. 116 2e-28  
 emb|X07445|SPBYR1 Fission yeast byr1 gene. 116 2e-28  
 emb|Z67750|SC41KCIV *S.cerevisiae* DNA (cosmid 31A2; chromosome IV... 77 7e-28  
 emb|X97751|SCIV23 *S.cerevisiae* chrIV genes STE7, CLB3, MSH5, RPC... 77 7e-28  
 emb|Z74207|SCYDL159W *S.cerevisiae* chromosome IV reading frame OR... 77 8e-28  
 10 gb|M14097|YSCSTE7 Yeast (*S.cerevisiae*) regulatory gene STE7, com... 77 8e-28  
 dbj|D26601|TOBPK Tobacco mRNA for protein kinase, complete cds. 54 1e-27  
 dbj|E05289|E05289 DNA encoding a protein kinase that is homologo... 54 1e-27  
 emb|AL358652|LMFP1408 *Leishmania major* Friedlin chromosome 14 PA... 100 3e-27  
 emb|AW349565|AW349565 GM210005A21F10R *Gm-r1021* Glycine max cDNA ... 85 4e-27  
 15 emb|AF169643|AF169643 *Glomerella cingulata* MAP kinase kinase (EM... 74 5e-27  
 emb|AQ849880|AQ849880 LMAJFV1\_lm51a11.x1 *Leishmania major* FV1 ra... 104 1e-26  
 emb|AW564378|AW564378 LG1\_292\_H08.b1\_A002 Light Grown 1 (LG1) So... 121 1e-26  
 emb|AC005140|AC005140 *Plasmodium falciparum* chromosome 12 clone ... 88 2e-26  
 emb|AW030150|AW030150 EST273405 tomato callus, TAMU Lycopersicon... 120 3e-26  
 20 emb|Z28126|SCYKL126W *S.cerevisiae* chromosome XI reading frame OR... 84 5e-26  
 gb|M21307|YSCPKN Yeast (*S.cerevisiae*) protein kinase (YPK1) gene... 84 7e-26  
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 emb|Z49702|SC9718 *S.cerevisiae* chromosome XIII cosmid 9718. 85 9e-26  
 gb|M24929|YSCYKR2A *Saccharomyces cerevisiae* protein kinase (YKR2... 85 9e-26  
 25 emb|AI779511|AI779511 EST260390 tomato susceptible, Cornell Lycö... 118 1e-25  
 emb|AZ048376|AZ048376 LMAJFV1\_lm77f10.x1 *Leishmania major* FV1 ra... 100 1e-25  
 gb|U11581|YSCHL5018 *Saccharomyces cerevisiae* chromosome VIII cos... 86 2e-25  
 gb|M94719|YSCSTE20P *Saccharomyces cerevisiae* protein kinase (Ste... 86 2e-25  
 gb|L04655|YSCSERKIN *Saccharomyces cerevisiae* serine/threonine ki... 86 2e-25  
 30 emb|AW922296|AW922296 DG1\_17\_G11.g1\_A002 Dark Grown 1 (DG1) Sorg... 116 4e-25  
 emb|Z98763|SPAC9G1 *S.pombe* chromosome I cosmid c9G1. 92 4e-25  
 emb|AE001376|AE001376 *Plasmodium falciparum* chromosome 2, sectio... 49 6e-25  
 emb|Z97211|SPBC2F12 *S.pombe* chromosome II cosmid c2F12. 56 2e-24  
 emb|Z98270|SPBC1D7 *S.pombe* chromosome II cosmid c1D7. 56 2e-24  
 35 emb|AW351150|AW351150 GM210011A20C11R *Gm-r1021* Glycine max cDNA ... 78 2e-24  
 gb|M74293|YSPBYR2 *Schizosaccharomyces pombe* byr2 gene, complete ... 56 2e-24  
 emb|X68851|SPSTE8A *S.pombe* ste8 gene encoding protein kinase. 56 2e-24  
 emb|AJ238845|BNA238845 *Brassica napus* mRNA for MAP3K epsilon 1 p... 78 3e-24  
 gb|L47210|YSASTPK *Candida albicans* serine/threonine protein kina... 86 8e-24  
 40 gb|U73457|CAU73457 *Candida albicans* Cst20p (CST20) gene, complet... 86 8e-24  
 emb|AJ005079|AJKL5079 *Kluyveromyces lactis* BCK1 gene, complete CDS. 51 8e-24  
 emb|AF157632|AF157632 *Schizosaccharomyces pombe* MAPK kinase Skh1... 73 2e-23  
 dbj|D82023|D82023 *Schizosaccharomyces pombe* mkk1+ gene for MAP k... 73 2e-23  
 emb|AF034090|AF034090 *Neurospora crassa* MAPKK kinase (nrc-1) gen... 58 2e-23  
 45 emb|AQ501953|AQ501953 V11H7 mTn-3xHA/lacZ Insertion Library Sacc... 72 2e-23  
 emb|AL034433|SPBC1604 *S.pombe* chromosome II cosmid c1604. 87 4e-23  
 gb|U22371|SPU22371 *Schizosaccharomyces pombe* Pak1p (PAK1) mRNA, ... 87 5e-23  
 gb|L41552|YSPSHK1A *Schizosaccharomyces pombe* Ste20 homologous pr... 87 5e-23

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 gb|aad34615.1|af153283\_1 (af153283) putative progesterone-binding  
 protein homolog [arabidopsis thaliana] /blast\_score 1.00e-116  
 (930 letters)

55

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

60

Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

	gb BE052137 BE052137 GA__Ea0031L11f Gossypium arboreum 7-10 dpa ...	257	8e-77
	emb AW727234 AW727234 GA__Ea0011E21 Gossypium arboreum 7-10 dpa ...	257	1e-76
5	emb AW728196 AW728196 GA__Ea0014P01 Gossypium arboreum 7-10 dpa ...	257	1e-76
	emb AW737982 AW737982 EST339409 tomato flower buds, anthesis, Co...	287	2e-76
	emb AW626347 AW626347 EST320254 tomato radicle, 5 d post-imbibit...	287	2e-76
	emb AW622517 AW622517 EST313317 tomato root during/after fruit s...	287	2e-76
10	emb AW623663 AW623663 EST321608 tomato flower buds 3-8 mm, Corne...	287	2e-76
	emb AW622008 AW622008 EST312806 tomato root during/after fruit s...	287	2e-76
	emb AI777165 AI777165 EST258130 tomato resistant, Cornell Lycope...	287	2e-76
	emb AW730733 AW730733 GA__Ea0027I13 Gossypium arboreum 7-10 dpa ...	254	7e-76
	emb AW705652 AW705652 sk50g08.y1 Gm-c1019 Glycine max cDNA clone...	248	1e-74
	emb AW755296 AW755296 sl01c07.y1 Gm-c1036 Glycine max cDNA clone...	245	6e-74
15	emb AW775898 AW775898 EST334963 DSIL Medicago truncatula cDNA cl...	243	2e-71
	emb AW774377 AW774377 EST333528 KV3 Medicago truncatula cDNA clo...	242	4e-71
	emb AW620616 AW620616 sj07e05.y1 Gm-c1032 Glycine max cDNA clone...	230	3e-69
	emb AW398755 AW398755 EST309255 L. pennellii trichome, Cornell U...	251	3e-68
	emb AW559353 AW559353 EST314401 DSIR Medicago truncatula cDNA cl...	231	6e-68
20	emb AI727590 AI727590 BNLGH8481 Six-day Cotton fiber Gossypium ...	226	2e-67
	emb AW696709 AW696709 NF109H10ST1F1091 Developing stem Medicago ...	211	7e-67
	gb T24185 T24185 crs173 lambdaZAPST Ricinus communis cDNA clone ...	254	2e-66
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	emb AW678629 AW678629 WS1_1_D02.b1_A002 Water-stressed 1 (WS1) S...	245	1e-63
25	emb AW672535 AW672535 LG1_360_B02.b1_A002 Light Grown 1 (LG1) So...	245	1e-63
	emb AW678699 AW678699 WS1_1_D02.b2_A002 Water-stressed 1 (WS1) S...	245	1e-63
	emb AI776227 AI776227 EST257327 tomato resistant, Cornell Lycope...	244	3e-63
	emb AI899451 AI899451 EST268894 tomato susceptible, Cornell Lyco...	242	9e-63
	gb BE125791 BE125791 DG1_57_D06.b1_A002 Dark Grown 1 (DG1) Sorgh...	241	2e-62
30	emb AI482787 AI482787 EST242110 tomato shoot, Cornell Lycopersic...	241	2e-62
	gb BE123902 BE123902 EST394027 DSIL Medicago truncatula cDNA clo...	231	2e-62
	emb AW704889 AW704889 sk40g12.y1 Gm-c1019 Glycine max cDNA clone...	241	2e-62
	emb AW185657 AW185657 se81h10.y1 Gm-c1023 Glycine max cDNA clone...	238	1e-61
	emb AW254869 AW254869 ML1292 peppermint glandular trichome Menth...	211	1e-61
35	emb AW255550 AW255550 ML584 peppermint glandular trichome Menta...	237	4e-61
	emb AW704813 AW704813 sk55h01.y1 Gm-c1019 Glycine max cDNA clone...	236	5e-61
	emb AI895103 AI895103 EST264546 tomato callus, TAMU Lycopersicon...	232	7e-60
	gb BE059713 BE059713 sn35h07.y1 Gm-c1016 Glycine max cDNA clone ...	232	7e-60
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40	emb AW755523 AW755523 sl05a05.y1 Gm-c1036 Glycine max cDNA clone...	223	4e-57
	emb AW727353 AW727353 GA__Ea0011L19 Gossypium arboreum 7-10 dpa ...	220	3e-56
	emb AW201709 AW201709 sf06d02.y1 Gm-c1027 Glycine max cDNA clone...	216	6e-55
	emb AW203472 AW203472 sf30f04.y1 Gm-c1028 Glycine max cDNA clone...	216	6e-55
	emb AI161953 AI161953 A010P20U Hybrid aspen plasmid library Popu...	149	2e-54
45	emb AI162696 AI162696 A022P09U Hybrid aspen plasmid library Popu...	152	2e-54
	emb AV410373 AV410373 AV410373 Lotus japonicus young plants (two...	186	4e-54
	emb AW217074 AW217074 EST295788 tomato callus, TAMU Lycopersicon...	213	5e-54
	emb AI441526 AI441526 sa67a03.y1 Gm-c1004 Glycine max cDNA clone...	177	2e-53
	emb AW678831 AW678831 WS1_1_D02.g1_A002 Water-stressed 1 (WS1) S...	208	2e-52
50	emb AW100277 AW100277 sd22a12.y2 Gm-c1012 Glycine max cDNA clone...	192	2e-52
	emb AW745340 AW745340 WS1_33_H02.b1_A002 Water-stressed 1 (WS1) ...	154	4e-48
	emb AW185605 AW185605 se79h09.y1 Gm-c1023 Glycine max cDNA clone...	193	6e-48
	emb AW278821 AW278821 sf99a06.y1 Gm-c1019 Glycine max cDNA clone...	192	8e-48
	gb BE035142 BE035142 MM03H05 MM Mesembryanthemum crystallinum cD...	178	1e-47
55	emb AW255911 AW255911 ML998 peppermint glandular trichome Menta...	124	2e-47
	emb AW683421 AW683421 NF011G07LF1F1055 Developing leaf Medicago ...	190	4e-47
	emb AI778919 AI778919 EST259798 tomato susceptible, Cornell Lyco...	188	1e-46
	emb AI938231 AI938231 sc41d07.y1 Gm-c1014 Glycine max cDNA clone...	184	2e-45
	emb AW677289 AW677289 DG1_7_D03.b1_A002 Dark Grown 1 (DG1) Sorgh...	182	1e-44
60	emb AW287668 AW287668 LG1_244_H12.b1_A002 Light Grown 1 (LG1) So...	180	4e-44
	emb AW625474 AW625474 EST319381 tomato radicle, 5 d post-imbibit...	156	1e-41



emb|AI729205|AI729205 BNLGHi12887 Six-day Cotton fiber Gossypium... 171 1e-41  
 emb|AI941012|AI941012 sb83c05.y1 Gm-cl010 Glycine max cDNA clone... 168 1e-40  
 emb|AI855517|AI855517 sc20b06.y1 Gm-cl013 Glycine max cDNA clone... 168 1e-40  
 emb|AV429287|AV429287 AV429287 Lotus japonicus young plants (two... 163 3e-39  
 5 emb|AW255564|AW255564 ML599 peppermint glandular trichome Mentha... 137 7e-39  
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 10 emb|AV417826|AV417826 AV417826 Lotus japonicus young plants (two... 121 7e-36  
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 emb|AW145544|AW145544 ga26e09.y1 Moss EST library PPN Physcomitr... 149 6e-35  
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 15 emb|AI482794|AI482794 EST242117 tomato shoot, Cornell Lycopersic... 146 5e-34  
 gb|BE125045|BE125045 DG1\_14\_A09.b1\_A002 Dark Grown 1 (DG1) Sorgh... 144 1e-33  
 emb|AW092409|AW092409 EST285589 tomato mixed elicitor, BTI Lycop... 141 2e-32  
 emb|AI774296|AI774296 EST255312 tomato resistant, Cornell Lycop... 141 2e-32  
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 20 emb|AW037272|AW037272 EST274122 tomato mixed elicitor, BTI Lycop... 141 2e-32  
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 emb|AW649965|AW649965 EST328419 tomato germinating seedlings, TA... 141 2e-32  
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 25 emb|AW093288|AW093288 EST286468 tomato mixed elicitor, BTI Lycop... 136 4e-31  
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 emb|AW981553|AW981553 PC14A01 Pine TriplEx pollen cone library P... 135 8e-31  
 emb|AW832150|AW832150 sm20d11.y1 Gm-cl027 Glycine max cDNA clone... 135 1e-30  
 emb|AI440919|AI440919 sa56f12.y1 Gm-cl004 Glycine max cDNA clone... 135 1e-30  
 30 emb|AW349246|AW349246 GM210004B21F9R Gm-r1021 Glycine max cDNA 3... 134 1e-30  
 emb|AW759979|AW759979 sl56e07.y1 Gm-cl027 Glycine max cDNA clone... 134 2e-30  
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 emb|AW832627|AW832627 sm14h06.y1 Gm-cl027 Glycine max cDNA clone... 134 2e-30  
 emb|AW666184|AW666184 sk33d03.y1 Gm-cl028 Glycine max cDNA clone... 121 3e-30  
 35 emb|AW925882|AW925882 HVSMEg0005M05 Hordeum vulgare pre-anthesis... 133 3e-30  
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 emb|AW754652|AW754652 PC04G03 Pine TriplEx pollen cone library P... 130 3e-29  
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 40 emb|AW754728|AW754728 PC07B03 Pine TriplEx pollen cone library P... 127 3e-28  
 emb|AW756987|AW756987 sk82g11.y1 Gm-cl016 Glycine max cDNA clone... 126 4e-28

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 [arabidopsis thaliana] /blast\_score 0  
 (2390 letters)

Database: plantfungal  
 50 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E  
 55 Sequences producing significant alignments: (bits) Value

gb|M99431|PHNHSP83A Pharbitis nil heat shock protein 83 (Hsp83) ... 597 0.0  
 gb|M96549|TOMHSC80P Tomato heat shock cognate protein 80 gene, 3... 577 0.0  
 gb|U55859|TAU55859 Triticum aestivum heat shock protein 80 mRNA,... 575 0.0  
 60 emb|X98582|TAX98582 T.aestivum mRNA for HSP80-2 protein. 572 0.0  
 emb|X63195|NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0



	emb AF123259 AF123259	Lycopersicon esculentum heat shock protein...	483	0.0
	emb AF165818 AF165818	Guillardia theta nucleomorph 5S ribosomal ...	505	0.0
	emb AF042329 AF042329	Eimeria tenella heat shock protein 90 (hsp...	514	0.0
	gb M57386 THEHSP90	T.parva heat shock protein 90 (hsp90) mRNA, c...	500	0.0
5	emb Z29667 PFHESHPR	P.falciparum (7) mRNA for heat-shock protein.	507	0.0
	gb U45449 EBU45449	Eimeria bovis heat shock protein 90 (hsp90) m...	495	0.0
	emb AF151114 AF151114	Tetrahymena thermophila strain B2086 hsp82...	486	0.0
	emb AF136649 AF136649	Babesia bovis heat shock protein 90 (HSP90...	487	0.0
	gb M15346 TRBHSC	T.cruzi tandemly repeated gene encoding an 85 k...	457	0.0
10	emb X14176 TBHSP83	Trypanosoma brucei HSP83 gene.	452	0.0
	gb M73492 LEIHSP90	Leishmania donovani heat shock protein 90 mRN...	456	0.0
	emb X87770 LIHSP83GN	L.infantum hsp83 gene.	454	0.0
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	gb U92465 AFU92465	Aspergillus fumigatus heat shock protein (Hsp...	458	e-165
15	emb AF212996 AF212996	Neurospora crassa heat shock protein 80 ge...	473	e-165
	emb AL110469 SPAC926	S.pombe chromosome I cosmid c926.	460	e-165
	gb L35550 YSPHSP90X	Schizosaccharomyces pombe heat shock protein...	460	e-162
	gb U81165 PAU81165	Podospira anserina suppressor of vegetative i...	292	e-161
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20	emb Z73596 SCYPL240C	S.cerevisiae chromosome XVI reading frame O...	448	e-159
	gb K01387 YSCHSP82A	Yeast (S.cerevisiae) HSP82 (heat shock-induc...	448	e-159
	emb X81025 CAHSP90	C.albicans hsp90 gene.	451	e-159
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	emb Z49808 SC8010	S.cerevisiae chromosome XIII cosmid 8010.	447	e-158
25	emb AF221856 AF221856	Euphorbia esula heat-shock protein 80 mRNA...	292	e-158
	gb M26044 YSCHSC82	S. cerevisiae HSC82 gene encoding hsc82, the ...	447	e-157
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30	emb AW982575 AW982575	HVSMEg0003K07f Hordeum vulgare pre-anthesi...	471	e-131
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	emb AW216642 AW216642	EST295356 tomato callus, TAMU Lycopersicon...	423	e-117
	emb AW217696 AW217696	EST296410 tomato flower buds 8 mm to pre-a...	422	e-117
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 15 emb|AW693115|AW693115 NF060C10ST1F1081 Developing stem Medicago ... 226 e-107  
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 25 emb|AW690804|AW690804 NF035B11ST1F1000 Developing stem Medicago ... 375 e-106  
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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Score E  
 Sequences producing significant alignments: (bits) Value

50 emb|AB014483|AB014483 *Nicotiana tabacum* NtHSF1 mRNA for heat sho... 213 2e-62  
 emb|X55347|LPHSF24 Tomato mRNA for heat stress transcription fac... 210 2e-53  
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 emb|Z46953|GMHSF34 G.max mRNA for heat shock transcription facto... 203 6e-53  
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 55 emb|AV415115|AV415115 AV415115 *Lotus japonicus* young plants (two... 197 2e-49  
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 emb|AI055366|AI055366 coau0003M17 Cotton Boll Abscission Zone cD... 191 1e-47  
 60 emb|AW703969|AW703969 sk14g08.y1 Gm-c1023 Glycine max cDNA clone... 191 1e-47  
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- emb|AW931781|AW931781 EST357624 tomato fruit mature green, TAMU ... 189 3e-47  
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20 emb|AW036683|AW036683 EST278726 tomato fruit mature green, TAMU ... 149 5e-35  
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30 emb|AW559623|AW559623 EST314671 DSIR Medicago truncatula cDNA cl... 144 2e-33  
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- emb|AV413314|AV413314 AV413314 Lotus japonicus young plants (two... 102 8e-21  
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5 emb|AW924303|AW924303 WS1\_52\_H11.b1\_A002 Water-stressed 1 (WS1) ... 99 7e-20  
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 25 emb|AW287985|AW287985 N100829e rootphos(-) Medicago truncatula c... 153 2e-36  
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 emb|AW597680|AW597680 sj49e04.y1 Gm-cl033 Glycine max cDNA clone... 128 2e-33  
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 emb|X15436|DC215G Carrot DC 2.15 mRNA for 14 kD protein. 139 2e-32  
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Database: plantfungal  
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	emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl...	94	5e-33
40	emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl...	111	2e-32
	emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon ...	132	2e-30
	emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ...	130	2e-29
	emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl...	125	2e-29
45	emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon ...	128	3e-29
	emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone...	108	8e-29
	dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds.	127	1e-28
	emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon ...	127	2e-28
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50	emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon ...	124	1e-27
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60	emb AW776668 AW776668 EST335733 DSIL Medicago truncatula cDNA cl...	118	6e-26
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25 Database: plantfungal  
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 gb|M23120|TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m... 265 e-105  
 35 emb|AJ277900|VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas... 284 e-104  
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 dbj|E02108|E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100  
 gb|M37753|SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... 226 e-100  
 gb|U41323|GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c... 171 e-100  
 40 emb|X77990|BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99  
 gb|U01901|U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan... 209 8e-99  
 gb|M80608|TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase ... 210 1e-98  
 emb|AF230109|AF230109 Populus alba x Populus tremula beta-1,3 gl... 289 1e-98  
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 45 gb|U22147|HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) ... 265 1e-95  
 emb|X54456|NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana... 106 3e-95  
 emb|AF067863|AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh... 210 6e-95  
 gb|U01900|U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan... 210 8e-95  
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 55 emb|Z68154|GHBGLUCS G.hirsutum mRNA for 1,3-beta-glucanase. 174 3e-93  
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 emb|X54742|NPB13GG Nicotiana plumbaginifolia beta-(1,3)-glucanas... 205 4e-93  
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 emb|X53129|PV13BDGL P. vulgaris mRNA for 1,3-beta-D-glucanase. 240 6e-91



- emb|X74905|LEQA *L.esculentum* TomQ'a mRNA for beta(1,3)glucanase. 105 2e-90  
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 gb|U01902|U01902 *Solanum tuberosum* Datura endo-1,3-beta-D-glucan... 210 2e-88  
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 5 emb|X74906|LEQB *L.esculentum* TomQ'b mRNA for beta(1,3)glucanase. 110 1e-86  
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 emb|AF004838|AF004838 *Musa acuminata* beta-1,3-glucanase mRNA, pa... 148 7e-86  
 gb|L02212|PEABETAGLU Pea beta-1,3-glucanase gene, complete cds. 180 1e-85  
 10 gb|S51479|S51479 beta-1,3-glucanase [*Pisum sativum*=peas, cultiva... 180 2e-85  
 emb|AF186083|AF186083 AF186083 *Populus alba* x *Populus tremula* ba... 218 5e-85  
 gb|M20620|TOBGLUBC *N.tabacum* beta-1,3-glucanase mRNA, clone pGL43. 207 4e-84  
 gb|U27179|MSU27179 *Medicago sativa* acidic glucanase mRNA, comple... 138 7e-79  
 gb|M60463|TOBGL153A Tobacco GL153 protein mRNA, complete cds. 99 3e-77  
 15 emb|AF141654|AF141654 *Nicotiana tabacum* beta-1,3-glucanase (GGL4... 99 5e-77  
 gb|M60460|TOBPR2A Tobacco PR2 protein mRNA, complete cds. 100 3e-76  
 gb|M59443|TOBGLUCB *N.tabacum* acidic beta-1,3-glucanase gene, com... 100 1e-75  
 emb|A16120|A16120 Extracellular Beta-1, 3 glucanase gene (SEQ ID... 100 1e-75  
 gb|M63634|TOBGCBREG *Nicotiana plumbaginifolia* beta(1,3)-glucanas... 268 2e-75  
 20 emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 100 1e-74  
 emb|X81560|NTSP41AGN *N.tabacum* Sp41a gene. 100 2e-74  
 emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 100 2e-74  
 gb|M96941|BLYGCNHVI *Hordeum vulgare* glucan endo-1,3-beta-glucosi... 93 8e-74  
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 25 gb|M20618|TOBGLUBA *N.tabacum* beta-1,3-glucanase mRNA, clones pGL... 207 9e-73  
 emb|Z15131|ASBGLUCAN *A.sativa* mRNA for beta glucanase. 158 1e-70  
 gb|M62740|BLYGLB2 *Hordeum vulgare* 1,3-1,4-beta-D glucan 4-glucan... 158 2e-70  
 emb|Z22874|TABETGLUB *T.aestivum* (1,3;1,4) beta glucanase mRNA, c... 158 2e-70  
 emb|Z22873|TABETGLUA *T.aestivum* beta glucanase mRNA, complete CDS. 158 3e-70  
 30 emb|X52572|HVBDG Barley DNA for (1-3,1-4)-beta-D-glucanase (EC 3... 158 1e-69  
 emb|X56775|HVGLB1 *H.vulgare* Glb 1 gene for 1-3,1-4-beta-D-glucan... 158 1e-69  
 emb|X56260|HVGLUEND Barley DNA for (1,3;1,4)-beta-glucanase.(EC ... 158 1e-69  
 gb|M80604|TOMB13GLUA *Lycopersicon esculentum* beta-1,3-glucanase ... 94 2e-69  
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 40 emb|AW216754|AW216754 EST295468 tomato callus, TAMU *Lycopersicon*... 202 7e-64  
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 gb|M13237|BLYGLUCB Barley beta glucanase mRNA. 158 4e-62  
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 gb|M23548|BLYGEH Barley (1->3)-beta-glucan endohydrolase mRNA, c... 92 7e-61  
 emb|Y18212|TAY18212 *Triticum aestivum* mRNA for beta-1,3-endogluc... 93 9e-61  
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 50 gb|M62907|BLYCBGL32 *H.vulgare* L. (1-3)-beta-glucanase mRNA, comp... 92 2e-60  
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 55 emb|AW033770|AW033770 EST277341 tomato callus, TAMU *Lycopersicon*... 122 3e-59  
 emb|AW830464|AW830464 sm27f06.y1 Gm-cl028 *Glycine max* cDNA clone... 221 4e-59  
 emb|AW034001|AW034001 EST277663 tomato callus, TAMU *Lycopersicon*... 202 8e-58  
 emb|X67099|HV13GEIII *H.vulgare* gene for 1,3-glucan endohydrolase... 153 2e-57  
 emb|AW034584|AW034584 EST278268 tomato callus, TAMU *Lycopersicon*... 164 2e-57  
 60 emb|AI894452|AI894452 EST263907 tomato callus, TAMU *Lycopersicon*... 210 4e-57  
 emb|AW034632|AW034632 EST278316 tomato callus, TAMU *Lycopersicon*... 124 4e-57

emb|AW034478|AW034478 EST278049 tomato callus, TAMU Lycopersicon... 162 9e-57  
emb|AW216963|AW216963 EST295677 tomato callus, TAMU Lycopersicon... 202 1e-56  
gb|BE020030|BE020030 sm41c02.y1 Gm-c1028 Glycine max cDNA clone ... 220 2e-56  
5 emb|AW032447|AW032447 EST276006 tomato callus, TAMU Lycopersicon... 166 6e-56  
emb|AW031387|AW031387 EST274841 tomato callus, TAMU Lycopersicon... 191 6e-56  
emb|AW036009|AW036009 EST282868 tomato callus, TAMU Lycopersicon... 207 1e-55  
emb|AW031078|AW031078 EST274385 tomato callus, TAMU Lycopersicon... 109 2e-55  
emb|AW035366|AW035366 EST280928 tomato callus, TAMU Lycopersicon... 191 6e-55  
10 emb|AI780513|AI780513 EST261392 tomato susceptible, Cornell Lyco... 110 6e-55

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15 (921 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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Score E  
Sequences producing significant alignments: (bits) Value

25 dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44  
emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 132 9e-43  
dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 134 6e-41  
emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 161 5e-39  
emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 160 1e-38  
30 emb|AB035270|AB035270 Matricaria chamomilla McEREBP1 mRNA for et... 155 5e-37  
gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 138 3e-32  
emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 135 1e-31  
emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 134 1e-30  
emb|AW729466|AW729466 GA\_Ea0025B11 Gossypium arboreum 7-10 dpa ... 132 4e-30  
35 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 125 4e-28  
emb|AW981151|AW981151 EST392345 DSIL Medicago truncatula cDNA cl... 124 8e-28  
emb|AW396250|AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone... 116 2e-25  
emb|AW233956|AW233956 sf32e02.y1 Gm-c1028 Glycine max cDNA clone... 115 5e-25  
emb|AW185128|AW185128 se87b10.y1 Gm-c1023 Glycine max cDNA clone... 114 1e-24  
40 emb|AI897834|AI897834 EST267277 tomato ovary, TAMU Lycopersicon ... 113 2e-24  
emb|AW349516|AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ... 113 2e-24  
emb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 111 6e-24  
emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24  
45 emb|AW981228|AW981228 EST392318 DSIL Medicago truncatula cDNA cl... 89 6e-24  
emb|AI899000|AI899000 EST268443 tomato ovary, TAMU Lycopersicon ... 110 2e-23  
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emb|AI794657|AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone... 110 2e-23  
emb|AW200919|AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone... 109 3e-23  
50 emb|AW507860|AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone... 109 3e-23  
emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 97 3e-23  
dbj|D38125|TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 109 4e-23  
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55 emb|AW278190|AW278190 sf40g11.y1 Gm-c1009 Glycine max cDNA clone... 109 4e-23  
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emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 108 8e-23  
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60 emb|AW596384|AW596384 sj02f12.y1 Gm-c1032 Glycine max cDNA clone... 107 1e-22  
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	emb AW574222 AW574222 EST316813 GVN Medicago truncatula cDNA clo...	105	4e-22
5	emb AI778693 AI778693 EST259572 tomato susceptible, Cornell Lyco...	105	4e-22
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	emb AW774176 AW774176 EST333259 KV3 Medicago truncatula cDNA clo...	105	4e-22
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10	emb AW030386 AW030386 EST273641 tomato callus, TAMU Lycopersicon...	103	2e-21
	emb AW030009 AW030009 EST273264 tomato callus, TAMU Lycopersicon...	103	2e-21
	emb AI782381 AI782381 EST263260 tomato susceptible, Cornell Lyco...	100	1e-20
	emb AW980654 AW980654 EST391807 GVN Medicago truncatula cDNA clo...	100	2e-20
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15	emb AI484961 AI484961 EST243224 tomato ovary, TAMU Lycopersicon ...	100	3e-20
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	emb AW443265 AW443265 EST308195 tomato mixed elicitor, BTI Lycop...	100	3e-20
	emb AI440657 AI440657 sa63d09.y1 Gm-c1004 Glycine max cDNA clone...	99	4e-20
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	emb AV421566 AV421566 AV421566 Lotus japonicus young plants (two...	97	2e-19
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	emb AI442716 AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone...	95	5e-19
	emb AI055252 AI055252 coau0003H16 Cotton Boll Abscission Zone cD...	67	8e-19
	emb AI967551 AI967551 Ljimpest05-400-d11 Ljimp Lambda HybriZap...	95	1e-18
	emb AI896308 AI896308 EST265751 tomato callus, TAMU Lycopersicon...	94	1e-18
30	emb AI776626 AI776626 EST257726 tomato resistant, Cornell Lycop...	93	3e-18
	emb AW686013 AW686013 NF033D04NR1F1000 Nodulated root Medicago t...	92	5e-18
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35	emb AW685077 AW685077 NF024H04NR1F1000 Nodulated root Medicago t...	90	2e-17
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	emb AW308784 AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone...	88	1e-16
	emb AW782252 AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone...	59	1e-16
	emb AW980481 AW980481 EST391634 GVN Medicago truncatula cDNA clo...	87	2e-16
40	gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone ...	87	2e-16
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	emb AW348322 AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3...	85	8e-16
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	emb AI898992 AI898992 EST268435 tomato ovary, TAMU Lycopersicon ...	84	2e-15
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- emb|AI939180|AI939180 sc67h02.y1 Gm-c1016 Glycine max cDNA clone... 125 3e-54  
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5 emb|AW030736|AW030736 EST273991 tomato callus, TAMU Lycopersicon... 133 8e-53  
emb|AI898029|AI898029 EST267472 tomato ovary, TAMU Lycopersicon ... 133 8e-53  
emb|AW625527|AW625527 EST319434 tomato radicle, 5 d post-imbibit... 133 8e-53  
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10 emb|AW442463|AW442463 EST307393 tomato mixed elicitor, BTI Lycop... 133 1e-52  
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15 emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51  
emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51  
emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50  
emb|AI899227|AI899227 EST268670 tomato ovary, TAMU Lycopersicon ... 139 3e-50  
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20 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50  
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25 emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47  
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30 emb|AW620537|AW620537 sj06d09.y1 Gm-c1032 Glycine max cDNA clone... 133 1e-46  
emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycop... 139 2e-46  
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emb|AI974778|AI974778 T113251e KV2 Medicago truncatula cDNA clon... 142 6e-45  
emb|AI898101|AI898101 EST267544 tomato ovary, TAMU Lycopersicon ... 98 8e-45  
gb|BE124175|BE124175 EST394300 DSIL Medicago truncatula cDNA clo... 127 1e-44  
40 emb|AW686370|AW686370 NF040G10NR1F1000 Nodulated root Medicago t... 127 4e-44  
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emb|AW256836|AW256836 EST304973 KV2 Medicago truncatula cDNA clo... 144 5e-44  
emb|AW559274|AW559274 EST306110 DSIR Medicago truncatula cDNA cl... 142 5e-44  
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emb|AW257069|AW257069 EST305206 KV2 Medicago truncatula cDNA clo... 142 2e-42  
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emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41  
emb|AW152892|AW152892 se32d04.y1 Gm-c1015 Glycine max cDNA clone... 82 2e-41  
gb|BE125749|BE125749 DG1\_55\_H11.b1\_A002 Dark Grown 1 (DG1) Sorgh... 127 2e-41  
gb|BE022002|BE022002 sm65c10.y1 Gm-c1028 Glycine max cDNA clone ... 137 3e-41  
55 emb|AI488060|AI488060 EST246382 tomato ovary, TAMU Lycopersicon ... 100 7e-41  
emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40  
emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40  
emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40  
emb|AI960196|AI960196 sc80a08.y1 Gm-c1018 Glycine max cDNA clone... 132 5e-40  
60 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39  
emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

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 5 /blast\_score 1.00e-115 /ec\_number /family /chip nova /gb\_link /ncgi

(925 letters)

10 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

		Score	E	
	Sequences producing significant alignments:		(bits)	Value
	emb AJ012689 CAR012689 Cicer arietinum mRNA for ribonuclease T2.	384	e-106	
	gb U13256 NAU13256 Nicotiana alata RNase NE mRNA, complete cds.	361	4e-99	
	gb U19924 ZEU19924 Zinnia elegans wounding-induced ribonuclease ...	358	4e-98	
20	emb AB034638 AB034638 Nicotiana tabacum mRNA for RNase, complete...	353	1e-96	
	emb X79337 LERNAL L.esculentum mRNA for ribonuclease le.	212	2e-93	
	dbj D49529 D49529 Pyrus pyrifolia mRNA for ribonuclease, complet...	335	4e-91	
	emb AI486253 AI486253 EST244574 tomato ovary, TAMU Lycopersicon ...	212	2e-89	
	emb AI485206 AI485206 EST243510 tomato ovary, TAMU Lycopersicon ...	212	1e-81	
25	gb U19923 ZEU19923 Zinnia elegans ribonuclease mRNA, complete cds.	232	3e-80	
	emb X79338 LERNALX L.esculentum mRNA for ribonuclease lx.	177	1e-73	
	emb AB032257 AB032257 Nicotiana glutinosa NGR3 mRNA for RNase NG...	176	7e-70	
	emb AI484830 AI484830 EST243091 tomato ovary, TAMU Lycopersicon ...	212	7e-70	
	emb AW684365 AW684365 NF016B03NR1F1000 Nodulated root Medicago t...	251	7e-66	
30	emb AI489460 AI489460 EST247799 tomato ovary, TAMU Lycopersicon ...	212	3e-63	
	emb Y17444 LES17444 Lycopersicon esculentum RNALX gene, exons 1 ...	152	2e-57	
	emb AI772676 AI772676 EST253776 tomato resistant, Cornell Lycopersicon...	152	2e-57	
	emb AI775352 AI775352 EST256452 tomato resistant, Cornell Lycopersicon...	212	3e-56	
	gb BE037115 BE037115 MP15C03 MP Mesembryanthemum crystallinum cD...	153	4e-55	
35	emb AF000939 AF000939 Hordeum vulgare aleurone ribonuclease mRNA...	89	7e-55	
	gb M83668 NELSTORAGE Nelumbo nucifera storage protein mRNA, comp...	127	2e-54	
	emb AI812905 AI812905 22D1 Pine Lambda Zap Xylem library Pinus t...	165	3e-54	
	emb AI488432 AI488432 EST246771 tomato ovary, TAMU Lycopersicon ...	211	5e-54	
	emb AW775298 AW775298 EST334363 DSIL Medicago truncatula cDNA cl...	200	7e-54	
40	emb AW279538 AW279538 s90h05.y1 Gm-c1019 Glycine max cDNA clone...	188	6e-47	
	emb AF000940 AF000940 Hordeum vulgare ribonuclease gene, complet...	116	2e-44	
	gb BE060583 BE060583 HVSMEg0012L03f Hordeum vulgare pre-anthesis...	74	5e-42	
	emb Y17445 LES17445 Lycopersicon esculentum RNALX gene, exons 1 ...	122	6e-42	
	emb AI777654 AI777654 EST258449 tomato susceptible, Cornell Lycopersicon...	152	2e-41	
45	emb AW596890 AW596890 sj84b03.y1 Gm-c1034 Glycine max cDNA clone...	162	3e-39	
	gb BE060118 BE060118 HVSMEg0011I10f Hordeum vulgare pre-anthesis...	89	6e-37	
	gb BE060590 BE060590 HVSMEg0012L10f Hordeum vulgare pre-anthesis...	89	2e-36	
	emb AW704136 AW704136 sk16e03.y1 Gm-c1028 Glycine max cDNA clone...	145	4e-34	
	emb AW289659 AW289659 NXNV003D07F Nsf Xylem Normal wood Vertical...	109	8e-32	
50	gb U19794 MDU19794 Malus domestica S-like RNase gene, partial cds.	76	2e-25	
	emb AI967855 AI967855 Ljirmp14-054-a9 Ljirmp Lambda HybriZap ...	109	4e-23	
	emb Y17446 LES17446 Lycopersicon esculentum RNALX gene, exons 1 ...	104	1e-21	
	dbj D64012 LUFRNLC2 Luffa cylindrica mRNA for ribonuclease (RNase...	95	1e-20	
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55	gb BE020073 BE020073 sm38f09.y1 Gm-c1028 Glycine max cDNA clone ...	45	7e-20	
	emb AW039494 AW039494 EST281775 tomato mixed elicitor, BTI Lycopersicon...	43	6e-19	
	emb AW216541 AW216541 EST295255 tomato callus, TAMU Lycopersicon...	43	6e-19	
	dbj D64011 LUFRNLC1 Luffa cylindrica mRNA for ribonuclease (RNase...	89	8e-19	
	emb AB026836 AB026836 Prunus dulcis mRNA for Sa-RNase, complete ...	76	1e-18	
60	emb AW980478 AW980478 EST391631 GVN Medicago truncatula cDNA clo...	44	4e-18	
	gb BE124916 BE124916 EST393951 GVN Medicago truncatula cDNA clon...	44	4e-18	

	emb AB032256 AB032256 Nicotiana glutinosa NGR2 mRNA for RNase NG...	41	9e-18
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	emb AW775566 AW775566 EST334631 DSIL Medicago truncatula cDNA cl...	44	1e-17
	emb AW926310 AW926310 HVSMEg0006001 Hordeum vulgare pre-anthesis...	52	4e-17
5	emb AB034248 AB034248 Volvox carteri vrn1 mRNA for S-like RNase,...	58	8e-17
	emb AF176533 AF176533 Solanum chacoense self-incompatibility rib...	82	2e-16
	emb AI416638 AI416638 sal7c06.y1 Gm-c1004 Glycine max cDNA clone...	45	6e-16
	emb X96465 AHS2RNASE A.hispanicum mRNA for S2-Rnase.	60	2e-15
	emb AB028153 AB028153 Prunus avium mRNA for S1-RNase, complete cds.	56	3e-15
10	emb AW223027 AW223027 EST299838 tomato fruit red ripe, TAMU Lyco...	43	4e-15
	emb AW224120 AW224120 EST300931 tomato fruit red ripe, TAMU Lyco...	43	5e-15
	emb AW223831 AW223831 EST300642 tomato fruit red ripe, TAMU Lyco...	43	5e-15
	emb AF191732 AF191732 Solanum chacoense self-incompatibility rib...	82	6e-15
	emb AB010306 AB010306 Prunus avium mRNA for S3-RNase, complete cds.	57	2e-14
15	emb X76065 LPSRNASE L.peruvianum mRNA for S-RNase S3.	60	2e-14
	emb AB010304 AB010304 Prunus avium mRNA for S2-RNase, partial cds.	60	4e-14
	emb AI729649 AI729649 BNLGHi13860 Six-day Cotton fiber Gossypium...	45	9e-14
	emb AI729386 AI729386 BNLGHi13239 Six-day Cotton fiber Gossypium...	45	1e-13
	emb AW671991 AW671991 LG1_353_B05.b1_A002 Light Grown 1 (LG1) So...	45	1e-13
20	gb S61768 S61768 S (S5)=self-incompatibility {3' region} [Lycopersicon...	60	1e-13
	emb X56897 SCSIAP3 S.chacoense mRNA for self-incompatibility ass...	63	1e-13
	emb AW563386 AW563386 LG1_214_C01.b1_A002 Light Grown 1 (LG1) So...	45	1e-13
	emb AB011470 AB011470 Prunus dulcis mRNA for Sc-RNase, complete ...	60	3e-13
	emb AB011469 AB011469 Prunus dulcis mRNA for Sb-RNase, complete ...	57	4e-13
25	emb AW623083 AW623083 EST321028 tomato flower buds 3-8 mm, Corne...	43	8e-13
	emb AW034883 AW034883 EST279112 tomato callus, TAMU Lycopersicon...	43	8e-13
	emb AF232304 AF232304 Solanum chacoense gametophytic self-incomp...	58	1e-12
	emb Z26583 LPSLGS6 L.peruvianum (Mill) self-incompatability glyc...	56	1e-12
	emb AB011471 AB011471 Prunus dulcis mRNA for Sd-RNase, partial cds.	57	1e-12
30	emb AV427528 AV427528 AV427528 Lotus japonicus young plants (two...	74	2e-12
	emb AF148465 AF148465 Prunus dulcis Sa-S-RNase gene, partial cds.	73	3e-12
	emb AB026982 AB026982 Prunus salicina mRNA for Sb-RNase, partial...	60	5e-12
	dbj E01266 E01266 cDNA encoding S2-protein linked to part of its...	56	1e-11
	gb M24600 TOBGPS N.alata stylar glycoprotein 2 mRNA, complete cds.	56	1e-11
35	dbj E01267 E01267 cDNA encoding S2-protein linked to its signal ...	56	1e-11
	emb X03803 NASINCS2 Nicotiana alata mRNA for S2 self-incompatibi...	56	1e-11
	gb L25930 TOBRNASESB Nicotiana alata RNase S mRNA.	56	1e-11
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40	emb AJ271062 PHY271062 Petunia hybrida mRNA for Sv-ribonuclease ...	62	2e-11
	emb AB016522 AB016522 Petunia x hybrida mRNA for SB1-ribonucleas...	62	2e-11
	emb AB026981 AB026981 Prunus salicina mRNA for Sa-RNase, partial...	56	3e-11
	emb X96464 AHS5RNASE A.hispanicum mRNA for S5-Rnase.	57	4e-11
	gb U19791 MDU19791 Malus domestica S5-RNase (S) mRNA, partial cds.	38	4e-11
45	emb X96466 AHS4RNASE A.hispanicum mRNA for S4-Rnase.	46	7e-11
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	emb Z26581 LPSLGS6 L.peruvianum (Mill) mRNA for self-incompatabi...	51	2e-10
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50	emb AI460477 AI460477 sa79g07.y1 Gm-c1004 Glycine max cDNA clone...	42	3e-10
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	emb AF105363 AF105363 Lycium andersonii self-incompatibility rib...	66	4e-10
	gb U07362 PHU07362 Petunia hybrida S1 self-incompatibility ribon...	62	4e-10
55	gb L40542 POTDSCS Solanum carolinense self-incompatibility ribon...	65	7e-10

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(1480 letters)



Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments:

(bits) Value

	emb AI782831 AI782831 EST263710 tomato susceptible, Cornell Lyco...	270	1e-71
10	emb AW093706 AW093706 EST286886 tomato mixed elicitor, BTI Lycop...	256	4e-67
	emb AW279194 AW279194 sf67g10.y1 Gm-c1013 Glycine max cDNA clone...	205	2e-53
	emb AI776928 AI776928 EST258028 tomato resistant, Cornell Lycoper...	174	1e-42
	emb AW441294 AW441294 EST310690 tomato fruit red ripe, TAMU Lyco...	88	9e-42
	emb AW035369 AW035369 EST280931 tomato callus, TAMU Lycopersicon...	88	3e-35
15	gb BE037451 BE037451 MP21C02 MP Mesembryanthemum crystallinum cD...	88	2e-34
	gb BE058288 BE058288 sn14b07.y1 Gm-c1016 Glycine max cDNA clone ...	88	2e-34
	emb AI895992 AI895992 EST265435 tomato callus, TAMU Lycopersicon...	80	3e-34
	emb AW441248 AW441248 EST310644 tomato fruit red ripe, TAMU Lyco...	88	2e-33
	emb AW223990 AW223990 EST300801 tomato fruit red ripe, TAMU Lyco...	88	2e-33
20	emb AW761120 AW761120 sl63e05.y1 Gm-c1027 Glycine max cDNA clone...	127	9e-32
	gb BE037096 BE037096 MP14H01 MP Mesembryanthemum crystallinum cD...	86	2e-30
	emb AW038060 AW038060 EST279717 tomato mixed elicitor, BTI Lycop...	84	1e-29
	emb AW030010 AW030010 EST273265 tomato callus, TAMU Lycopersicon...	84	1e-29
	emb AW035432 AW035432 EST281170 tomato callus, TAMU Lycopersicon...	83	1e-29
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	emb AW306189 AW306189 se47b02.y1 Gm-c1017 Glycine max cDNA clone...	112	4e-27
	emb AW686451 AW686451 NF038B03NR1F1000 Nodulated root Medicago t...	57	1e-24
	emb AW934306 AW934306 EST360149 tomato fruit mature green, TAMU ...	80	4e-22
30	emb AI896882 AI896882 EST266325 tomato callus, TAMU Lycopersicon...	84	6e-22
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	emb AW216877 AW216877 EST295591 tomato callus, TAMU Lycopersicon...	84	2e-21
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35	emb AI054656 AI054656 coau0001K05 Cotton Boll Abscission Zone cD...	95	2e-18
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40	emb AW034079 AW034079 EST277574 tomato callus, TAMU Lycopersicon...	77	3e-13
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	emb AV418279 AV418279 AV418279 Lotus japonicus young plants (two...	48	8e-09
	emb X91491 CAXANEPOX C.annuum mRNA for xanthophyll epoxidase.	61	2e-08
45	emb Z83835 LEZEAXAN L.esculentum mRNA for zeaxanthin epoxidase.	59	1e-07
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50	emb AQ274524 AQ274524 mgxb0022E01r CUGI Rice Blast BAC Library P...	47	3e-04
	emb AW982239 AW982239 HVSMEG0002G20f Hordeum vulgare pre-anthesi...	36	5e-04
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55	emb AW265977 AW265977 L30-2632T3 Ice plant Lambda Uni-Zap XR exp...	39	0.12
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	emb AV425826 AV425826 AV425826 Lotus japonicus young plants (two...	37	0.42
	emb AB017765 AB017765 Trypanosoma cruzi genes for GATase-CPSase,...	36	0.80
60	emb AL115728 CNS01CMW Botrytis cinerea strain T4 cDNA library un...	36	0.80
	gb U35892 NHU35892 Nectria haematococca maackiain detoxification...	36	0.80



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emb|AJ223325|CRAJ3325 Chlamydomonas reinhardtii mRNA for ascorba... 35 1.1  
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emb|AW279175|AW279175 sf67d04.y1 Gm-c1013 Glycine max cDNA clone... 35 1.5  
5 emb|AF211986|AF211986 Acleisanthes anisophylla 18S ribosomal RNA... 35 1.5  
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emb|AZ217020|AZ217020 Sheared DNA-75G4.TF Sheared DNA Trypanosom... 35 2.1  
emb|X80690|SCDNASEQ S.cerevisiae DNA sequence. 35 2.1  
emb|Z73040|SCYGR255C S.cerevisiae chromosome VII reading frame O... 35 2.1  
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15 gb|BE122310|BE122310 894019A08.y1 C. reinhardtii CC-1690, normal... 35 2.1  
emb|AF003698|AF003698 Saccharomyces cerevisiae COQ6 monooxygenas... 35 2.1  
emb|AW460022|AW460022 si07g06.y1 Gm-c1029 Glycine max cDNA clone... 27 2.5  
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emb|AJ011587|KLA011587 Kluyveromyces lactis muf1 gene. 34 2.9  
20 emb|AI068756|AI068756 mgae0004aD11f Magnaporthe grisea Appressor... 34 2.9  
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25 emb|AV429219|AV429219 AV429219 Lotus japonicus young plants (two... 34 2.9  
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emb|AQ447995|AQ447995 mgxb0015N12r CUGI Rice Blast BAC Library P... 30 3.2  
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30 emb|AW477291|AW477291 ga44f01.y1 Moss EST library PPU Physcomitr... 34 3.9  
emb|AW187125|AW187125 BNLGHi10212 Six-day Cotton fiber Gossypium... 34 3.9  
gb|L04488|TORPHD Trichosporon cutaneum phenol hydroxylase mRNA, ... 34 3.9  
emb|Z74962|BO13G6IG B.oleracea mRNA (unknown). 34 3.9  
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35 emb|AF008953|AF008953 Octomeles sumatrana 18S ribosomal RNA gene... 34 3.9  
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40 emb|AC004145|AC004145 Leishmania major chromosome 3 clone L5801 ... 33 5.4  
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45 emb|AL160727|P417R Leishmania major Friedlin PAC P417 right end-... 33 5.4  
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(2746 letters)

55 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

Searching.....done.

60 Score E  
Sequences producing significant alignments: (bits) Value

- emb|AI896318|AI896318 EST265761 tomato callus, TAMU Lycopersicon... 182 5e-65  
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 5 emb|AW432288|AW432288 sh71g05.y1 Gm-c1015 Glycine max cDNA clone... 200 5e-50  
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 15 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 82 2e-43  
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 30 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 78 5e-39  
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 40 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 82 3e-38  
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 dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 75 5e-38  
 45 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 81 6e-38  
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 50 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 78 5e-37  
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 emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 100 9e-37  
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 55 emb|AW030223|AW030223 EST273478 tomato callus, TAMU Lycopersicon... 92 2e-36  
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 60 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 82 4e-36  
 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 122 8e-36

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 5 emb|AW565461|AW565461 LG1\_344\_F11.g1\_A002 Light Grown 1 (LG1) So... 106 4e-35  
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 10 emb|AW597214|AW597214 sl71g06.y1 Gm-c1031 Glycine max cDNA clone... 126 2e-34  
 emb|AW092144|AW092144 EST285240 tomato mixed elicitor, BTI Lycop... 122 2e-34  
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 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 74 3e-34  
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 15 emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Come... 93 3e-34  
 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 67 3e-34  
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 20 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 74 5e-34  
 emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 77 6e-34  
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 25 emb|AA738547|AA738547 SbRLK5 Sorghum bicolor cv. TX430 leaf Sorg... 115 2e-33  
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Database: plantfungal

50 661,018 sequences; 426,114,510 total letters

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Score E

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 emb|AW200814|AW200814 se93h01.y1 Gm-c1027 Glycine max cDNA clone... 212 3e-78  
 60 emb|AI490817|AI490817 EST241526 tomato shoot, Cornell Lycopersic... 189 3e-71  
 emb|AW757393|AW757393 sl32g05.y1 Gm-c1027 Glycine max cDNA clone... 185 8e-63



- emb|AI731648|AI731648 BNLGHi10360 Six-day Cotton fiber Gossypium... 182 2e-61  
emb|AW458591|AW458591 sh11b01.y1 Gm-cl016 Glycine max cDNA clone... 138 1e-59  
emb|AW033644|AW033644 EST277215 tomato callus, TAMU Lycopersicon... 144 1e-51  
5 emb|AW704608|AW704608 sk54c06.y1 Gm-cl019 Glycine max cDNA clone... 153 5e-51  
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10 emb|AW648007|AW648007 EST326461 tomato germinating seedlings, TA... 100 2e-38  
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gb|BE052703|BE052703 GA\_Ea0031N16f Gossypium arboreum 7-10 dpa ... 86 1e-36  
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emb|X70035|CHTRP1 C.heterostrophus gene for trifunctional trypto... 58 2e-07  
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35 emb|X56047|PDTRPC P. chrysosporium trpC gene for trifunctional p... 55 1e-06  
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40 gb|M74901|CPCTRPI Cryprococcus neoformans phosphoribosyl anthran... 40 0.042  
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb X85382 NTRNATCAL N.tabacum mRNA for calreticulin.	570	e-161
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	gb L27348 BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par...	560	e-159
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	emb X80756 CAPCRTC C.annuum PCRTC mRNA.	344	e-154
25	gb U74631 RCU74631 Ricinus communis calreticulin gene, complete ...	149	e-123
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 emb|AF162779|AF162779 Trypanosoma cruzi Tc45-calreticulin precur... 143 2e-60  
 emb|AW725203|AW725203 GA\_\_Ea0015H01 Gossypium arboreum 7-10 dpa ... 232 4e-60

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments:

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	emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	151	1e-59
	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	151	1e-59
20	emb AW034260 AW034260 EST277831 tomato callus, TAMU Lycopersicon...	151	1e-59
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	emb AI896249 AI896249 EST265692 tomato callus, TAMU Lycopersicon...	142	6e-57
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	emb AW032727 AW032727 EST276286 tomato callus, TAMU Lycopersicon...	147	1e-53
	emb X52555 NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat...	116	1e-52
	gb BE034214 BE034214 MH01C07 MH Mesembryanthemum crystallinum cD...	112	4e-52
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	emb AW559969 AW559969 EST315017 DSIR Medicago truncatula cDNA cl...	81	4e-52
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	emb X05454 NTPR1CR Nicotiana tabacum mRNA for PR-1c protein.	111	2e-51
60	emb X12487 NTPR1C Tobacco mRNA fragment for pathogenesis-related...	111	2e-51
	emb AJ011520 LES011520 Lycopersicon esculentum pr1a (P4) gene.	98	1e-50



- gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50  
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 emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50  
 5 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50  
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 10 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50  
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 15 emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50  
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 emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49  
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 20 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49  
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55 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E  
 Sequences producing significant alignments: (bits) Value



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	emb AW038928 AW038928 EST280884 tomato mixed elicitor, BTI Lycop...	190	2e-80
	emb AI782780 AI782780 EST263659 tomato susceptible, Cornell Lyco...	259	4e-77
	emb AI486671 AI486671 EST244993 tomato ovary, TAMU Lycopersicon ...	241	4e-70
10	emb AW725576 AW725576 GA_Ea0018M08 Gossypium arboreum 7-10 dpa ...	196	3e-69
	emb AW265987 AW265987 L30-2643T3 Ice plant Lambda Uni-Zap XR exp...	150	3e-69
	emb AW033272 AW033272 EST276843 tomato callus, TAMU Lycopersicon...	260	2e-68
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55	gb BE022211 BE022211 sm72b10.y1 Gm-c1028 Glycine max cDNA clone ...	106	7e-22
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	emb AI725563 AI725563 BNLGHi12127 Six-day Cotton fiber Gossypium...	67	5e-18

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 5 emb|AI894661|AI894661 EST264104 tomato callus, TAMU Lycopersicon... 68 3e-10  
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 10 emb|AW184978|AW184978 se85a09.y1 Gm-c1023 Glycine max cDNA clone... 54 4e-06  
 emb|AW091651|AW091651 EST284747 tomato mixed elicitor, BTI Lycop... 51 3e-05  
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 25 emb|AQ847838|AQ847838 LMAJFV1\_lm42a03.y1 Leishmania major FV1 ra... 38 0.25  
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 30 emb|AF099095|AF099095 Samanea saman pulvinus inward-rectifying c... 37 0.66  
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 35 emb|AI781524|AI781524 EST262403 tomato susceptible, Cornell Lyco... 31 2.0  
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emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17  
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20 gb|C96396|C96396 C96396 Marchantia polymorpha immature sex organ... 73 3e-17  
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25 gb|J05116|ACKCAL A.klebsiana calmodulin gene, complete cds. 75 4e-17  
emb|X70923|NCCALMOE N.crassa mRNA for calmodulin. 74 6e-17  
emb|AI328739|AI328739 a6d02ne.fl Neurospora crassa evening cDNA ... 74 6e-17  
emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17  
gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17  
30 gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17  
gb|S68025|S68025 CAM=calmodulin [Paramecium tetraurelia, Genomic... 74 8e-17  
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gb|K02944|TRBCMRSO Trypanosoma brucei gambiense calmodulin genes... 73 2e-16  
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gb|U10150|BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,... 73 2e-16  
emb|X89890|BPCALMGEM B.pilosa mRNA for calmodulin. 73 2e-16  
emb|AW099396|AW099396 sd39h01.y1 Gm-c1016 Glycine max cDNA clone... 76 2e-16  
emb|AW101324|AW101324 sd77e09.y1 Gm-c1009 Glycine max cDNA clone... 59 2e-16  
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emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16  
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55 emb|AW164628|AW164628 se74e01.y1 Gm-c1023 Glycine max cDNA clone... 60 3e-16  
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emb|AW738989|AW738989 gb23c06.y1 Moss EST library PPN Physcomitr... 73 3e-16  
gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16  
gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16  
60 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16  
emb|AF064552|AF064552 Apium graveolens calmodulin mRNA, complete... 73 4e-16



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 gb|U48242|TAU48242 *Triticum aestivum* calmodulin TaCaM1-1 mRNA, c... 73 4e-16  
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 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16  
 20 emb|AW927068|AW927068 HVSMEg0009G21 *Hordeum vulgare* pre-anthesis... 73 4e-16  
 gb|U48689|TAU48689 *Triticum aestivum* calmodulin TaCaM1-3 mRNA, c... 73 4e-16  
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 25 emb|AW775754|AW775754 EST334819 DSIL *Medicago truncatula* cDNA cl... 73 4e-16  
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 gb|U13882|PSU13882 *Pisum sativum* Alaska calmodulin mRNA, complet... 73 4e-16  
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 30 emb|AW666619|AW666619 GA\_Ea0005C16 *Gossypium arboreum* 7-10 dpa ... 73 4e-16  
 emb|AW108833|AW108833 gate0001L24f *Gossypium arboreum* 7-10 dpa f... 73 4e-16  
 emb|Z12839|LLCALMOD *Lilium longiflorum* mRNA encoding calmodulin. 73 4e-16  
 gb|L18912|LILCALMODU *Lilium longiflorum* calmodulin mRNA, complet... 73 4e-16  
  
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 50 gb|U58314|CBU58314 *Clarkia breweri* S-linalool synthase (Lis) mRN... 146 e-171  
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 emb|AF067602|AF067602 *Clarkia concinna* linalool synthase gene, c... 112 1e-53  
 emb|AF097310|AF097310 *Stevia rebaudiana* kaurene synthase (KS1-1)... 88 5e-31  
 emb|AF097311|AF097311 *Stevia rebaudiana* kaurene synthase (KS22-1... 88 5e-31  
 emb|AF067604|AF067604 *Oenothera arizonica* linalool synthase-like... 75 5e-24  
 55 emb|AF067601|AF067601 *Clarkia breweri* linalool synthase 1 (LIS1)... 86 1e-17  
 gb|U43904|CMU43904 *Cucurbita maxima* ent-kaurene synthase B mRNA,... 63 5e-17  
 emb|AI485628|AI485628 EST243949 tomato ovary, TAMU *Lycopersicon* ... 60 3e-15  
 emb|AI485623|AI485623 EST243944 tomato ovary, TAMU *Lycopersicon* ... 55 9e-14  
 gb|U92267|AGU92267 *Abies grandis* gamma-humulene synthase mRNA, c... 45 2e-10  
 60 gb|U50768|AGU50768 *Abies grandis* abietadiene synthase (ac22) mRN... 58 6e-10  
 emb|AW255432|AW255432 ML454 peppermint glandular trichome *Mentha*... 56 1e-08



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5	emb AF006195 AF006195 Abies grandis E-alpha-bisabolene synthase ...	55	7e-08
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10	gb U92266 AGU92266 Abies grandis d-selinene synthase mRNA, compl...	60	1e-07
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40	emb AW255052 AW255052 ML1347 peppermint glandular trichome Menth...	55	2e-06
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	emb AF051901 AF051901 Salvia officinalis (+)-sabinene synthase m...	54	5e-06
45	emb AF175323 AF175323 Mentha longifolia limonene synthase mRNA, ...	54	6e-06
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50	emb AF154125 AF154125 Artemisia annua (3R)-linalool synthase (QH...	51	4e-05
	emb AF049906 AF049906 Cucurbita maxima copalyl diphosphate synth...	51	4e-05
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55	emb AW254876 AW254876 ML1300 peppermint glandular trichome Menth...	49	2e-04
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5	emb AW685590 AW685590 NF029D03NR1F1000 Nodulated root <i>Medicago t...</i>	34	0.014
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25	emb AB022598 AB022598 <i>Solanum tuberosum</i> PVS1 mRNA for vetispirad...	36	1.1
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35 Database: plantfungal  
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	emb AJ239051 CAR239051 <i>Cicer arietinum</i> mRNA for cytochrome P450 ...	255	e-145
	emb AB025016 AB025016 <i>Lotus japonicus</i> mRNA for cytochrome P450, ...	340	e-142
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50	emb AJ000477 HTCYP81C <i>Helianthus tuberosus</i> mRNA for cytochrome P...	225	4e-84
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	302	5e-81
	emb AJ249801 CAR249801 <i>Cicer arietinum</i> partial mRNA for cytochro...	298	6e-80
	emb AF082028 AF082028 <i>Hemerocallis</i> hybrid cultivar senescence-as...	209	4e-76
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55	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	275	6e-73
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60	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber <i>Gossypium</i> ...	188	2e-62
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5 emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycop... 152 9e-56  
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emb|AF022461|AF022461 Glycine max cytochrome P450 monooxygenase ... 108 1e-47  
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25 emb|Y10982|GMP450CP6 Glycine max mRNA for cytochrome P450-like p... 159 9e-47  
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emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 162 6e-46  
dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 157 1e-45  
emb|AW616482|AW616482 EST322893 L. hirsutum trichome, Cornell Un... 124 2e-45  
emb|AW617814|AW617814 EST324213 L. hirsutum trichome, Cornell Un... 124 2e-45  
35 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 183 2e-45  
emb|AW616075|AW616075 EST296834 L. hirsutum trichome, Cornell Un... 124 5e-45  
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40 emb|AW102198|AW102198 sd84f03.y1 Gm-cl009 Glycine max cDNA clone... 181 1e-44  
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45 emb|AW309498|AW309498 sE20c05.x1 Gm-cl028 Glycine max cDNA clone... 178 1e-43  
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50 emb|AW255096|AW255096 ML139 peppermint glandular trichome Mentha... 162 2e-43  
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55 emb|AB023636|AB023636 Glycyrrhiza echinata CYP Ge-8 mRNA for cyt... 107 4e-42  
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60 emb|AI731481|AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ... 171 9e-42  
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5 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 104 4e-41  
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15 emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 168 9e-41  
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25 (1381 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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35 gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ...	260	1e-68
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emb AW220184 AW220184 EST302667 tomato root during/after fruit s...	208	7e-53
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45 emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco...	138	9e-32
emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycop...	111	2e-23
emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco...	86	7e-16
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50 emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo...	62	7e-09
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emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersic...	29	0.010
emb AW651526 AW651526 EST329980 tomato germinating seedlings, TA...	29	0.011
emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ...	29	0.011
55 emb AW926585 AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis...	29	0.025
emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon...	28	0.026
emb AW736598 AW736598 EST333090 KV3 Medicago truncatula cDNA clo...	37	0.39
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	emb AW713709 AW713709 h1e09ne.fl Neurospora crassa evening cDNA ...	35	1.0
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	emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ...	26	1.5
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	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC...	35	1.9
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	emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom...	35	1.9
	emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso...	35	1.9
	emb AQ643883 AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano...	35	1.9
15	emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom...	35	1.9
	emb AW729536 AW729536 GA_Ea0025E24 Gossypium arboreum 7-10 dpa ...	35	1.9
	emb AW727289 AW727289 GA_Ea0011H24 Gossypium arboreum 7-10 dpa ...	35	1.9
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	emb AW256609 AW256609 EST304746 KV2 Medicago truncatula cDNA clo...	34	2.6
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	emb AF230371 AF230371 Lycopersicon esculentum allene oxide synth...	34	3.6
	emb AA741645 AA741645 LmLv39p3/255A Leishmania major promastigot...	34	3.6
	gb U08843 PPU08843 Porphyra purpurea putative polysaccharide bin...	34	3.6
35	emb AF124792 AF124792 Sporothrix schenckii protein kinase C (PCK...	29	4.7
	emb AQ399149 AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P...	33	5.0
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	emb AW035453 AW035453 EST281191 tomato callus, TAMU Lycopersicon...	33	5.0
	emb AF051695 AF051695 Trypanosoma cruzi sialidase homolog (P85.1...	33	5.0
40	emb Z37538 LTGRR4 L.tarentolae mRNA encoding putative NADH subun...	28	5.5
	emb X85021 SCXLTORFS S.cerevisiae DNA from left arm of chromosom...	33	6.8
	gb L25088 YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi...	33	6.8
	emb AQ443826 AQ443826 GSSTc01287 Trypanosoma cruzi random genom...	33	6.8
	emb AQ502942 AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc...	33	6.8
45	emb Z85962 MSZ85962 Musa sp. DNA for sequence tagged microsatell...	33	6.8
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	emb AW224537 AW224537 EST302980 tomato root, plants pre-anthesis...	31	7.5
	emb AW257183 AW257183 EST305320 KV2 Medicago truncatula cDNA clo...	32	9.4
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50	emb AW738509 AW738509 EST339936 tomato flower buds, anthesis, Co...	32	9.4
	emb AW217351 AW217351 EST296174 tomato flower buds 0-3 mm, Corne...	32	9.4
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55	emb AW622239 AW622239 EST313037 tomato root during/after fruit s...	32	9.4
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	emb Y11565 NC11565 N.crassa acu-15 gene.	32	9.4
	emb AW775944 AW775944 EST335009 DSIL Medicago truncatula cDNA cl...	32	9.4
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(2083 letters)

5 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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	emb AW217248 AW217248 EST295962 tomato callus, TAMU Lycopersicon...	245	1e-88
15	emb AI485780 AI485780 EST244101 tomato ovary, TAMU Lycopersicon ...	242	1e-85
	emb AI485695 AI485695 EST244016 tomato ovary, TAMU Lycopersicon ...	261	3e-85
	emb AI485239 AI485239 EST243543 tomato ovary, TAMU Lycopersicon ...	291	1e-77
	emb AI899197 AI899197 EST268640 tomato ovary, TAMU Lycopersicon ...	161	1e-77
	emb AW034573 AW034573 EST278257 tomato callus, TAMU Lycopersicon...	272	8e-72
20	emb AI488812 AI488812 EST247151 tomato ovary, TAMU Lycopersicon ...	251	1e-65
	emb AW687082 AW687082 NF005G09RT1F1071 Developing root Medicago ...	182	6e-65
	emb AI898248 AI898248 EST267691 tomato ovary, TAMU Lycopersicon ...	204	1e-63
	emb AI483614 AI483614 EST249464 tomato ovary, TAMU Lycopersicon ...	238	1e-61
	emb AI897089 AI897089 EST266532 tomato ovary, TAMU Lycopersicon ...	226	7e-58
25	emb AW774994 AW774994 EST334145 KV3 Medicago truncatula cDNA clo...	182	2e-56
	emb AW559604 AW559604 EST314652 DSIR Medicago truncatula cDNA cl...	177	3e-53
	emb AI485284 AI485284 EST243588 tomato ovary, TAMU Lycopersicon ...	204	3e-51
	emb AI485664 AI485664 EST243985 tomato ovary, TAMU Lycopersicon ...	195	8e-49
	emb AW774741 AW774741 EST333892 KV3 Medicago truncatula cDNA clo...	90	2e-48
30	emb AI487608 AI487608 EST245930 tomato ovary, TAMU Lycopersicon ...	187	3e-46
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	emb AI485008 AI485008 EST243271 tomato ovary, TAMU Lycopersicon ...	157	2e-37
	emb AI938737 AI938737 sb58c06.y1 Gm-c1018 Glycine max cDNA clone...	151	2e-35
35	emb AI967736 AI967736 Ljirmp11-837-a7 Ljirmp Lambda HybriZap ...	147	4e-34
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	emb Z71382 SCYNL106C S.cerevisiae chromosome XIV reading frame O...	60	1e-33
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	emb AL022103 SPBC2G2 S.pombe chromosome II cosmid c2G2.	79	1e-27
	emb X79743 SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes.	72	2e-27
	emb Z38062 SC9687 S.cerevisiae chromosome IX cosmid 9687.	72	2e-27
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50	emb AW034093 AW034093 EST277588 tomato callus, TAMU Lycopersicon...	111	3e-23
	emb Z98763 SPAC9G1 S.pombe chromosome I cosmid c9G1.	59	8e-23
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	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	3e-21
55	emb AW731056 AW731056 GA_Ea0008D13 Gossypium arboreum 7-10 dpa ...	102	1e-20
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	emb AW616540 AW616540 EST322951 L. hirsutum trichome, Cornell Un...	98	2e-19
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60	emb AI780067 AI780067 EST260946 tomato susceptible, Cornell Lyco...	94	5e-18
	emb AW687035 AW687035 NF005C05RT1F1037 Developing root Medicago ...	73	2e-17

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	emb AW220291 AW220291 EST302774 tomato root during/after fruit s...	68	1e-14
5	emb AQ644913 AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso...	53	1e-13
	emb AA495505 AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil...	49	4e-13
	emb AW830613 AW830613 sm04c07.y1 Gm-c1027 Glycine max cDNA clone...	77	4e-13
	emb AW666237 AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone...	77	4e-13
	emb AW285758 AW285758 LG1_223_C03.b1_A002 Light Grown 1 (LG1) So...	74	4e-12
10	emb AQ658256 AQ658256 Sheared DNA-13C5.TR Sheared DNA Trypanosom...	73	1e-11
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	emb AV390446 AV390446 AV390446 Chlamydomonas reinhardtii C9 Chla...	70	5e-11
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15	emb AW695904 AW695904 NF099H04ST1F1043 Developing stem Medicago ...	49	2e-10
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20	emb AW333870 AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c...	36	4e-09
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	emb AW616547 AW616547 EST322958 L. hirsutum trichome, Cornell Un...	62	2e-08
25	emb AW693686 AW693686 NF068A05ST1F1036 Developing stem Medicago ...	62	2e-08
	emb AW208046 AW208046 M111077e DSIR Medicago truncatula cDNA clo...	61	4e-08
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(1690 letters)

60 Database: plantfungal  
661,018 sequences; 426,114,510 total letters



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	emb AJ001770 NTTCG9	Nicotiana tabacum mRNA for cytosolic glucose...	893 0.0
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15	emb Z69381 SCCXIV39K	S.cerevisiae 38,855 bp segment of chromosom...	244 e-136
	gb M34709 YSCG6PD	S.cerevisiae glucose-6-phosphate dehydrogenase...	244 e-136
	emb X57336 SCMET19	S. cerevisiae MET19 gene for glucose-6-phosph...	244 e-136
	emb Z71517 SCYNL241C	S.cerevisiae chromosome XIV reading frame O...	244 e-136
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20	emb X99405 NTG6PD	N.tabacum mRNA for chloroplast glucose-6-phosp...	242 e-135
	emb AF012861 AF012861	Petroselinum crispum plastidic glucose-6-p...	248 e-135
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30	emb X83923 STG6PDHPI	S.tuberosum mRNA for glucose-6-phosphate de...	249 e-118
	emb AJ000182 SO000182	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-117
	emb AJ001771 NTTPG16	Nicotiana tabacum mRNA for plastidic glucos...	247 e-116
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	emb AJ000183 SO000183	Spinacia oleracea mRNA for glucose-6-phosp...	190 3e-99
	emb X84001 ANDNAG6PD	A.nidulans g6pd gene.	130 2e-98
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50	emb AW216550 AW216550	EST295264 tomato callus, TAMU Lycopersicon...	188 6e-84
	emb AW219903 AW219903	EST302386 tomato root during/after fruit s...	305 7e-82
	emb AW180861 AW180861	MgA1030f MgA Library Mycosphaerella gramin...	226 5e-80
	emb AW616585 AW616585	EST322996 L. hirsutum trichome, Cornell Un...	175 7e-80
	emb AW309937 AW309937	sf26h03.x1 Gm-c1028 Glycine max cDNA clone...	294 1e-78
55	emb AW031447 AW031447	EST274901 tomato callus, TAMU Lycopersicon...	166 6e-78
	emb AI894720 AI894720	EST264163 tomato callus, TAMU Lycopersicon...	291 1e-77
	emb AW690515 AW690515	NF030E09ST1F1000 Developing stem Medicago ...	174 3e-77
	emb AW736245 AW736245	EST332231 KV3 Medicago truncatula cDNA clo...	278 7e-76
	emb AW455246 AW455246	EST311906 tomato root during/after fruit s...	155 6e-75
60	emb AW980010 AW980010	EST310488 tomato root deficiency, Cornell ...	153 3e-74
	emb AL023595 SPCC794	S.pombe chromosome III cosmid c794.	177 1e-73



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emb|AW689492|AW689492 NF019H04ST1F1000 Developing stem Medicago ... 128 3e-69  
5 emb|AW737104|AW737104 EST338531 tomato flower buds, anthesis, Co... 141 1e-64  
emb|AW255222|AW255222 ML216 peppermint glandular trichome Mentha... 142 2e-64  
emb|AW737079|AW737079 EST338506 tomato flower buds, anthesis, Co... 141 3e-64  
emb|AW565200|AW565200 LG1\_328\_D07.b1\_A002 Light Grown 1 (LG1) So... 119 1e-60  
emb|AW684970|AW684970 NF023F11NR1F1000 Nodulated root Medicago t... 128 1e-60  
10 emb|AQ952407|AQ952407 Sheared DNA-32N19.TF Sheared DNA Trypanoso... 84 2e-60  
emb|AA787466|AA787466 n3fl1a1.r1 Aspergillus nidulans 24hr asexu... 229 4e-59  
emb|AW254983|AW254983 ML1164 peppermint glandular trichome Menth... 134 2e-58  
emb|AW617385|AW617385 EST323796 L. hirsutum trichome, Cornell Un... 141 2e-57  
emb|AI773327|AI773327 EST254427 tomato resistant, Cornell Lycopers... 222 5e-57  
emb|AW704079|AW704079 sk27e10.y1 Gm-c1028 Glycine max cDNA clone... 219 6e-56  
15 emb|X77829|ANNGSDA A.niger (N400) gsdA gene. 131 4e-55  
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emb|AV424412|AV424412 AV424412 Lotus japonicus young plants (two... 205 9e-52  
20 emb|AQ875204|AQ875204 V123H11 mTn-3xHA/lacZ Insertion Library, s... 192 1e-49  
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emb|Z99568|SPAC3C7 S.pombe chromosome I cosmid c3C7. 95 1e-48  
emb|AQ500574|AQ500574 V36G4 mTn-3xHA/lacZ Insertion Library Sacc... 127 6e-48  
emb|AI187687|AI187687 p280 Porphyra yezoensis in Lambda UniZAP P... 87 1e-47  
25 emb|AJ279688|BPE279688 Betula pendula partial mRNA for Glucose-6... 93 7e-47  
emb|AW700124|AW700124 gb34g09.y1 Moss EST library PPN Physcomitr... 187 3e-46  
emb|AW223852|AW223852 EST300663 tomato fruit red ripe, TAMU Lyco... 141 6e-46  
emb|AW774199|AW774199 EST333350 KV3 Medicago truncatula cDNA clo... 143 3e-45  
emb|AW621290|AW621290 EST312088 tomato root during/after fruit s... 138 3e-43  
30 emb|AW980083|AW980083 EST341594 tomato root deficiency, Cornell ... 133 2e-42  
emb|AZ217409|AZ217409 Sheared DNA-90C8.TR Sheared DNA Trypanosom... 90 3e-42  
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emb|AW224136|AW224136 EST300947 tomato fruit red ripe, TAMU Lyco... 141 3e-40  
emb|AW616535|AW616535 EST322946 L. hirsutum trichome, Cornell Un... 139 2e-38  
35 emb|AU036687|AU036687 Schizosaccharomyces pombe genomic clone ha... 98 3e-38  
emb|AI416414|AI416414 NCW07G12T3 Westergaards Neurospora crassa ... 103 3e-38  
emb|AW286271|AW286271 LG1\_329\_F06.g1\_A002 Light Grown 1 (LG1) So... 149 4e-35  
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40 emb|AJ130773|LDI130773 Laminaria digitata mRNA for glucose-6-pho... 131 2e-29  
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50 (887 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

60 emb|AW725454|AW725454 GA\_Ea0018A14 Gossypium arboreum 7-10 dpa ... 238 8e-81  
emb|Z38114|SC9745 S.cerevisiae chromosome XIII cosmid 9745. 122 2e-33

- gb|U34860|SCU34860 *Saccharomyces cerevisiae* origin recognition c... 122 2e-33  
 dbj|D38172|YSCTEMIP Yeast gene for GTP-binding protein Tem1p, co... 122 2e-33  
 emb|AI988573|AI988573 sd04c11.y1 Gm-c1020 Glycine max cDNA clone... 142 3e-33  
 emb|Y12314|SPSPG1GEN *S.pombe* spg1 gene. 67 9e-20  
 5 emb|AJ001587|SPAJ1587 *Schizosaccharomyces pombe* sid3 gene. 67 9e-20  
 emb|AW776339|AW776339 EST335404 *DSIL* *Medicago truncatula* cDNA cl... 67 5e-14  
 emb|AI416417|AI416417 NCW07E2T3 *Westergaards Neurospora crassa* c... 55 1e-06  
 gb|U17243|YSCL8003 *Saccharomyces cerevisiae* chromosome XII cosmi... 32 2e-06  
 emb|Z75093|SCYOR185C *S.cerevisiae* chromosome XV reading frame OR... 32 2e-06  
 10 gb|L08690|YSCGSP1X Yeast GTP-binding protein (GSP1) gene, comple... 32 2e-06  
 gb|L08691|YSCGSP2X Yeast GTP-binding protein (GSP2) gene, comple... 32 2e-06  
 emb|X71946|SCCNR2A *S.cerevisiae* CNR2 gene. 32 2e-06  
 emb|X71945|SCCNR1A *S.cerevisiae* CNR1 gene. 32 2e-06  
 dbj|D17748|TETTRAN *Tetrahymena thermophila* mRNA for Ran/TC4, com... 33 3e-06  
 15 dbj|D21825|TETPRAN *Tetrahymena pyriformis* mRNA for Ran/TC4, comp... 33 3e-06  
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 30 emb|AW738459|AW738459 EST339886 tomato flower buds, anthesis, Co... 36 0.33  
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 40 emb|AW040005|AW040005 EST282496 tomato mixed elicitor, BTI Lycop... 35 0.56  
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 gb|S79308|S79308 Rac13=21.8 kda GTP-binding protein [Gossypium h... 35 0.62  
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 5 gb|BE055015|BE055015 GA\_\_Ea0001G03f Gossypium arboreum 7-10 dpa ... 35 0.62  
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 25 emb|AW559842|AW559842 EST314890 DSIR Medicago truncatula cDNA cl... 34 1.6  
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45 Database: plantfungal  
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gb|U18557|RSU18557 Raphanus sativus antifungal protein 1 preprot... 166 7e-43  
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 gb|U18556|RSU18556 Raphanus sativus antifungal protein 2 preprot... 160 1e-38  
 emb|X97319|RSEFP3 R.sativus mRNA for antifungal protein 3. 133 8e-37  
 gb|U59459|BNU59459 Brassica napus antifungal protein mRNA, compl... 135 2e-36  
 emb|AT001728|AT001728 AT001728 Flower bud cDNA Brassica rapa sub... 82 2e-15  
 60 gb|L47901|L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA... 81 5e-15  
 emb|A26963|A26963 D.merkii AMP1 sequence. 74 5e-13



	emb A27062 A27062 C.benedictus AMP2 sequence.	73 1e-12
	emb X53375 HASF18 Sunflower anther-specific mRNA SF18.	72 3e-12
	emb A26906 A26906 C.benedictus AMP1 sequence.	72 3e-12
	emb AT001738 AT001738 AT001738 Flower bud cDNA Brassica rapa sub...	69 2e-11
5	emb A27064 A27064 C.ternatea AMP1 sequence.	58 8e-10
	emb X91487 PASPI1GEN P.abies mRNA for gamma-thionin protein (put...	40 1e-05
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40	emb AW622390 AW622390 EST313189 tomato root during/after fruit s...	35 0.029
	emb AI486656 AI486656 EST244977 tomato ovary, TAMU Lycopersicon ...	38 0.031
	emb AW399651 AW399651 EST310151 L. pennellii trichome, Cornell U...	38 0.043
	emb AW621171 AW621171 EST311969 tomato root during/after fruit s...	34 0.048
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45	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon ...	37 0.059
	emb AW622079 AW622079 EST312877 tomato root during/after fruit s...	33 0.061
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	emb Y15149 ABY15149 Aquilaria beccariana rbcL gene.	34 0.54
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	emb AF022125 AF022125 Theobroma cacao ribulose 1,5-bisphosphate ...	34 0.54
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	gb L01961 TEPCPRBCL Thespesia populnea ribulose 1,5-bisphosphate...	33	1.4
	emb AJ233137 RTAJ3137 Reevesia thyrsoides chloroplast rbcL gene,...	33	1.4
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	emb AJ233127 HBAJ3127 Helicteres baruensis chloroplast rbcL gene...	33	1.4
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Database: plantfungal  
 45 661,018 sequences; 426,114,510 total letters

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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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5	emb AW622151 AW622151 EST312949 tomato root during/after fruit s...	47 6e-07
	emb AW623994 AW623994 EST321939 tomato flower buds 3-8 mm, Corne...	48 6e-07
	emb AW621737 AW621737 EST312535 tomato root during/after fruit s...	47 6e-07
	emb AI482693 AI482693 EST242016 tomato shoot, Cornell Lycopersic...	48 7e-07
	emb AW622612 AW622612 EST313412 tomato root during/after fruit s...	46 1e-06
10	emb AW596685 AW596685 sj15e02.y1 Gm-c1032 Glycine max cDNA clone...	49 2e-06
	emb AW328890 AW328890 N200082e rootphos(-) Medicago truncatula c...	41 2e-06
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	emb AW650481 AW650481 EST328935 tomato germinating seedlings, TA...	53 5e-06
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20	emb AI726794 AI726794 BNLGHi6582 Six-day Cotton fiber Gossypium ...	50 7e-06
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	emb AI487871 AI487871 EST246193 tomato ovary, TAMU Lycopersicon ...	39 1e-04
	emb AJ276421 CAR276421 Cicer arietinum partial mRNA for putative...	48 1e-04
30	emb AW277884 AW277884 sf88f10.y1 Gm-c1019 Glycine max cDNA clone...	42 2e-04
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35	gb BE124032 BE124032 EST394157 DSIL Medicago truncatula cDNA clo...	47 3e-04
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	emb AW929104 AW929104 EST337808 tomato flower buds 8 mm to pre-a...	33 5e-04
	emb AW624906 AW624906 EST313735 tomato radicle, 5 d post-imbibit...	35 5e-04
	emb AW706408 AW706408 sj56h10.y1 Gm-c1033 Glycine max cDNA clone...	46 6e-04
40	gb BE054438 BE054438 GA_Ea0004H20f Gossypium arboreum 7-10 dpa ...	45 7e-04
	emb AW109570 AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f...	45 7e-04
	emb AW279386 AW279386 sf66f11.y1 Gm-c1013 Glycine max cDNA clone...	37 7e-04
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 5 gb|BE057305|BE057305 sn01c10.y1 Gm-c1015 Glycine max cDNA clone ... 43 0.004  
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 emb|AW648494|AW648494 EST326948 tomato germinating seedlings, TA... 43 0.005  
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 10 emb|AI487258|AI487258 EST245580 tomato ovary, TAMU Lycopersicon ... 43 0.005  
 emb|AW218200|AW218200 EST303381 tomato radicle, 5 d post-imbibit... 43 0.005  
 emb|AI486112|AI486112 EST244433 tomato ovary, TAMU Lycopersicon ... 43 0.005  
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 emb|AW348454|AW348454 GM210002A22E12R Gm-r1021 Glycine max cDNA ... 39 0.006  
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 emb|AW666820|AW666820 GA\_Ea0006B14 Gossypium arboreum 7-10 dpa ... 35 0.006  
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 20 emb|AW730008|AW730008 GA\_Ea0027E20 Gossypium arboreum 7-10 dpa ... 36 0.008  
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 emb|AW100112|AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone... 30 0.012  
 emb|AW394864|AW394864 sh36e01.y1 Gm-c1017 Glycine max cDNA clone... 41 0.014

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 gb|aa042519 come from this gene. [arabidopsis thaliana]" /blast\_score  
 30 0 /ec\_number /family /chip nova /gb\_link /ncgi  
 (1335 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

35

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|AF019376|AF019376 Brassica napus calreticulin mRNA, complete... 619 0.0

gb|U74630|RCU74630 Ricinus communis calreticulin mRNA, complete ... 747 0.0

emb|Z71395|NPCAL1MNR N.plumbaginifolia mRNA for calreticulin. 742 0.0

emb|AF134733|AF134733 Prunus armeniaca calcium-binding protein c... 741 0.0

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emb|AJ002057|BVMRNAC Beta vulgaris mRNA for calreticulin. 730 0.0

emb|X85382|NTRNATCAL N.tabacum mRNA for calreticulin. 726 0.0

emb|AF052040|AF052040 Berberis stolonifera calreticulin mRNA, co... 722 0.0

emb|X80756|CAPCRTC C.annuum PCRTC mRNA. 471 0.0

gb|L27348|BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par... 670 0.0

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gb|L27349|BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par... 669 0.0

gb|U74631|RCU74631 Ricinus communis calreticulin gene, complete ... 201 e-172

emb|AW039860|AW039860 EST282333 tomato mixed elicitor, BTI Lycop... 517 e-145

emb|AB018243|AB018243 Solanum melongena EEF22 mRNA for calreticu... 510 e-143

emb|AI782264|AI782264 EST263143 tomato susceptible, Cornell Lyco... 497 e-140

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emb|AW441195|AW441195 EST310591 tomato fruit red ripe, TAMU Lyco... 487 e-136

emb|AJ000765|CRAJ765 Chlamydomonas reinhardtii mRNA for calretic... 393 e-135

emb|AW930392|AW930392 EST340945 tomato fruit mature green, TAMU ... 478 e-134

emb|AW667951|AW667951 GA\_Ea0012A11 Gossypium arboreum 7-10 dpa ... 472 e-132

emb|AW944954|AW944954 EST337004 tomato flower buds 3-8 mm, Corne... 469 e-131

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emb|AW773947|AW773947 EST332933 KV3 Medicago truncatula cDNA clo... 469 e-131

emb|AW650947|AW650947 EST329401 tomato germinating seedlings, TA... 468 e-131



- emb|AW622049|AW622049 EST312847 tomato root during/after fruit s... 467 e-131  
emb|AW216727|AW216727 EST295441 tomato callus, TAMU Lycopersicon... 460 e-128  
emb|AW731454|AW731454 GA\_Ea0030H17 Gossypium arboreum 7-10 dpa ... 456 e-127  
5 emb|AI735991|AI735991 sb21e08.y1 Gm-cl007 Glycine max cDNA clone... 450 e-125  
emb|Y09078|DBCALLKPR D.bioculata mRNA for calreticulin-like prot... 228 e-124  
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10 emb|AW773889|AW773889 EST332875 KV3 Medicago truncatula cDNA clo... 437 e-122  
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emb|AW626316|AW626316 EST320223 tomato radicle, 5 d post-imbibit... 422 e-117  
emb|AA660477|AA660477 00363 MtRHE Medicago truncatula cDNA 5' si... 421 e-117  
15 emb|AW727433|AW727433 GA\_Ea0012B12 Gossypium arboreum 7-10 dpa ... 421 e-117  
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emb|AW621571|AW621571 EST312369 tomato root during/after fruit s... 419 e-116  
emb|AW309216|AW309216 sg05g07.y1 Gm-cl019 Glycine max cDNA clone... 414 e-115  
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20 emb|AW738476|AW738476 EST339903 tomato flower buds, anthesis, Co... 412 e-114  
emb|AW685878|AW685878 NF031C11NR1F1000 Nodulated root Medicago t... 411 e-114  
emb|AW933869|AW933869 EST359712 tomato fruit mature green, TAMU ... 407 e-113  
emb|AW220942|AW220942 EST297411 tomato fruit mature green, TAMU ... 406 e-112  
emb|AW277466|AW277466 sf82d10.y1 Gm-cl019 Glycine max cDNA clone... 406 e-112  
25 emb|AW568477|AW568477 si59c07.y1 Gm-r1030 Glycine max cDNA clone... 403 e-111  
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emb|AW773817|AW773817 EST332803 KV3 Medicago truncatula cDNA clo... 399 e-110  
emb|AI495184|AI495184 sa89b11.y1 Gm-cl004 Glycine max cDNA clone... 398 e-110  
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30 emb|AW035959|AW035959 EST282818 tomato callus, TAMU Lycopersicon... 396 e-109  
emb|AW932476|AW932476 EST358319 tomato fruit mature green, TAMU ... 395 e-109  
emb|AW979917|AW979917 EST341567 tomato root deficiency, Cornell ... 395 e-109  
emb|AW649196|AW649196 EST327650 tomato germinating seedlings, TA... 391 e-108  
emb|AI960982|AI960982 sc93e09.y1 Gm-cl019 Glycine max cDNA clone... 386 e-106  
35 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 385 e-106  
emb|AW596414|AW596414 sj12b07.y1 Gm-cl032 Glycine max cDNA clone... 384 e-106  
emb|AW648010|AW648010 EST326464 tomato germinating seedlings, TA... 382 e-105  
emb|AW725587|AW725587 GA\_Ea0018N14 Gossypium arboreum 7-10 dpa ... 379 e-104  
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40 emb|AW727696|AW727696 GA\_Ea0015K01 Gossypium arboreum 7-10 dpa ... 303 e-103  
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45 emb|AW933031|AW933031 EST358874 tomato fruit mature green, TAMU ... 366 e-100  
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emb|AW035234|AW035234 EST280496 tomato callus, TAMU Lycopersicon... 364 1e-99  
emb|AW907386|AW907386 EST343509 potato stolon, Cornell Universit... 361 9e-99  
emb|AW756722|AW756722 sl26d08.y1 Gm-cl027 Glycine max cDNA clone... 359 3e-98  
50 emb|AW760501|AW760501 sl51b04.y1 Gm-cl027 Glycine max cDNA clone... 358 6e-98  
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emb|AW043340|AW043340 ST32B12 Pine TriplEx shoot tip library Pin... 324 1e-87  
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60 emb|AW648456|AW648456 EST326910 tomato germinating seedlings, TA... 316 3e-85  
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- emb|AW624478|AW624478 EST322423 tomato flower buds 3-8 mm, Corne... 312 3e-84  
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 emb|AW754529|AW754529 PC03C03 Pine TriplEx pollen cone library P... 280 2e-74  
 emb|AW042889|AW042889 ST26F06 Pine TriplEx shoot tip library Pin... 279 3e-74  
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 (1647 letters)

30 Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

35 Score E  
 Sequences producing significant alignments: (bits) Value

- emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 308 e-114  
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 emb|AI897763|AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... 305 7e-82  
 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 278 3e-81  
 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 269 6e-81  
 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 300 2e-80  
 45 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 300 2e-80  
 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 121 9e-79  
 emb|X70824|SMPEG1 S.melongena pEG1 mRNA for hydroxylase P450. 171 1e-77  
 dbj|E05111|E05111 cDNA encoding solanum flavonoid 3',5'-hydroxyg... 171 1e-77  
 gb|M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 283 3e-75  
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- emb|Y10490|GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 259 4e-68  
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emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 256 3e-67  
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5 emb|AI897760|AI897760 EST267203 tomato ovary, TAMU Lycopersicon ... 138 2e-66  
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emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 247 2e-64  
gb|U48435|SCU48435 Solanum chacoense putative cytochrome P450 ge... 247 2e-64  
emb|AW730128|AW730128 GA\_Ea0027P19 Gossypium arboreum 7-10 dpa ... 184 6e-63  
10 emb|AI777331|AI777331 EST263739 tomato seed, TAMU Lycopersicon e... 240 3e-62  
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emb|AW668189|AW668189 GA\_Ea0013B20 Gossypium arboreum 7-10 dpa ... 184 5e-62  
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emb|AW234222|AW234222 sf22f08.y1 Gm-c1028 Glycine max cDNA clone... 237 3e-61  
emb|AF124815|AF124815 Mentha spicata cytochrome p450 mRNA, compl... 162 3e-61  
gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 236 3e-61  
20 dbj|D14589|D14589 Eustoma russellianum mRNA for flavonoid 3',5'-... 179 5e-61  
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25 gb|BE054146|BE054146 GA\_Ea0034H12f Gossypium arboreum 7-10 dpa ... 234 2e-60  
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emb|Z22545|PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA. 182 3e-60  
dbj|D14588|PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h... 182 3e-60  
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30 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 231 8e-60  
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dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 178 5e-59  
emb|Z33875|CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. 228 8e-59  
35 emb|AI726383|AI726383 BNLGHi5702 Six-day Cotton fiber Gossypium ... 227 2e-58  
emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lycop... 225 7e-58  
emb|AW728587|AW728587 GA\_Ea0017C12 Gossypium arboreum 7-10 dpa ... 225 1e-57  
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40 emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 146 2e-57  
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45 emb|AW459662|AW459662 sh90c05.y1 Gm-c1016 Glycine max cDNA clone... 221 9e-57  
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emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 168 5e-56  
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50 emb|AW832652|AW832652 sm15g02.y1 Gm-c1027 Glycine max cDNA clone... 121 3e-55  
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55 emb|AW395730|AW395730 sg74f08.y1 Gm-c1007 Glycine max cDNA clone... 213 3e-54  
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60 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 109 3e-53  
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5 emb|AW616345|AW616345 EST322756 L. hirsutum trichome, Cornell Un... 208 1e-52  
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emb|AF000403|AF000403 Lotus japonicus putative cytochrome P450 ... 145 2e-52  
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10 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 93 4e-51  
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emb|AB025016|AB025016 Lotus japonicus mRNA for cytochrome P450, ... 152 6e-51  
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http://www3.ncbi.nlm.nih.gov/htbin-  
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http://www.ncgr.org/cgi-bin/ff?ac000375  
(1533 letters)  
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Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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Score E  
Sequences producing significant alignments: (bits) Value

35 gb|BE020282|BE020282 sm42g12.y1 Gm-c1028 Glycine max cDNA clone ... 91 2e-39  
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emb|AW731252|AW731252 GA\_\_Ea0030E03 Gossypium arboreum 7-10 dpa ... 93 2e-31  
emb|AW650703|AW650703 EST329157 tomato germinating seedlings, TA... 88 2e-28  
emb|AW648696|AW648696 EST327066 tomato germinating seedlings, TA... 85 7e-25  
40 emb|AT000481|AT000481 AT000481 Brassica rapa guard cell Brassica... 62 3e-23  
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emb|AI774644|AI774644 EST255744 tomato resistant, Cornell Lycopersicon... 65 4e-19  
emb|AW560992|AW560992 EST316040 DSIR Medicago truncatula cDNA cl... 68 2e-18  
45 emb|AW034968|AW034968 EST279197 tomato callus, TAMU Lycopersicon... 61 2e-15  
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50 emb|AW032231|AW032231 EST275685 tomato callus, TAMU Lycopersicon... 62 6e-11  
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55 emb|AI896893|AI896893 EST266336 tomato callus, TAMU Lycopersicon... 62 1e-10  
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20 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score E  
 Sequences producing significant alignments: (bits) Value

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 30 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 211 4e-95  
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 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 185 5e-81  
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 35 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 156 4e-79  
 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 156 4e-79  
 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 119 4e-78  
 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 119 7e-78  
 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 119 1e-77  
 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 103 6e-77  
 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 105 1e-75  
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 45 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 133 2e-70  
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 50 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 167 9e-65  
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 60 emb|AW746018|AW746018 WS1\_38\_H11.g1\_A002 Water-stressed 1 (WS1) ... 147 3e-57  
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5 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 138 3e-54  
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gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 116 1e-51  
15 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 117 9e-51  
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 124 2e-50  
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 141 6e-50  
emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 149 1e-49  
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20 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 120 4e-49  
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 115 9e-49  
emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 112 1e-48  
gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 112 1e-48  
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 115 1e-48  
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gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 112 5e-48  
emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 112 5e-48  
emb|AW922735|AW922735 DG1\_45\_B06.g1\_A002 Dark Grown 1 (DG1) Sorg... 139 9e-48  
30 emb|AW746695|AW746695 WS1\_54\_E02.g1\_A002 Water-stressed 1 (WS1) ... 139 9e-48  
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35 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 116 3e-46  
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40 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 116 4e-46  
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emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 121 9e-46  
emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 109 1e-45  
emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 112 2e-45  
45 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 135 2e-45  
gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 116 2e-45  
gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 109 2e-45  
gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 116 3e-45  
gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 109 6e-45  
50 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 108 8e-45  
emb|AW922776|AW922776 DG1\_46\_C01.g1\_A002 Dark Grown 1 (DG1) Sorg... 147 2e-44  
gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 141 4e-44  
emb|AA739579|AA739579 344 PtiFG2 Pinus taeda cDNA clone 8562M 3'... 107 1e-43  
emb|AW560048|AW560048 EST315096 DSIR Medicago truncatula cDNA cl... 116 1e-43  
55 emb|A23396|A23396 B.vulgaris gene for chitinase 76. 105 3e-43  
emb|AW267781|AW267781 EST305909 DSIR Medicago truncatula cDNA cl... 115 4e-43  
emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 108 8e-43  
emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 125 1e-42  
emb|AI352718|AI352718 MB46-29 PZ204.BNlib Brassica napus cDNA cl... 144 4e-42  
60 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 80 5e-42  
emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 111 2e-41

emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 116 3e-41  
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 117 4e-41  
 emb|Z15138|LECHI14 L.esculentum mRNA for chitinase (partial). 114 1e-40  
 gb|U30465|LEU30465 Lycopersicon esculentum class II chitinase (C... 114 2e-40  
 5 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 100 1e-39

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 (1116 letters)

15 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

20 Searching.....done

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25	emb AW671006 AW671006 LG1_278_H12.b1_A002 Light Grown 1 (LG1) So...	81	6e-28
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	gb U43491 SCU43491 Saccharomyces cerevisiae cosmid clone pEOA156...	37	0.31
	emb Z74916 SCYOR008C S.cerevisiae chromosome XV reading frame OR...	37	0.31
	gb U39481 SCU39481 Saccharomyces cerevisiae Slglp (SLG1) gene, c...	37	0.31
	emb AA680906 AA680906 LmFrAm0494 Leishmania major Amastigote ful...	33	1.0
30	emb AF193903 AF193903 Cafeteria roenbergensis mitochondrial DNA,...	35	1.1
	emb AF229795 AF229795 Vigna radiata beta galactosidase mRNA, com...	35	1.5
	emb AW683786 AW683786 NF001A06NR1F1038 Nodulated root Medicago t...	35	1.5
	emb AC005802 AC005802 Leishmania major chromosome 3 clone L6202 ...	34	2.1
	emb AC005893 AC005893 Leishmania major chromosome 3 clone L822 s...	34	2.1
35	emb AA520166 AA520166 TgESTzz39b08.s1 TgME49 invivo Bradyzoite c...	34	2.9
	emb AW618793 AW618793 EST320779 L. pennellii trichome, Cornell U...	34	2.9
	emb AW306460 AW306460 se51a02.y1 Gm-c1017 Glycine max cDNA clone...	34	2.9
	emb AQ502036 AQ502036 V10E12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9
	gb U87148 HVU87148 Hordeum vulgare nucellin mRNA, complete cds.	33	3.9
40	emb AF017430 AF017430 Hordeum vulgare EEA1 mRNA, complete cds.	33	3.9
	emb AQ500344 AQ500344 V41B12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9
	emb Z71686 SCYNR071C S.cerevisiae chromosome XIV reading frame O...	33	3.9
	emb AQ501720 AQ501720 V15F6 mTn-3xHA/lacZ Insertion Library Sacc...	33	3.9
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45	emb AW126050 AW126050 N100246e rootphos(-) Medicago truncatula c...	33	5.4
	emb AW127669 AW127669 M110413 DSLC Medicago truncatula cDNA clon...	33	5.4
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50	emb AQ503147 AQ503147 V44D10 mTn-3xHA/lacZ Insertion Library Sac...	33	5.4
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	emb AW672219 AW672219 LG1_358_B09.b1_A002 Light Grown 1 (LG1) So...	33	5.4
	emb AW925272 AW925272 HVSMEg0001G19 Hordeum vulgare pre-anthesis...	33	5.4
55	emb AA783066 AA783066 a1h02c9.r1 Aspergillus nidulans 24hr asexu...	26	5.7
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60	emb AW156670 AW156670 se29c01.y1 Gm-c1015 Glycine max cDNA clone...	32	7.4
	emb AW277786 AW277786 sf86e12.y1 Gm-c1019 Glycine max cDNA clone...	32	7.4



emb|AE001432|AE001432 Plasmodium falciparum chromosome 2, sectio... 32 7.4  
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5 emb|AW277436|AW277436 sf82a10.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4  
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15 http://www3.ncbi.nlm.nih.gov/htbin-  
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(1812 letters)

20 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score E  
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emb|AW930291|AW930291 EST340748 tomato fruit mature green, TAMU ... 415 e-115  
emb|AW625643|AW625643 EST319550 tomato radicle, 5 d post-imbibit... 398 e-110  
30 emb|AW666282|AW666282 sk34f11.y1 Gm-c1028 Glycine max cDNA clone... 393 e-108  
emb|AW650696|AW650696 EST329150 tomato germinating seedlings, TA... 226 e-103  
emb|AW691093|AW691093 NF041B09ST1F1000 Developing stem Medicago ... 355 e-102  
emb|AW926942|AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis... 339 e-102  
gb|BE055044|BE055044 GA\_Ea0031H08f Gossypium arboreum 7-10 dpa ... 341 2e-99  
35 emb|AW696933|AW696933 NF112E03ST1F1021 Developing stem Medicago ... 357 4e-98  
emb|AW731385|AW731385 GA\_Ea0030K22 Gossypium arboreum 7-10 dpa ... 344 2e-95  
emb|AW688234|AW688234 NF005A05ST1F1000 Developing stem Medicago ... 348 6e-95  
gb|BE036418|BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... 279 1e-94  
gb|BE052354|BE052354 GA\_Ea0034P16f Gossypium arboreum 7-10 dpa ... 346 3e-94  
40 emb|AW423801|AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone... 339 4e-92  
emb|AI813214|AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... 336 4e-92  
emb|AW692700|AW692700 NF054C07ST1F1000 Developing stem Medicago ... 304 7e-87  
emb|AW737130|AW737130 EST338557 tomato flower buds, anthesis, Co... 318 1e-85  
emb|AW727978|AW727978 GA\_Ea0029C18 Gossypium arboreum 7-10 dpa ... 285 3e-80  
45 gb|BE020170|BE020170 sm39e05.y1 Gm-c1028 Glycine max cDNA clone ... 291 1e-77  
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emb|AW926887|AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... 280 3e-74  
emb|AW689358|AW689358 NF018C09ST1F1000 Developing stem Medicago ... 253 3e-73  
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50 emb|AW625020|AW625020 EST313849 tomato radicle, 5 d post-imbibit... 253 4e-66  
gb|BE060782|BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis... 234 1e-60  
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55 emb|AW398821|AW398821 EST309321 L. pennellii trichome, Cornell U... 201 2e-50  
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5 emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 112 2e-39  
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emb|AA840711|AA840711 CAN22 Anther cDNA library of Hot pepper Ca... 101 5e-33  
15 emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 98 1e-32  
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gb|BE058285|BE058285 sn14b01.y1 Gm-c1016 Glycine max cDNA clone ... 138 1e-31  
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gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 84 6e-31  
20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 7e-31  
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emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 84 5e-30  
emb|AW599036|AW599036 gb01c10.y1 Moss EST library PPN Physcomitr... 116 5e-25  
25 emb|AF079881|AF079881 Entodinium caudatum D-3-phosphoglycerate d... 56 1e-24  
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30 emb|AT000607|AT000607 AT000607 Brassica rapa guard cell Brassica... 100 9e-21  
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35 emb|AQ874261|AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st... 84 2e-15  
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45 emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 77 4e-13  
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55 dbj|D49433|D49433 Pumpkin colne HPR2 hydroxypyruvate reductases ... 72 1e-11  
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60 emb|X14609|CSNDHR Cucumis sativus mRNA for NAPH-dependent hydrox... 70 5e-11  
emb|AJ001429|RGDMANDER Rhodotorula graminis mRNA for D-mandelate... 70 6e-11

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 5 emb|AI898454|AI898454 EST267897 tomato ovary, TAMU Lycopersicon ... 69 9e-11

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 (2463 letters)

15 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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	emb AQ841817 AQ841817 T134068 Soybean RFLP probe Glycine max gen...	186	8e-46
	emb X77087 SJ100567 S.cerevisiae (S288C) J0909, J0911, J0914 and...	150	5e-35
	emb Z49369 SCYJL094C S.cerevisiae chromosome X reading frame ORF...	150	5e-35
30	emb AW774205 AW774205 EST333356 KV3 Medicago truncatula cDNA clo...	120	8e-28
	emb AW559356 AW559356 EST314404 DSIR Medicago truncatula cDNA cl...	104	2e-23
	emb AQ361449 AQ361449 mgxb0004G06r CUGI Rice Blast BAC Library P...	59	4e-16
	emb AT000678 AT000678 AT000678 Brassica rapa guard cell Brassica...	79	2e-13
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	emb AW307241 AW307241 sf54e09.y1 Gm-c1009 Glycine max cDNA clone...	48	1e-06
	emb AW334422 AW334422 S34F3 AGS-1 Pneumocystis carinii f. sp. ca...	52	2e-05
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	emb AB028188 AB028188 Penicillium digitatum DNA fragment contain...	35	2.6
	emb Z48093 GVEITS133 G.verna DNA for internal transcribed spacer...	28	3.2
	emb AL353012 SPBC1711 S.pombe chromosome II cosmid c1711.	35	3.6
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	gb BE036176 BE036176 MO20A07 MO Mesembryanthemum crystallinum cD...	35	3.6
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	emb AJ274013 AJ274013 AJ274013 Metarhizium anisopliae ARSEF 2575...	35	3.6
	gb U80041 AFU80041 Avena fatua Af10-protein mRNA, complete cds.	34	5.0
60	emb AI612607 AI612607 TENG0370 T. Cruzi epimastigote normalised ...	34	5.0
	emb X04693 SOPCG Spinach gene for plastocyanin.	34	5.0

emb|AW010989|AW010989 ST15D02 Pine TriplEx shoot tip library Pin... 34 5.0  
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 emb|AZ215593|AZ215593 Sheared DNA-74E9.TR Sheared DNA Trypanosom... 34 6.8  
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 5 gb|M33825|TRBMVAT5A T.brucei MVAT5-like variant surface glycopro... 34 6.8  
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 10 emb|AF183445|CLITSYDK1 Codonopsis lanceolata internal transcribe... 34 6.8  
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 gb|L04971|TRBVSGM Trypanosoma brucei variant surface glycoprotei... 34 6.8  
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 15 emb|AI050199|AI050199 TENU1447 T. cruzi epimastigote normalized ... 34 6.8  
 emb|AW597619|AW597619 sj96f04.y1 Gm-cl023 Glycine max cDNA clone... 34 6.8  
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 gb|N60227|N60227 TgESTzy10g08.r1 TgRH Tachyzoite cDNA Toxoplasma... 33 9.4  
 emb|X68032|MTENOD12 M.truncatula ENOD12 gene. 33 9.4  
 20 emb|AW126974|AW126974 gal6h04.y1 Moss EST library PPU Physcomitr... 33 9.4  
 emb|AA274329|AA274329 TgESTzz24g03.s1 TgME49 invivo Bradyzoite c... 33 9.4  
 gb|BE054344|BE054344 GA\_Ea0035E03f Gossypium arboreum 7-10 dpa ... 33 9.4  
 emb|AA009393|AA009393 TgESTzz08e11.r1 TgME49 Tachyzoite cDNA Tox... 33 9.4  
 emb|Y16262|DCY16262 Daucus carota mRNA for neutral invertase. 33 9.4  
 25 gb|BE035627|BE035627 MO12F02 MO Mesembryanthemum crystallinum cD... 33 9.4  
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30 Query= AC002387.185\_at 13631\_at /id\_source genbank /description  
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 [arabidopsis thaliana] /blast\_score 0 /ec\_number /family /chip nova  
 /gb\_link http://www3.ncbi.nlm.nih.gov/htbin-  
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 35 (2371 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
45	emb Z50099 STTKETMR S.tuberosum mRNA for transketolase.	1372	0.0
	gb L76554 SPITRAN Spinacia oleracea transketolase mRNA, chloropl...	1350	0.0
	emb Y15781 CAY15781 Capsicum annuum mRNA for plastid transketola...	1344	0.0
	emb A52295 A52295 Sequence 1 from Patent EP0723017.	1283	0.0
	emb Z46648 CPTKT7 C.plantagineum tkt7 gene for transketolase.	1063	0.0
50	emb Z46647 CPTKT10 C.plantagineum tkt10 gene for transketolase.	1038	0.0
	emb Z46646 CPTKT3 C.plantagineum tkt3 gene for transketolase.	1014	0.0
	emb AJ249787 CPA249787 Cyanophora paradoxa mRNA for putative tra...	557	0.0
	emb AL033501 CAC41C10 C.albicans cosmid Ca41C10.	253	e-175
	emb AC007872 AC007872 The sequence of an Aspergillus parasiticus...	167	e-158
55	gb H55032 H55032 HHU58a Sorghum bicolor cv. TX430 Sorghum bicolo...	233	e-151
	emb AC005299 AC005299 emericella nidulans chromosome viii cosmid...	166	e-147
	emb AC004395 AC004395 Emericella nidulans Chromosome VIII Cosmid...	166	e-147
	emb AW443928 AW443928 EST308858 tomato mixed elicitor, BTI Lycop...	468	e-131
	emb AW667519 AW667519 GA_Ea0009J09 Gossypium arboreum 7-10 dpa ...	463	e-129
60	emb AI778813 AI778813 EST259692 tomato susceptible, Cornell Lyco...	453	e-126
	emb AW776720 AW776720 EST335785 DSIL Medicago truncatula cDNA cl...	450	e-125



- emb|AW695194|AW695194 NF092E10ST1F1082 Developing stem Medicago ... 370 e-124  
emb|AI774685|AI774685 EST255785 tomato resistant, Cornell Lycopersicon ... 444 e-123  
emb|AW618386|AW618386 EST320372 *L. pennellii* trichome, Cornell U... 434 e-120  
5 gb|BE052708|BE052708 GA\_Ea0031N21f *Gossypium arboreum* 7-10 dpa ... 431 e-119  
emb|AW737315|AW737315 EST338838 tomato flower buds, anthesis, Co... 409 e-113  
emb|AW694020|AW694020 NF071G12ST1F1099 Developing stem Medicago ... 406 e-112  
gb|BE060293|BE060293 HVSMEg0011O04f *Hordeum vulgare* pre-anthesis... 405 e-112  
emb|AW649769|AW649769 EST328223 tomato germinating seedlings, TA... 377 e-111  
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10 emb|AW760220|AW760220 sl59e08.y1 *Gm-c1027* Glycine max cDNA clone... 388 e-106  
emb|AW929526|AW929526 EST338314 tomato flower buds 8 mm to pre-a... 386 e-106  
emb|AW596420|AW596420 sj12c01.y1 *Gm-c1032* Glycine max cDNA clone... 380 e-104  
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15 emb|AW720123|AW720123 LjNEST14e4r *Lotus japonicus* nodule library... 369 e-101  
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20 emb|AW979915|AW979915 EST341564 tomato root deficiency, Cornell ... 349 6e-95  
emb|AI781665|AI781665 EST262544 tomato susceptible, Cornell Lyco... 348 1e-94  
emb|Z26486|PSTKTG *P. stipitis* TKT gene for transketolase. 261 8e-93  
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25 emb|AW691000|AW691000 NF040C09ST1F1000 Developing stem Medicago ... 338 9e-92  
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emb|AW203636|AW203636 sf36e03.y1 *Gm-c1028* Glycine max cDNA clone... 332 6e-90  
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emb|Z71255|SCCHRXVI *S. cerevisiae* chromosome XVI 165536 bp sequen... 225 2e-88  
30 gb|U51033|YSCP9513 *Saccharomyces cerevisiae* chromosome XVI cosmi... 225 2e-88  
emb|Z49219|SC9499X *S. cerevisiae* chromosome XVI cosmid 9499. 225 2e-88  
emb|X73224|SCTKL1 *S. cerevisiae* TKL1 gene for transketolase. 225 2e-88  
emb|AL033385|SPBC2G5 *S. pombe* chromosome II cosmid c2G5. 198 2e-87  
emb|AV388967|AV388967 AV388967 *Chlamydomonas reinhardtii* C9 Chla... 322 8e-87  
35 emb|AV391940|AV391940 AV391940 *Chlamydomonas reinhardtii* C9 Chla... 321 1e-86  
emb|AW587453|AW587453 IPPGHZ0039 Cotton fiber and embryo Lambda ... 276 3e-86  
gb|U65983|KLU65983 *Kluyveromyces lactis* transketolase (TKL1) gen... 211 1e-85  
emb|AW035937|AW035937 EST282796 tomato callus, TAMU Lycopersicon... 316 5e-85  
emb|AW156809|AW156809 se31b02.y1 *Gm-c1015* Glycine max cDNA clone... 315 1e-84  
40 emb|AA660853|AA660853 00748 MtrHE Medicago truncatula cDNA 5' si... 282 1e-83  
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45 emb|AW694632|AW694632 NF078D05ST1F1045 Developing stem Medicago ... 285 4e-82  
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emb|AV388182|AV388182 AV388182 *Chlamydomonas reinhardtii* C9 Chla... 304 2e-81  
emb|AW688641|AW688641 NF009H10ST1F1000 Developing stem Medicago ... 282 8e-80  
emb|AW508848|AW508848 si41b02.y1 *Gm-r1030* Glycine max cDNA clone... 298 9e-80  
50 emb|AW695046|AW695046 NF082H06ST1F1059 Developing stem Medicago ... 297 3e-79  
emb|X78993|SCRACII *S. cerevisiae* genomic DNA 70kb region of the r... 200 3e-79  
emb|X73532|SCTKL2 *S. cerevisiae* gene for transketolase. 200 3e-79  
emb|Z35985|SCYBR116C *S. cerevisiae* chromosome II reading frame OR... 200 3e-79  
emb|AW564318|AW564318 LG1\_290\_F06.b1\_A002 Light Grown 1 (LG1) So... 293 4e-78  
55 emb|AW201472|AW201472 sf03e09.y1 *Gm-c1027* Glycine max cDNA clone... 292 6e-78  
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emb|AW746874|AW746874 WS1\_56\_C06.b1\_A002 Water-stressed 1 (WS1) ... 291 2e-77  
emb|AW776336|AW776336 EST335401 DSIL Medicago truncatula cDNA cl... 290 4e-77  
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60 emb|AV395290|AV395290 AV395290 *Chlamydomonas reinhardtii* C9 Chla... 288 1e-76  
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 emb|AV394221|AV394221 AV394221 Chlamydomonas reinhardtii C9 Chla... 275 4e-73  
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 5 emb|AI162975|AI162975 A028P14U Hybrid aspen plasmid library Popu... 273 1e-72  
 emb|AJ234429|HVU234429 Hordeum vulgare partial mRNA; clone cMWG0... 271 1e-71  
 emb|AW398784|AW398784 EST309284 L. pennellii trichome, Cornell U... 271 2e-71  
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 emb|AA819992|AA819992 L0-171M13R Ice plant Lambda Uni-Zap XR exp... 258 1e-67  
 emb|AW180358|AW180358 MgA0465f MgA Library Mycosphaerella gramin... 144 1e-66  
 emb|AI563214|AI563214 EST00338 watermelon lambda zap library Cit... 249 1e-65  
 20 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 163 7e-65  
 emb|AW696579|AW696579 NF106E10ST1F1082 Developing stem Medicago ... 249 7e-65  
 gb|M63302|YSCTRANSK S.cerevisiae transketolase gene, complete cds. 168 5e-64

25 Query= AL022347.46\_at 13659\_at /id\_source genbank /description  
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 30 http://www.ncgr.org/cgi-bin/ff?al022347  
 (2037 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

Score E  
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40 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 385 e-125  
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 45 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 347 e-109  
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 333 e-108  
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 342 e-107  
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 328 e-106  
 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 334 e-105  
 50 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 329 e-104  
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 205 e-104  
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 326 e-103  
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 330 e-103  
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 55 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 325 e-101  
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 60 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 276 4e-93  
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- emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 275 9e-91  
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5 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 127 2e-88  
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10 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 118 6e-84  
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emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 113 7e-83  
emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 113 1e-82  
emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 122 9e-82  
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20 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 221 3e-72  
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25 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 242 2e-66  
emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 172 3e-65  
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emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 197 5e-64  
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30 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 166 1e-61  
emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 236 6e-61  
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35 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 126 3e-57  
emb|AI967314|AI967314 Ljirnp00-017 Ljirnp Lambda HybriZap two... 138 4e-57  
emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 223 4e-57  
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emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 131 2e-56  
40 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 219 8e-56  
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emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 171 3e-54  
emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 169 7e-54  
emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 169 7e-54  
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50 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 136 1e-51  
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emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 172 7e-51  
emb|AW667985|AW667985 GA\_\_Ea0012C15 Gossypium arboreum 7-10 dpa ... 106 1e-50  
emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 72 2e-50  
55 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 135 2e-50  
emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 108 3e-49  
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60 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 192 1e-47  
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5 gb|U13923|LEU13923 Lycopersicon pimpinellifolium serine/threonin... 107 3e-47  
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10 emb|Z18861|BOSRK RPA B.oleracea encoding S-receptor kinase relate... 118 2e-46  
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15 gb|U59318|LEU59318 Lycopersicon esculentum serine/threonine prot... 105 1e-45  
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25 http://www3.ncbi.nlm.nih.gov/htbin-  
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http://www.ncgr.org/cgi-bin/ff?ac005662  
(966 letters)  
30 Database: plantfungal  
661,018 sequences; 426,114,510 total letters  
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emb|AI781496|AI781496 EST262375 tomato susceptible, Cornell Lyco... 308 4e-83  
45 emb|AI898923|AI898923 EST268366 tomato ovary, TAMU Lycopersicon ... 307 8e-83  
emb|AI894834|AI894834 EST264277 tomato callus, TAMU Lycopersicon... 306 2e-82  
emb|AW033760|AW033760 EST277331 tomato callus, TAMU Lycopersicon... 306 2e-82  
emb|AI490417|AI490417 EST248743 tomato ovary, TAMU Lycopersicon ... 304 7e-82  
emb|AW686492|AW686492 NF042A07NR1F1000 Nodulated root Medicago t... 299 8e-82  
50 emb|AI898538|AI898538 EST267981 tomato ovary, TAMU Lycopersicon ... 303 1e-81  
emb|AI488586|AI488586 EST246925 tomato ovary, TAMU Lycopersicon... 303 2e-81  
emb|AI775239|AI775239 EST256339 tomato resistant, Cornell Lycope... 302 4e-81  
emb|AI771731|AI771731 EST252831 tomato ovary, TAMU Lycopersicon ... 301 5e-81  
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55 emb|AW029697|AW029697 EST272952 tomato callus, TAMU Lycopersicon... 299 2e-80  
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emb|AW223714|AW223714 EST300525 tomato fruit red ripe, TAMU Lyco... 297 9e-80  
emb|AW220845|AW220845 EST297314 tomato fruit mature green, TAMU ... 292 3e-78  
60 emb|AW684608|AW684608 NF018H07NR1F1000 Nodulated root Medicago t... 292 3e-78  
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5	emb AI488011 AI488011 EST246333 tomato ovary, TAMU Lycopersicon ...	286	2e-76
	emb AI771230 AI771230 EST252246 tomato ovary, TAMU Lycopersicon ...	281	4e-75
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	emb AW931636 AW931636 EST357479 tomato fruit mature green, TAMU ...	277	7e-74
10	emb AI898026 AI898026 EST267469 tomato ovary, TAMU Lycopersicon ...	276	2e-73
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	emb AI484072 AI484072 EST249943 tomato ovary, TAMU Lycopersicon ...	267	8e-71
15	emb AI485145 AI485145 EST243449 tomato ovary, TAMU Lycopersicon ...	266	2e-70
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	emb AW038382 AW038382 EST280065 tomato mixed elicitor, BTI Lycop...	264	5e-70
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	emb AW625379 AW625379 EST319202 tomato radicle, 5 d post-imbibit...	242	4e-63
	emb AI485781 AI485781 EST244102 tomato ovary, TAMU Lycopersicon ...	240	1e-62
25	emb AW728861 AW728861 GA_Ea0028O02 Gossypium arboreum 7-10 dpa ...	189	2e-59
	emb AI489435 AI489435 EST247774 tomato ovary, TAMU Lycopersicon ...	224	7e-58
	emb AI485480 AI485480 EST243801 tomato ovary, TAMU Lycopersicon ...	221	5e-57
	emb AW030923 AW030923 EST274230 tomato callus, TAMU Lycopersicon...	219	3e-56
	emb AI771831 AI771831 EST252931 tomato ovary, TAMU Lycopersicon ...	219	3e-56
30	emb AI488694 AI488694 EST247033 tomato ovary, TAMU Lycopersicon ...	216	2e-55
	emb AI897044 AI897044 EST266487 tomato ovary, TAMU Lycopersicon ...	216	2e-55
	emb AW127616 AW127616 M110351 DSLC Medicago truncatula cDNA clon...	207	1e-52
	emb AW221131 AW221131 EST297600 tomato fruit mature green, TAMU ...	203	2e-51
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35	emb AW310620 AW310620 sg22b10.x1 Gm-c1024 Glycine max cDNA clone...	138	4e-49
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	emb AW031053 AW031053 EST274360 tomato callus, TAMU Lycopersicon...	175	6e-43
	emb AI771906 AI771906 EST253006 tomato ovary, TAMU Lycopersicon ...	174	1e-42
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45	emb AI895638 AI895638 EST265081 tomato callus, TAMU Lycopersicon...	164	9e-40
	emb AW441823 AW441823 EST311219 tomato fruit red ripe, TAMU Lyco...	164	9e-40
	emb AW981333 AW981333 EST392486 DSIL Medicago truncatula cDNA cl...	156	3e-37
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	emb AV425590 AV425590 AV425590 Lotus japonicus young plants (two...	148	6e-35
50	emb AW563884 AW563884 LG1_272_D05.b1_A002 Light Grown 1 (LG1) So...	136	3e-31
	emb AI489302 AI489302 EST247641 tomato ovary, TAMU Lycopersicon ...	129	4e-29
	emb AI967559 AI967559 Ljimpest05-409-e8 Ljirnp Lambda HybriZap ...	120	2e-26
	emb AI898395 AI898395 EST267838 tomato ovary, TAMU Lycopersicon ...	115	7e-25
	emb AI782642 AI782642 EST263521 tomato susceptible, Cornell Lyco...	105	7e-22
55	emb AI725304 AI725304 1170 PtIFG2 Pinus taeda cDNA clone 9256r, ...	78	2e-18
	emb AW096566 AW096566 EST289746 tomato mixed elicitor, BTI Lycop...	90	3e-17
	emb AI899609 AI899609 EST269052 tomato susceptible, Cornell Lyco...	90	3e-17
	emb AI899596 AI899596 EST269039 tomato susceptible, Cornell Lyco...	90	3e-17
	emb AW443878 AW443878 EST308808 tomato mixed elicitor, BTI Lycop...	90	3e-17
60	emb AI486045 AI486045 EST244366 tomato ovary, TAMU Lycopersicon ...	90	3e-17
	emb AW222135 AW222135 EST298946 tomato fruit red ripe, TAMU Lyco...	89	4e-17



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 5 emb|Z92685|Z92685 223/4 Norway spruce mRNA Picea abies cDNA clon... 76 5e-13  
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 10 emb|AW443870|AW443870 EST308800 tomato mixed elicitor, BTI Lycop... 41 0.011  
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 gb|U74447|ZAU74447 Zinnia angustifolia internal transcribed spac... 33 0.95  
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 (159 letters)

25 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

30 Searching.....done

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	emb AL116063 CNS01CW7 Botrytis cinerea strain T4 cDNA library un...	29	0.24
	emb AQ940444 AQ940444 Sheared DNA-35C4.TF Sheared DNA Trypanosom...	24	0.40
	emb AQ362000 AQ362000 mgxb0004E15r CUGI Rice Blast BAC Library P...	28	0.62
40	emb AQ945662 AQ945662 Sheared DNA-49E8.TR Sheared DNA Trypanosom...	25	1.5
	emb AW266254 AW266254 L30-2966T3 Ice plant Lambda Uni-Zap XR exp...	27	1.6
	emb AL355929 NCB21J21 Neurospora crassa DNA linkage group II BAC...	27	1.6
	emb AW726145 AW726145 GA_Ea0020M12 Gossypium arboreum 7-10 dpa ...	26	2.2
	emb AW661015 AW661015 832009D11.y1 C. reinhardtii CC-125 nutrien...	23	2.7
	emb AV391625 AV391625 AV391625 Chlamydomonas reinhardtii C9 Chla...	23	2.7
45	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	23	2.7
	emb AL354533 LMFL6294 Leishmania major Friedlin chromosome 21 co...	26	4.1
	gb N98018 N98018 2045C3 czapPFDd2.1, Debopam Chakrabarti Plasmod...	26	4.1
	emb AA519693 AA519693 TgESTzz27f07.r1 TgME49 invivo Bradyzoite c...	26	4.1
	emb AA519224 AA519224 TgESTzz39g08.s1 TgME49 invivo Bradyzoite c...	26	4.1
50	emb AW650822 AW650822 EST329276 tomato germinating seedlings, TA...	26	4.1
	emb AA531994 AA531994 TgESTzz46c10.r1 TgME49 invivo Bradyzoite c...	26	4.1
	emb AA520816 AA520816 TgESTzz64d11.r1 TgME49 invivo Bradyzoite c...	26	4.1
	gb U15615 TCU15615 Trypanosoma cruzi reverse transcriptase-like ...	26	4.1
	emb AQ848398 AQ848398 LMAJFV1_lm61f01.x1 Leishmania major FV1 ra...	26	4.1
55	emb AL136536 SPBC1703 S.pombe chromosome II cosmid c1703.	26	4.1
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	emb Z81402 CAZ81402 C.aeruginosa 28S rRNA gene.	26	4.1
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60	emb Z74775 SCYOL033W S.cerevisiae chromosome XV reading frame OR...	25	5.7
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5 gb|BE054352|BE054352 GA\_Ea0035E11f Gossypium arboreum 7-10 dpa ... 25 5.7  
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10 emb|AI730886|AI730886 BNLGHi8147 Six-day Cotton fiber Gossypium ... 25 5.7  
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15 emb|Z49821|SCPDR10 S.cerevisiae PDR10, MYO2, PDR10, SCD5, MIP1, ... 25 7.8  
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20 emb|AI131048|CAR131048 Cicer arietinum mRNA for protein kinase, ... 25 7.8  
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25 emb|AI068528|AI068528 mgae0002dE03f Magnaporthe grisea Appressor... 25 7.8  
emb|AI068407|AI068407 mgae0002aH09f Magnaporthe grisea Appressor... 25 7.8  
emb|AL109846|SPBC17G9 S.pombe chromosome II cosmid c17G9. 23 9.1  
emb|Z72244|CNIGRITS1 C.nigricans DNA for internal transcribed sp... 21 9.5

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(2508 letters)

Database: plantfungal

40 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E

45 Sequences producing significant alignments: (bits) Value

emb|AF119041|AF119041 Lycopersicon esculentum haplotype Southern... 105 4e-61  
emb|AF119040|AF119040 Lycopersicon esculentum haplotype Northern... 112 1e-59  
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50 emb|AJ002236|LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist... 103 2e-57  
gb|U42444|U42444 Lycopersicon pimpinellifolium leucine rich repe... 122 4e-57  
emb|A57130|A57130 Sequence 1 from Patent WO9531564. 122 4e-57  
gb|U42445|U42445 Lycopersicon pimpinellifolium leucine rich repe... 122 4e-57  
emb|A57133|A57133 Sequence 4 from Patent WO9531564. 122 4e-57  
55 emb|AF053995|AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ... 121 2e-56  
emb|AF053997|AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ... 109 1e-52  
emb|A67432|A67432 Sequence 5 from Patent WO9743429. 109 1e-52  
emb|AF053996|AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr... 101 5e-49  
emb|AF053998|AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ... 127 7e-49  
60 emb|A67434|A67434 Sequence 7 from Patent WO9743429. 127 7e-49  
emb|AF053993|AF053993 Lycopersicon esculentum disease resistance... 127 7e-49

- emb|A67429|A67429 Sequence 2 from Patent WO9743429. 127 7e-49  
 emb|A67428|A67428 Sequence 1 from Patent WO9743429. 127 7e-49  
 emb|AB029327|AB029327 Nicotiana tabacum mRNA for elicitor-induci... 102 3e-48  
 emb|AF053994|AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ... 103 2e-42  
 5 emb|Y12640|LECF4A L.esculentum Cf-4A gene. 100 1e-40  
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 20 emb|AZ044600|AZ044600 Gm\_UMb001\_116\_G01.R UMN Soybean BAC Librar... 106 8e-22  
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 25 emb|X81367|TAAWJL172 T.aestivumn (subclone pAWJL172) AWJL172 gene. 71 9e-21  
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 emb|AW398651|AW398651 EST309151 L. pennellii trichome, Cornell U... 85 2e-20  
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 emb|AF159170|AF159170 Eucalyptus saligna polygalacturonase-inhib... 74 3e-18  
 emb|AF159167|AF159167 Eucalyptus grandis polygalacturonase-inhib... 74 3e-18  
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 40 emb|X81370|TAAWJL236 T.aestivumn (subclone pAWJL236) AWJL236 gene. 78 4e-18  
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 5 emb|AW164782|AW164782 se77g01.y1 Gm-cl023 Glycine max cDNA clone... 85 2e-15  
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters  
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	emb AJ002236 LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist...	103	2e-57	
45	gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe...	122	4e-57	
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50	emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ...	109	1e-52	
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55	emb AF053993 AF053993 Lycopersicon esculentum disease resistance...	127	7e-49	
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	emb A67428 A67428 Sequence 1 from Patent WO9743429.	127	7e-49	
	emb AB029327 AB029327 Nicotiana tabacum mRNA for elicitor-induci...	102	3e-48	
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60	emb Y12640 LECF4A L.esculentum Cf-4A gene.	100	1e-40	
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- emb|A58270|A58270 Sequence 1 from Patent WO9635790. 93 6e-37  
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10 emb|AW306675|AW306675 se53h08.y1 Gm-c1017 Glycine max cDNA clone... 90 6e-23  
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15 emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 85 1e-21  
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20 emb|AW398661|AW398661 EST309161 L. pennellii trichome, Cornell U... 85 2e-20  
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30 emb|AF159171|AF159171 Eucalyptus nitens polygalacturonase-inhibi... 74 3e-18  
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35 emb|Z49063|ADPGIP A.deliciosa pgip mRNA for polygalacturonase in... 74 5e-18  
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45 emb|AW688235|AW688235 NF005A07ST1F1000 Developing stem Medicago ... 89 1e-16  
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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi)  
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 30 Database: plantfungal  
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 45 gb|L08188|RCCHCP Ricinus communis (clone ST330) hexose carrier p... 203 e-163  
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 emb|Z93775|VFZ93775 V.faba mRNA for hexose transporter. 362 e-129  
 emb|X66856|NTMST1 N.tabacum MST1 mRNA. 215 e-129  
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emb|AW455278|AW455278 EST311938 tomato root during/after fruit s... 152 8e-36  
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 25 (1612 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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| emb X70981 SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase.     | 127    | 6e-99 |
| emb Y09423 NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C...    | 136    | 8e-98 |
| emb X71654 SMCYYP71B3 S.melongena CYP71A2 mRNA for hydroxylase.        | 124    | 9e-95 |
| dbj D14990 POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl...    | 124    | 9e-95 |
| 40 emb Y10489 GMC450CP1 G.max mRNA for putative cytochrome P450, cl... | 90     | 1e-84 |
| emb X70982 SMCYPEG3 S.melongena CYP71A3 mRNA for P450 hydroxylase.     | 126    | 3e-74 |
| emb Y09424 NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A...    | 154    | 3e-65 |
| dbj E13663 E13663 cDNA encoding cytochrome P450 which is induced...    | 71     | 9e-63 |
| dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)...    | 71     | 9e-63 |
| 45 emb AF022157 AF022157 Glycine max cytochrome P450 monooxygenase ... | 126    | 3e-61 |
| emb AW053855 AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp...    | 103    | 1e-53 |
| emb Y09920 HT7ECODET Helianthus tuberosus mRNA for 7-ethoxycouma...    | 94     | 1e-50 |
| emb Y10098 HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee...    | 94     | 1e-50 |
| emb AF022459 AF022459 Glycine max cytochrome P450 monooxygenase ...    | 105    | 4e-50 |
| 50 emb AJ238612 CRO238612 Catharanthus roseus mRNA for cytochrome P... | 89     | 2e-49 |
| emb AF029858 AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C...    | 139    | 3e-49 |
| gb U48434 SCU48434 Solanum chacoense cytochrome P450 mRNA, compl...    | 117    | 2e-48 |
| emb AF166332 AF166332 Nicotiana tabacum cytochrome P450 gene, co...    | 114    | 4e-47 |
| emb AW223719 AW223719 EST300530 tomato fruit red ripe, TAMU Lyco...    | 88     | 4e-46 |
| 55 emb Y10490 GMC450CP3 G.max mRNA for putative cytochrome P450, cl... | 104    | 6e-46 |
| emb X71658 SMCYPEG8 S.melongena CYP76A1 mRNA.                          | 88     | 2e-45 |
| emb AF122821 AF122821 Capsicum annuum cytochrome P450 (PepCYP) m...    | 118    | 4e-45 |
| emb Z33875 CYMPCP450 M.piperita gene for cytochrome P-450 oxidase.     | 88     | 7e-45 |
| emb AI897763 AI897763 EST267206 tomato ovary, TAMU Lycopersicon ...    | 84     | 1e-44 |
| 60 emb AW830233 AW830233 sm24f03.y1 Gm-cl028 Glycine max cDNA clone... | 139    | 5e-44 |
| gb U48435 SCU48435 Solanum chacoense putative cytochrome P450 ge...    | 95     | 2e-43 |



- emb|AF029857|AF029857 Sorghum bicolor cytochrome P450 CYP99A1 (C... 127 2e-43  
emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 87 3e-43  
emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 79 8e-43  
emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 105 1e-42  
5 emb|AW034502|AW034502 EST278118 tomato callus, TAMU Lycopersicon... 107 2e-42  
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gb|L24438|THLCYP450A Thlaspi arvense germline cytochrome P450 mR... 94 7e-42  
emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 87 3e-41  
10 emb|AW774664|AW774664 EST333815 KV3 Medicago truncatula cDNA clo... 102 6e-41  
emb|AW234222|AW234222 sE22f08.y1 Gm-c1028 Glycine max cDNA clone... 88 1e-40  
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15 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 82 2e-39  
gb|BE054146|BE054146 GA\_\_Ea0034H12f Gossypium arboreum 7-10 dpa ... 72 3e-39  
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20 emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 91 6e-39  
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25 emb|AW132351|AW132351 se03a02.y1 Gm-c1013 Glycine max cDNA clone... 159 5e-38  
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30 emb|AF014801|AF014801 Eschscholzia californica (S)-N-methylcocla... 75 2e-37  
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emb|AI726383|AI726383 BNLGHi5702 Six-day Cotton fiber Gossypium ... 84 4e-37  
35 emb|AI896171|AI896171 EST265614 tomato callus, TAMU Lycopersicon... 89 7e-37  
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emb|AW832315|AW832315 sm07e11.y1 Gm-c1027 Glycine max cDNA clone... 116 1e-36  
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emb|AW442182|AW442182 EST311578 tomato fruit red ripe, TAMU Lyco... 88 4e-36  
40 emb|AW680602|AW680602 WS1\_6\_C01.b1\_A002 Water-stressed 1 (WS1) S... 102 4e-36  
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45 emb|AW255799|AW255799 ML868 peppermint glandular trichome Mentha... 68 8e-35  
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50 emb|AW728587|AW728587 GA\_\_Ea0017C12 Gossypium arboreum 7-10 dpa ... 82 5e-34  
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55 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 95 2e-33  
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60 emb|AB032833|AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom... 77 4e-33  
emb|AW688786|AW688786 NF011F03ST1F1000 Developing stem Medicago ... 129 4e-33

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emb|AI777331|AI777331 EST263739 tomato seed, TAMU Lycopersicon e... 86 1e-32  
5 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 72 2e-32  
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10 emb|AW255299|AW255299 ML307 peppermint glandular trichome Mentha... 88 2e-32  
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30 emb|AW256802|AW256802 EST304939 KV2 Medicago truncatula cDNA clo... 112 5e-46  
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35 emb|AB013598|AB013598 Verbena hybrida HGT8 mRNA for UDP-glucose:... 104 2e-34  
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emb|AW216808|AW216808 EST295522 tomato callus, TAMU Lycopersicon... 101 3e-32  
40 emb|AW398421|AW398421 EST298268 L. pennellii trichome, Cornell U... 84 6e-32  
emb|AW349414|AW349414 GM210007A20D2R Gm-r1021 Glycine max cDNA 3... 97 1e-31  
emb|AW035896|AW035896 EST282403 tomato callus, TAMU Lycopersicon... 100 1e-31  
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emb|AB013596|AB013596 Perilla frutescens PF3R4 mRNA for UDP-gluc... 93 7e-31  
45 emb|AB013597|AB013597 Perilla frutescens PF3R6 mRNA for UDP-gluc... 93 1e-30  
emb|AI771830|AI771830 EST252930 tomato ovary, TAMU Lycopersicon ... 93 1e-30  
emb|AB027455|AB027455 Petunia x hybrida PH1 mRNA for anthocyanin... 89 6e-30  
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50 emb|X85138|LETW11 L.esculentum twil mRNA. 81 1e-28  
emb|AB033758|AB033758 Citrus unshiu LGTase mRNA for limonoid UDP... 89 2e-28  
emb|X72729|LEERT1B L.esculentum (ERT 1b) ripening-related mRNA. 87 9e-28  
emb|A62529|A62529 Sequence 34 from Patent WO9716559. 96 1e-27  
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55 emb|AQ580287|AQ580287 T135903b shotgun sub-library of BAC clone ... 93 1e-27  
emb|X77460|MECGT4 M.esculenta Crantz CGT4 mRNA for UTP-glucose g... 84 2e-27  
emb|AW621210|AW621210 EST312008 tomato root during/after fruit s... 98 4e-27  
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60 emb|AQ368131|AQ368131 tox0001H06r CUGI Tomato BAC Library Lycop... 84 7e-27  
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- emb|AI488782|AI488782 EST247121 tomato ovary, TAMU Lycopersicon ... 80 1e-26  
emb|AI729108|AI729108 BNLGHi12670 Six-day Cotton fiber Gossypium... 82 1e-26  
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5 emb|X77369|SMGT S.melongena GT mRNA for glycosyltransferase. 97 5e-26  
dbj|E12713|E12713 Solanum melongena cDNA encoding flavonoid-3-gl... 97 5e-26  
emb|AW223197|AW223197 EST300008 tomato fruit red ripe, TAMU Lyco... 79 6e-26  
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10 emb|AF101972|AF101972 Phaseolus lunatus zeatin O-glucosyltransfe... 87 2e-25  
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20 emb|AW221893|AW221893 EST298704 tomato fruit red ripe, TAMU Lyco... 84 2e-24  
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emb|AW625781|AW625781 EST319688 tomato radicle, 5 d post-imbibit... 84 4e-24  
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25 emb|AW034671|AW034671 EST278402 tomato callus, TAMU Lycopersicon... 81 5e-24  
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emb|AW329251|AW329251 N200469e rootphos(-) Medicago truncatula c... 93 2e-23  
emb|AI780684|AI780684 EST261479 tomato susceptible, Cornell Lyco... 79 2e-23  
30 emb|AI486974|AI486974 EST245296 tomato ovary, TAMU Lycopersicon ... 83 3e-23  
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emb|AB009370|AB009370 Vigna mungo UF3GaT mRNA for flavonoid 3-O-... 80 1e-21  
emb|AF000372|AF000372 Vitis vinifera UDP glucose:flavonoid 3-o-g... 85 1e-21  
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emb|X77464|MECGT7 M.esculenta Crantz CGT7 mRNA for UTP-glucose g... 88 1e-21  
45 emb|AB012114|AB012114 Vigna mungo UFGlyT mRNA for UDP-glucose:fl... 73 2e-21  
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- emb|AW781424|AW781424 sl78a07.y1 Gm-c1037 Glycine max cDNA clone... 95 9e-19  
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 5 emb|AB012115|AB012115 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 89 1e-18  
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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi)  
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- dbj|D13991|AAICAD A. cordata mRNA for cinnamyl alcohol dehydroge... 279 e-152  
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 40 emb|X72675|PACINALDA P.abies mRNA for cinnamyl alcohol dehydroge... 240 e-124  
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 45 gb|U63534|FXU63534 Fragaria x ananassa cinnamyl alcohol dehydrog... 251 9e-89  
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 gb|L36823|SSNCAD1A Stylosanthes humilis cinnamyl alcohol dehydro... 226 9e-84  
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 50 emb|X92855|LEMTD L.esculentum exon 1 of MTD gene. 130 6e-77  
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 55 emb|AF207555|AF207555 Brassica rapa cinnamyl alcohol dehydrogena... 155 1e-71  
 emb|AF207554|AF207554 Brassica oleracea cinnamyl alcohol dehydro... 156 1e-71  
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 emb|AI489728|AI489728 EST248067 tomato ovary, TAMU Lycopersicon ... 269 3e-71  
 emb|AW830216|AW830216 sm24b12.y1 Gm-c1028 Glycine max cDNA clone... 264 6e-70  
 60 emb|AW350274|AW350274 GM210007B20B7R Gm-r1021 Glycine max cDNA 3... 262 1e-69  
 gb|U79770|MCU79770 Mesembryanthemum crystallinum cinnamyl-alcho... 255 4e-69



- emb|AW031628|AW031628 EST275082 tomato callus, TAMU Lycopersicon... 182 7e-69  
gb|BE021646|BE021646 sm60f08.y1 Gm-cl028 Glycine max cDNA clone ... 259 4e-68  
gb|BE123932|BE123932 EST394057 DSIL Medicago truncatula cDNA clo... 185 7e-65  
emb|AW560160|AW560160 EST315208 DSIR Medicago truncatula cDNA cl... 169 3e-64  
5 emb|AW684815|AW684815 NF021D07NR1F1000 Nodulated root Medicago t... 230 1e-62  
emb|AI162401|AI162401 A017P09U Hybrid aspen plasmid library Popu... 178 5e-62  
emb|AI900147|AI900147 sc01e08.y1 Gm-cl012 Glycine max cDNA clone... 142 2e-61  
emb|AW101492|AW101492 sd78h08.y1 Gm-cl009 Glycine max cDNA clone... 176 3e-61  
emb|AW568106|AW568106 si68e05.y1 Gm-r1030 Glycine max cDNA clone... 136 3e-59  
10 emb|AF146691|AF146691 Lycopersicon esculentum cultivar Rio Grand... 194 1e-58  
emb|AI443116|AI443116 sa84e07.y1 Gm-cl004 Glycine max cDNA clone... 170 1e-54  
emb|AJ001925|PAAJ1925 Picea abies cad7 gene. 115 1e-53  
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15 emb|AI488134|AI488134 EST246456 tomato ovary, TAMU Lycopersicon ... 210 2e-53  
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20 gb|BE123743|BE123743 NXNV\_153\_E12\_F Nsf Xylem Normal wood Vertic... 187 4e-49  
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emb|X75480|EGCAD E.gunnii CAD gene. 139 3e-46  
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25 emb|AW775567|AW775567 EST334632 DSIL Medicago truncatula cDNA cl... 105 7e-45  
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30 emb|AI729035|AI729035 BNLGHi12406 Six-day Cotton fiber Gossypium... 174 9e-43  
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emb|AW100321|AW100321 sd23a02.y1 Gm-cl012 Glycine max cDNA clone... 130 2e-41  
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35 emb|AV412798|AV412798 AV412798 Lotus japonicus young plants (two... 137 6e-40  
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45 emb|AW648829|AW648829 EST327283 tomato germinating seedlings, TA... 89 3e-37  
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50 emb|AW684143|AW684143 NF012H08NR1F1000 Nodulated root Medicago t... 121 3e-36  
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emb|AV417794|AV417794 AV417794 Lotus japonicus young plants (two... 140 1e-32  
55 emb|AF067082|AF067082 Apium graveolens mannitol dehydrogenase (M... 127 9e-32  
emb|AW234172|AW234172 sf22a12.y1 Gm-cl028 Glycine max cDNA clone... 134 1e-30  
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60 emb|AW625821|AW625821 EST319728 tomato radicle, 5 d post-imbibit... 132 4e-30  
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 emb|AI960981|AI960981 sc93e08.y1 Gm-c1019 Glycine max cDNA clone... 85 4e-29  
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Database: plantfungal  
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	emb AW677327 AW677327 DG1_5_D03.g1_A002 Dark Grown 1 (DG1) Sorgh...	76	1e-13	
	emb AW424028 AW424028 sh59f09.y1 Gm-c1015 Glycine max cDNA clone...	62	1e-12	
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35	emb AW119941 AW119941 sd54h12.y1 Gm-c1016 Glycine max cDNA clone...	47	4e-08	
	emb AW092074 AW092074 EST285350 tomato mixed elicitor, BTI Lycop...	57	4e-08	
	emb AW127599 AW127599 M110330 DSLC Medicago truncatula cDNA clon...	43	5e-07	
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50	emb AW287856 AW287856 N100699e rootphos(-) Medicago truncatula c...	31	1.0	
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 5 emb|AI050216|AI050216 TENU1464 T. cruzi epimastigote normalized ... 31 3.7  
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 emb|AW096641|AW096641 EST289821 tomato mixed elicitor, BTI Lycop... 27 8.9  
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45 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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 60 gb|M77504|POPBS Populus deltoides bark storage protein mRNA, co... 99 3e-30  
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	gb M25340 POPCHIC Populus sp. chitinase mRNA fragment, clone 4.	46	6e-04
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 emb|AB030726|AB030726 Nicotiana tabacum mRNA for DNA (cytosine-5... 34 2.5  
 emb|AW397331|AW397331 sg77e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5  
 10 emb|AI210350|AI210350 i0c03a1.r1 Aspergillus nidulans 24hr asexu... 34 2.5  
 emb|AA786346|AA786346 l3g09a1.f1 Aspergillus nidulans 24hr asexu... 34 2.5  
 emb|AW397063|AW397063 sg66e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5  
 emb|AI327733|AI327733 i0c03a1.f1 Aspergillus nidulans 24hr asexu... 34 2.5  
 emb|AW672119|AW672119 LG1\_357\_F07.b1\_A002 Light Grown 1 (LG1) So... 33 3.4  
 15 emb|AJ270207|ECA270207 Entodinium caudatum partial mRNA fro puta... 33 3.4  
 emb|AW672133|AW672133 LG1\_357\_D07.b1\_A002 Light Grown 1 (LG1) So... 33 3.4  
 emb|AQ847463|AQ847463 LMAJFV1\_lm34c05.y1 Leishmania major FV1 ra... 33 4.7  
 emb|AZ212142|AZ212142 Sheared DNA-70G10.TF Sheared DNA Trypanoso... 32 6.4  
 emb|AI163630|AI163630 A045p06u Hybrid aspen plasmid library Popu... 32 6.4  
 20 emb|AL354532|LMFL1177 Leishmania major Friedlin chromosome 21 co... 30 6.9  
 emb|AJ243516|NCR243516 Neurospora crassa partial nca-3 gene for ... 32 8.8  
 emb|AL116648|CNS01DCG Botrytis cinerea strain T4 cDNA library un... 27 9.3  
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 25 /blast\_score 0 /ec\_number /family /chip nova /gb\_link /ncgi  
 (1236 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

30

Searching.....done

	Score	E
Sequences producing significant alignments:	(bits)	Value
35 gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge...	744	0.0
emb A00741 A00741 A.rusticana synthetic gene (reverse complement...	692	0.0
emb A00740 A00740 A.rusticana synthetic gene for peroxidase.	692	0.0
dbj E01651 E01651 cDNA encoding horseradish peroxidase.	692	0.0
40 gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge...	371	e-133
emb X97349 PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P...	473	e-132
emb X97350 PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P...	469	e-131
dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds.	468	e-131
gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge...	363	e-130
45 emb X97348 PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P...	463	e-129
dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part...	441	e-123
emb X97351 PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P...	383	e-120
dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part...	356	e-112
emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor ...	227	e-107
50 gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple...	229	e-107
emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1)...	229	e-106
gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA...	381	e-105
emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A.	211	e-105
dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i...	296	e-103
55 emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod ...	138	2e-97
emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor ...	142	4e-97
emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B.	231	1e-95
emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C.	226	7e-94
gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA.	210	2e-89
60 emb AJ959837 AJ959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone...	228	6e-89
emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs...	208	9e-88

- emb|AW559660|AW559660 EST314772 DSIR Medicago truncatula cDNA cl... 236 1e-87  
 emb|AW774581|AW774581 EST333732 KV3 Medicago truncatula cDNA clo... 236 7e-87  
 emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 215 2e-86  
 emb|AW981426|AW981426 EST392579 DSIL Medicago truncatula cDNA cl... 236 2e-85  
 5 emb|AB042103|AB042103 Asparagus officinalis AspPOX1 mRNA for per... 209 2e-85  
 emb|AF244923|AF244923 Spinacia oleracea peroxidase prx14 precurs... 205 9e-85  
 emb|AJ250121|PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... 253 1e-83  
 emb|AW775762|AW775762 EST334827 DSIL Medicago truncatula cDNA cl... 236 6e-83  
 emb|Y10466|SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18. 218 3e-82  
 10 emb|AW775425|AW775425 EST334490 DSIL Medicago truncatula cDNA cl... 208 1e-81  
 emb|AW685437|AW685437 NF029D09NR1F1000 Nodulated root Medicago t... 230 9e-80  
 emb|AB024439|AB024439 Scutellaria baicalensis mRNA for peroxidase... 209 2e-79  
 emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 212 3e-79  
 emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 115 6e-78  
 15 emb|AW776273|AW776273 EST335338 DSIL Medicago truncatula cDNA cl... 222 1e-77  
 emb|AW267813|AW267813 EST305941 DSIR Medicago truncatula cDNA cl... 200 1e-76  
 emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 196 5e-76  
 emb|AF049881|AF049881 Linum usitatissimum peroxidase FLXPER4 (PE... 207 7e-76  
 emb|AW256487|AW256487 EST304624 KV2 Medicago truncatula cDNA clo... 200 9e-76  
 20 emb|AW775890|AW775890 EST334955 DSIL Medicago truncatula cDNA cl... 200 3e-74  
 emb|AW257195|AW257195 EST305332 KV2 Medicago truncatula cDNA clo... 214 5e-74  
 gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 86 2e-73  
 gb|U41657|GMU41657 Glycine max seed coat peroxidase isozyme (SPO... 159 3e-73  
 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 197 5e-73  
 25 gb|L36110|SSNPEROXIA Stylosanthes humilis peroxidase mRNA. 199 5e-73  
 gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 204 7e-73  
 emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root Medicago t... 236 9e-73  
 emb|AW278775|AW278775 sf97d02.y1 Gm-cl019 Glycine max cDNA clone... 155 1e-72  
 emb|X71593|LECEV11A L.esculentum CEVI-1 mRNA. 99 2e-72  
 30 gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 100 2e-72  
 emb|AW559945|AW559945 EST314993 DSIR Medicago truncatula cDNA cl... 233 2e-72  
 emb|AW980744|AW980744 EST391897 GVN Medicago truncatula cDNA clo... 235 5e-70  
 emb|Y10467|SOPR XR6 S.oleracea mRNA for peroxidase, clone PC23. 105 1e-69  
 dbj|D83225|POPP02 Populus nigra peroxidase gene, complete cds. 196 2e-69  
 35 gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 205 6e-69  
 emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 211 1e-68  
 gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68  
 emb|AW574244|AW574244 EST316835 GVN Medicago truncatula cDNA clo... 202 1e-67  
 emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 98 3e-67  
 40 emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root Medicago t... 236 5e-67  
 emb|AW561032|AW561032 EST316080 DSIR Medicago truncatula cDNA cl... 203 7e-67  
 emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66  
 emb|AW185769|AW185769 se59d08.y1 Gm-cl019 Glycine max cDNA clone... 219 4e-65  
 emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 96 2e-64  
 45 gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64  
 emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidase... 205 7e-64  
 gb|M91374|CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 76 2e-63  
 gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 167 2e-63  
 gb|M91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 134 2e-63  
 50 emb|AF043235|AF043235 Striga asiatica ferriprotein porphyrin-con... 199 3e-63  
 emb|AW288002|AW288002 N100846e rootphos(-) Medicago truncatula c... 182 7e-63  
 emb|AW126121|AW126121 N100318e rootphos(-) Medicago truncatula c... 216 1e-62  
 gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62  
 emb|AW687443|AW687443 NF009F07RT1F1062 Developing root Medicago ... 235 1e-61  
 55 emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem Medicago ... 236 3e-61  
 emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidase... 163 3e-61  
 emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 133 5e-61  
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 emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root Medicago t... 222 8e-61  
 60 dbj|D38050|POPP1 Aspen prx3a gene for peroxidase, complete cds. 121 9e-61  
 emb|AW704659|AW704659 sk54h10.y1 Gm-cl019 Glycine max cDNA clone... 149 9e-61

emb|Y10464|SOPR XR3 *S.oleracea* mRNA for peroxidase, clone PC42. 80 3e-60  
emb|AW705730|AW705730 sk51b02.y1 *Gm-c1019* Glycine max cDNA clone... 149 8e-60  
gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60  
gb|U12314|CCU12314 *Cenchrus ciliaris* clone PX7 peroxidase mRNA, ... 105 9e-60  
5 emb|AI938533|AI938533 sb46h09.y1 *Gm-c1015* Glycine max cDNA clone... 145 1e-59  
emb|AW705617|AW705617 sk50d03.y1 *Gm-c1019* Glycine max cDNA clone... 149 2e-59  
emb|AI781859|AI781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59  
emb|AF149278|AF149278 *Phaseolus vulgaris* peroxidase 3 precursor ... 90 3e-59  
gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59  
10 emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59  
emb|AF244921|AF244921 *Spinacia oleracea* peroxidase prx12 precurs... 156 8e-59  
gb|M32742|CUSCUPER *C.sativus* peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58  
emb|AW705946|AW705946 sk52h07.y1 *Gm-c1019* Glycine max cDNA clone... 224 6e-58

15 Query= X68592.6\_at 15978\_at /id\_source genbank /description  
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[arabidopsis thaliana] /blast\_score 0 /ec\_number /family translocase  
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20 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)  
<http://www.ncgr.org/cgi-bin/ff?x68592>  
(1530 letters)

25 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

Searching.....done

30 Score E  
Sequences producing significant alignments: (bits) Value

emb|AF006489|AF006489 *Gossypium hirsutum* adenine nucleotide tran... 325 0.0  
emb|X62123|STANTG *S.tuberosum* ant gene for ADP/ATP translocator. 328 0.0  
35 gb|U89839|LEU89839 *Lycopersicon esculentum* ADP/ATP translocator ... 327 0.0  
emb|X57557|STANT1 *S.tuberosum* PANT1 mRNA for adenine nucleotide ... 635 0.0  
emb|AJ003197|LAAJ3197 *Lupinus albus* mRNA for adenine nucleotide ... 331 e-175  
emb|X80023|TTADPATP *T.turgidum* mRNA for ADP/ATP carrier. 322 e-172  
emb|X65194|CRANT *C.reinhardtii* mRNA CRANT for mitochondrial ADP/... 348 e-149  
40 emb|AL023634|SPBC530 *S.pombe* chromosome II cosmid c530. 265 e-139  
emb|Z49974|SPANC1GN *S.pombe* ANC1 gene for adenine nucleotide car... 265 e-139  
emb|AF085429|AF085429 *Candida parapsilosis* ADP/ATP carrier prote... 311 e-134  
dbj|D89102|D89102 *Schizosaccharomyces pombe* mRNA, partial cds, c... 265 e-133  
gb|L33797|YSKAAC *Kluyveromyces lactis* ADP/ATP translocase (AAC) ... 259 e-132  
45 emb|AF237675|AF237675 *Yarrowia lipolytica* ADP/ATP carrier protei... 247 e-132  
emb|AJ277099|CUT277099 *Candida utilis* anc gene for mitochondrial... 253 e-131  
emb|AJ277098|CUT277098 *Candida utilis* anc gene for mitochondrial... 253 e-131  
gb|M34075|YSCAAC3 *S.cerevisiae* ADP/ATP-translocator protein (AAC... 252 e-129  
emb|X77291|SCIILDNA *S.cerevisiae* YBL0421, YBL0438, YBL0418, YBL0... 252 e-129  
50 emb|Z35791|SCYBL030C *S.cerevisiae* chromosome II reading frame OR... 252 e-129  
emb|X74427|SCADNUCA *S.cerevisiae* gene for adenine nucleotide car... 252 e-129  
gb|J04021|YSCAAC2 *S.cerevisiae* ADP/ATP carrier protein (AAC2) ge... 252 e-129  
emb|X00363|NCADPATP *Neurospora crassa* mRNA for mitochondrial ADP... 280 e-126  
emb|Z49703|SC9796 *S.cerevisiae* chromosome XIII cosmid 9796. 248 e-125  
55 gb|M12514|YSCPET9 *S.cerevisiae* ADP/ATP translocator protein (AAC... 248 e-125  
emb|Z35954|SCYBR085W *S.cerevisiae* chromosome II reading frame OR... 247 e-125  
gb|M34076|YSCAAC2A *S.cerevisiae* ADP/ATP-translocator protein (AA... 247 e-125  
emb|AW774326|AW774326 EST333477 *Medicago truncatula* cDNA clo... 288 e-124  
emb|AL111975|CNS019QN *Botrytis cinerea* strain T4 cDNA library un... 254 e-122  
60 emb|AW647699|AW647699 EST307178 tomato germinating seedlings, TA... 299 e-120



- emb|AW349848|AW349848 GM210006A11G9R Gm-r1021 Glycine max cDNA 3... 326 e-118
- emb|AW624842|AW624842 EST313671 tomato radicle, 5 d post-imbibit... 229 e-116
- emb|X95863|TTANT1 *T.turgidum* ant gene (1549bp). 195 e-114
- 5 emb|AW041186|AW041186 EST284050 tomato mixed elicitor, BTI Lycop... 239 e-114
- emb|X95864|TTANT2 *T.turgidum* ant gene (1494bp). 191 e-112
- emb|AW706324|AW706324 sj54h05.y1 Gm-c1033 Glycine max cDNA clone... 245 e-110
- emb|AL157416|LMFL6066 *Leishmania major* Friedlin chromosome 19 co... 233 e-108
- emb|AW160172|AW160172 EST290029 *L. pennellii* trichome, Cornell U... 328 e-108
- 10 emb|AW928728|AW928728 EST337516 tomato flower buds 8 mm to pre-a... 247 e-107
- emb|AW218544|AW218544 EST303727 tomato radicle, 5 d post-imbibit... 325 e-105
- emb|AW830381|AW830381 sm26a12.y1 Gm-c1028 Glycine max cDNA clone... 268 e-105
- emb|AW201674|AW201674 sf05h11.y1 Gm-c1027 Glycine max cDNA clone... 309 e-104
- emb|AI812944|AI812944 22G12 Pine Lambda Zap Xylem library Pinus ... 251 e-103
- 15 emb|AI777865|AI777865 EST258744 tomato susceptible, Cornell Lyco... 284 e-102
- emb|AW234033|AW234033 sf33d01.y1 Gm-c1028 Glycine max cDNA clone... 237 e-101
- emb|AW831587|AW831587 sm28b02.y1 Gm-c1028 Glycine max cDNA clone... 300 e-101
- emb|AW668198|AW668198 GA\_Ea0013C13 *Gossypium arboreum* 7-10 dpa ... 331 e-100
- emb|AF049130|AF049130 *Trypanosoma brucei brucei* ADP/ATP carrier ... 238 1e-98
- 20 emb|AI898886|AI898886 EST268329 tomato ovary, TAMU Lycopersicon... 213 2e-98
- gb|U32987|TBU32987 *Trypanosoma brucei rhodesiense* ADP/ATP carrie... 238 3e-98
- emb|AW223982|AW223982 EST300793 tomato fruit red ripe, TAMU Lyco... 327 1e-96
- emb|AW624951|AW624951 EST313780 tomato radicle, 5 d post-imbibit... 327 1e-96
- emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 328 2e-96
- 25 emb|AW441243|AW441243 EST310639 tomato fruit red ripe, TAMU Lyco... 324 1e-95
- emb|AW223973|AW223973 EST300784 tomato fruit red ripe, TAMU Lyco... 321 7e-95
- emb|AW931569|AW931569 EST357412 tomato fruit mature green, TAMU ... 328 2e-94
- emb|AW218871|AW218871 EST301353 tomato root during/after fruit s... 327 8e-94
- 30 emb|AL116444|CNS01D6S *Botrytis cinerea* strain T4 cDNA library un... 267 4e-93
- emb|AW831561|AW831561 sm34f06.y1 Gm-c1028 Glycine max cDNA clone... 312 2e-92
- emb|AI484151|AI484151 EST248958 tomato resistant, Cornell Lycope... 264 3e-91
- emb|AW925414|AW925414 HVSMEg0001L02 *Hordeum vulgare* pre-anthesis... 299 6e-91
- emb|AI731594|AI731594 BNLGHi10182 Six-day Cotton fiber *Gossypium*... 335 7e-91
- 35 emb|AW730597|AW730597 GA\_Ea0027H02 *Gossypium arboreum* 7-10 dpa ... 333 1e-90
- emb|AW647665|AW647665 EST307143 tomato germinating seedlings, TA... 317 1e-90
- emb|AW395111|AW395111 sh40a06.y1 Gm-c1017 Glycine max cDNA clone... 303 6e-90
- emb|AI725588|AI725588 BNLGHi12376 Six-day Cotton fiber *Gossypium*... 288 1e-89
- emb|AW934656|AW934656 EST353548 tomato flower buds 0-3 mm, Corne... 328 2e-89
- 40 emb|AW757478|AW757478 874001D11.y1 *C. reinhardtii* CC-1690, Lambd... 202 3e-89
- emb|AW725897|AW725897 GA\_Ea0020B06 *Gossypium arboreum* 7-10 dpa ... 328 8e-89
- emb|AW647757|AW647757 EST326211 tomato germinating seedlings, TA... 301 1e-88
- emb|AW509174|AW509174 sh92b04.y1 Gm-c1016 Glycine max cDNA clone... 297 4e-88
- emb|AW666654|AW666654 GA\_Ea0005E11 *Gossypium arboreum* 7-10 dpa ... 279 7e-88
- 45 emb|AL114553|CNS01BQ9 *Botrytis cinerea* strain T4 cDNA library un... 231 3e-87
- gb|BE021489|BE021489 sm59b05.y1 Gm-c1028 Glycine max cDNA clone ... 322 5e-87
- emb|AW507801|AW507801 si45c02.y1 Gm-r1030 Glycine max cDNA clone... 259 2e-86
- emb|AW733916|AW733916 sk85a11.y1 Gm-c1035 Glycine max cDNA clone... 306 2e-86
- emb|AW096468|AW096468 EST289648 tomato mixed elicitor, BTI Lycop... 292 6e-86
- 50 emb|AW156741|AW156741 se30b08.y1 Gm-c1015 Glycine max cDNA clone... 184 1e-85
- emb|AI729625|AI729625 BNLGHi13824 Six-day Cotton fiber *Gossypium*... 276 4e-85
- emb|AW034214|AW034214 EST277785 tomato callus, TAMU Lycopersicon... 304 5e-85
- emb|AJ273864|AJ273864 AJ273864 *Metarhizium anisopliae* ARSEF 2575... 184 1e-84
- emb|AI775647|AI775647 EST256747 tomato resistant, Cornell Lycope... 297 1e-84
- 55 emb|AI822682|AI822682 L0-1204T3 Ice plant Lambda Uni-Zap XR expr... 314 2e-84
- emb|AW625107|AW625107 EST313924 tomato radicle, 5 d post-imbibit... 314 2e-84
- emb|AI726147|AI726147 BNLGHi5085 Six-day Cotton fiber *Gossypium* ... 263 6e-83
- emb|AW755396|AW755396 sl03d11.y1 Gm-c1036 Glycine max cDNA clone... 306 3e-82
- emb|AI728088|AI728088 BNLGHi9938 Six-day Cotton fiber *Gossypium* ... 259 5e-82
- 60 emb|AW979992|AW979992 EST310378 tomato root deficiency, Cornell ... 285 8e-82
- emb|AW333018|AW333018 S16C3 AGS-1 *Pneumocystis carinii* f. sp. ca... 278 1e-81



emb|AI780394|AI780394 EST261273 tomato susceptible, Cornell Lyco... 284 2e-81  
 emb|AW691046|AW691046 NF037A12ST1F1000 Developing stem Medicago ... 266 2e-81  
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 emb|AI731287|AI731287 BNLGHi9093 Six-day Cotton fiber Gossypium ... 262 5e-81  
 5 emb|AW760027|AW760027 sl57b04.y1 Gm-c1027 Glycine max cDNA clone... 301 1e-80  
 emb|AW667101|AW667101 GA\_Ea0007F21 Gossypium arboreum 7-10 dpa ... 300 2e-80  
 emb|AW622023|AW622023 EST312821 tomato root during/after fruit s... 280 4e-80  
 emb|AV388663|AV388663 AV388663 Chlamydomonas reinhardtii C9 Chla... 284 8e-80  
 emb|AW650428|AW650428 EST328882 tomato germinating seedlings, TA... 278 4e-79  
 10 emb|AI775628|AI775628 EST256728 tomato resistant, Cornell Lycopersicon... 295 7e-79  
 gb|BE024093|BE024093 sm96f04.y1 Gm-c1015 Glycine max cDNA clone ... 293 2e-78  
 emb|AJ273749|AJ273749 AJ273749 Metarhizium anisopliae ARSEF 2575... 256 1e-77  
 emb|AW737446|AW737446 EST338789 tomato flower buds, anthesis, Co... 290 2e-77

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 thaliana] /blast\_score 1.00e-110 /ec\_number /family transferase /chip  
 nova /gb\_link  
 20 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi)  
<http://www.ncgr.org/cgi-bin/ff?y14251>  
 (630 letters)

25 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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 Score E  
 Sequences producing significant alignments: (bits) Value

emb|X78203|HMGST H.muticus mRNA for glutathione S-transferase. 271 4e-72  
 emb|AW727692|AW727692 GA\_Ea0015I24 Gossypium arboreum 7-10 dpa ... 146 9e-71  
 35 emb|AF002692|AF002692 Solanum commersonii glutathione S-transfer... 264 3e-70  
 dbj|D10524|TOBPARB Nicotiana tabacum mRNA for glutathione S-tran... 262 2e-69  
 emb|AW731360|AW731360 GA\_Ea0030G14 Gossypium arboreum 7-10 dpa ... 142 3e-69  
 dbj|D29680|TOBAP12B Tobacco api2 mRNA (which expression is induc... 261 4e-69  
 emb|AW220064|AW220064 EST302547 tomato root during/after fruit s... 260 5e-69  
 40 emb|Z71749|NPGSTMR N.plumbaginifolia mRNA for glutathione S-tran... 260 8e-69  
 emb|AI774583|AI774583 EST255683 tomato resistant, Cornell Lycopersicon... 258 3e-68  
 emb|AW728413|AW728413 GA\_Ea0016J18 Gossypium arboreum 7-10 dpa ... 142 7e-68  
 emb|AI725552|AI725552 BNLGHi12077 Six-day Cotton fiber Gossypium... 142 4e-67  
 emb|AI728937|AI728937 BNLGHi12090 Six-day Cotton fiber Gossypium... 142 4e-67  
 45 gb|BE033971|BE033971 MG02G09 MG Mesembryanthemum crystallinum cD... 228 2e-65  
 emb|AW735791|AW735791 EST336559 tomato flower buds 0-3 mm, Corne... 248 2e-65  
 emb|AF242309|AF242309 Euphorbia esula glutathione S-transferase ... 130 3e-62  
 emb|AW726844|AW726844 GA\_Ea0022O11 Gossypium arboreum 7-10 dpa ... 140 5e-61  
 emb|AI726215|AI726215 BNLGHi5300 Six-day Cotton fiber Gossypium ... 142 5e-61  
 50 emb|AW218151|AW218151 EST303332 tomato radicle, 5 d post-imbibit... 232 1e-60  
 emb|AW728876|AW728876 GA\_Ea0028P14 Gossypium arboreum 7-10 dpa ... 147 2e-60  
 gb|M84968|SIPGTSTF Silene cucubalus glutathione-S-transferase mR... 115 5e-59  
 emb|AF133894|AF133894 Persea americana glutathione S-transferase... 220 8e-57  
 emb|AI352770|AI352770 MB58-4B PZ204.BNlib Brassica napus cDNA cl... 174 7e-55  
 55 emb|AW040790|AW040790 EST283654 tomato mixed elicitor, BTI Lycopersicon... 210 6e-54  
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 60 emb|AW684286|AW684286 NF015A06NR1F1000 Nodulated root Medicago t... 186 1e-46  
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- gb|BE033640|BE033640 MF05D04 MF Mesembryanthemum crystallinum cD... 185 2e-46  
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gb|C96149|C96149 C96149 Marchantia polymorpha immature sex organ... 145 1e-41  
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15 dbj|D49526|TOBPBARBA Tobacco chimeric parB promoter/beta-glucuron... 163 1e-39  
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20 emb|Y07721|PHGLSTRAN P.hybrida mRNA for glutathione S-transferase. 151 5e-36  
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25 emb|AW926756|AW926756 HVSMeg0008B23 Hordeum vulgare pre-anthesis... 92 3e-35  
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emb|AV427165|AV427165 AV427165 Lotus japonicus young plants (two... 142 3e-33  
emb|AJ010451|AMY010451 Alopecurus myosuroides mRNA for glutathio... 97 4e-33  
emb|AF184059|AF184059 Triticum aestivum glutathione S-transferas... 81 5e-33  
30 emb|AW164336|AW164336 se71b09.y1 Gm-c1023 Glycine max cDNA clone... 139 1e-32  
emb|AJ010454|AMY010454 Alopecurus myosuroides mRNA for glutathio... 95 2e-32  
emb|AJ010452|AMY010452 Alopecurus myosuroides mRNA for glutathio... 94 3e-32  
emb|AW678048|AW678048 WS1\_13\_A09.b1\_A002 Water-stressed 1 (WS1) ... 84 3e-32  
gb|BE021219|BE021219 sm56c09.y1 Gm-c1028 Glycine max cDNA clone ... 99 7e-32  
35 emb|AW561921|AW561921 IPPGHZ0010 Cotton fiber and embryo Lambda ... 137 7e-32  
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40 emb|AI823131|AI823131 L30-1014T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-31  
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emb|AW745644|AW745644 WS1\_36\_D11.b1\_A002 Water-stressed 1 (WS1) ... 84 4e-30  
45 emb|AW279568|AW279568 sf95d06.y1 Gm-c1019 Glycine max cDNA clone... 131 4e-30  
emb|AW054044|AW054044 L30-2014T3 Ice plant Lambda Uni-Zap XR exp... 106 3e-29  
emb|AW202090|AW202090 sf11a03.y1 Gm-c1027 Glycine max cDNA clone... 106 1e-28  
emb|AI440830|AI440830 sa86f05.y1 Gm-c1004 Glycine max cDNA clone... 126 1e-28  
emb|AW678628|AW678628 WS1\_1\_B05.b1\_A002 Water-stressed 1 (WS1) S... 85 2e-28  
50 emb|AW677650|AW677650 WS1\_10\_F04.b1\_A002 Water-stressed 1 (WS1) ... 80 6e-28  
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emb|AW053375|AW053375 L30-1572T3 Ice plant Lambda Uni-Zap XR exp... 99 2e-27  
emb|AV426523|AV426523 AV426523 Lotus japonicus young plants (two... 122 2e-27  
55 emb|AV427075|AV427075 AV427075 Lotus japonicus young plants (two... 122 2e-27  
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emb|AT000441|AT000441 AT000441 Brassica rapa guard cell Brassica... 122 3e-27  
emb|AI442436|AI442436 sa26h04.y1 Gm-c1004 Glycine max cDNA clone... 111 4e-27  
gb|BE034032|BE034032 MG03G03 MG Mesembryanthemum crystallinum cD... 90 6e-26  
60 emb|AW689646|AW689646 NF022G04ST1F1000 Developing stem Medicago ... 66 3e-25  
gb|BE060798|BE060798 HVSMeg0013G13f Hordeum vulgare pre-anthesis... 92 6e-25

gb|BE060847|BE060847 HVSMEg0013J11f Hordeum vulgare pre-anthesis... 64 3e-24  
 emb|AW171715|AW171715 N100609e rootphos(-) Medicago truncatula c... 112 3e-24  
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 emb|AW680604|AW680604 WS1\_6\_C03.b1\_A002 Water-stressed 1 (WS1) S... 84 4e-24  
 5 emb|AI352728|AI352728 MB47-17 PZ204.BNlib Brassica napus cDNA cl... 110 1e-23  
 emb|AW127163|AW127163 M110099 GVN Medicago truncatula cDNA clone... 110 1e-23  
 emb|AW924273|AW924273 WS1\_51\_A04.b1\_A002 Water-stressed 1 (WS1) ... 95 1e-23  
 emb|AW680779|AW680779 WS1\_7\_D01.b1\_A002 Water-stressed 1 (WS1) S... 97 1e-23  
 emb|AI444064|AI444064 sa31g12.y1 Gm-c1004 Glycine max cDNA clone... 109 2e-23  
 10 emb|AW459151|AW459151 sb21c07.y1 Gm-c1016 Glycine max cDNA clone... 66 6e-23

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 (1619 letters)

20 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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	Sequences producing significant alignments:	(bits)	Value
30	emb AJ007574 RCO7574 Ricinus communis mRNA for amino acid carrier.	410	0.0
	emb Y09591 VFAMACTRA V.faba mRNA for amino acid transporter.	392	0.0
	emb AJ132228 RCO132228 Ricinus communis mRNA for amino acid carr...	342	0.0
	emb AF080543 AF080543 Nepenthes alata amino acid transporter (AA...	641	0.0
	emb Y09826 STAAP2 S.tuberosum mRNA for amino acid transporter AA...	354	0.0
	emb AF080544 AF080544 Nepenthes alata amino acid transporter (AA...	596	0.0
35	emb Y09825 STAAP1 S.tuberosum mRNA for amino acid transporter AA...	288	e-158
	emb Z68759 RCAACMR R.communis mRNA for amino acid carrier.	334	e-155
	emb AF080542 AF080542 Nepenthes alata amino acid transporter (AA...	239	e-145
	emb AF061435 AF061435 Vicia faba amino acid transporter b (AAPB)...	501	e-141
	emb Y11121 RCAACARR Ricinus communis mRNA for amino acid carrier...	264	e-123
40	emb AF061434 AF061434 Vicia faba amino acid transporter a (AAPA)...	290	e-107
	emb AF061436 AF061436 Vicia faba amino acid transporter c (AAPC)...	259	5e-95
	emb AW560155 AW560155 EST315203 DSIR Medicago truncatula cDNA cl...	293	4e-86
	emb AW203255 AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone...	312	4e-84
	emb AI166826 AI166826 xylem.est.62 Poplar xylem Lambda ZAPII lib...	188	2e-68
45	emb AW648039 AW648039 EST326493 tomato germinating seedlings, TA...	226	2e-67
	emb AI974813 AI974813 T113295e KV2 Medicago truncatula cDNA clon...	153	2e-66
	emb AW926173 AW926173 HVSMEg0006I08 Hordeum vulgare pre-anthesis...	243	3e-66
	emb AW648857 AW648857 EST327311 tomato germinating seedlings, TA...	219	3e-65
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50	emb AW277711 AW277711 sf85f01.y1 Gm-c1019 Glycine max cDNA clone...	242	5e-63
	emb AW774110 AW774110 EST333340 KV3 Medicago truncatula cDNA clo...	238	7e-62
	emb AW720246 AW720246 LjNEST17f12r Lotus japonicus nodule librar...	235	6e-61
	emb AI930612 AI930612 sb37c02.y1 Gm-c1013 Glycine max cDNA clone...	167	5e-60
	emb AW399595 AW399595 EST310095 L. pennellii trichome, Cornell U...	192	8e-58
55	emb AW737124 AW737124 EST338551 tomato flower buds, anthesis, Co...	217	2e-55
	emb AW691461 AW691461 NF045C01ST1F1000 Developing stem Medicago ...	206	7e-55
	emb AW432416 AW432416 sh73f10.y1 Gm-c1015 Glycine max cDNA clone...	89	8e-51
	emb AW255060 AW255060 ML1355 peppermint glandular trichome Menth...	111	1e-50
	emb AW685782 AW685782 NF035B03NR1F1000 Nodulated root Medicago t...	201	1e-50
60	gb BE125804 BE125804 DG1_57_F07.b1_A002 Dark Grown 1 (DG1) Sorgh...	178	3e-50
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- emb|AW349599|AW349599 GM210005A21G12R Gm-r1021 Glycine max cDNA ... 140 5e-49
- emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 122 2e-48
- emb|AW737784|AW737784 EST339211 tomato flower buds, anthesis, Co... 192 6e-48
- 5 emb|AW309945|AW309945 s27a03.x1 Gm-c1028 Glycine max cDNA clone... 149 5e-47
- emb|AW738557|AW738557 EST339984 tomato flower buds, anthesis, Co... 188 8e-47
- emb|AQ842052|AQ842052 T134338 Soybean RFLP probe Glycine max gen... 148 2e-44
- emb|AF074703|AF074703 Glycine max pA381 marker, sequence tagged ... 149 1e-43
- emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 127 3e-43
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- emb|AW597381|AW597381 si92b03.y1 Gm-c1031 Glycine max cDNA clone... 175 1e-42
- emb|AW310916|AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone... 172 5e-42
- emb|AW306512|AW306512 se51h04.y1 Gm-c1017 Glycine max cDNA clone... 140 1e-41
- emb|AW395873|AW395873 sh01d01.y1 Gm-c1026 Glycine max cDNA clone... 112 4e-41
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- emb|AW684816|AW684816 NF021D09NR1F1000 Nodulated root Medicago t... 164 2e-39
- emb|AZ051221|AZ051221 Gm\_UMb001\_166\_P11R UMN Soybean BAC Library... 159 7e-38
- emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 155 1e-36
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- 20 emb|AW830977|AW830977 sm31a10.y1 Gm-c1028 Glycine max cDNA clone... 149 4e-35
- emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 147 3e-34
- emb|AJ004829|STAJ4829 Solanum tuberosum fdh3 pseudogene. 110 3e-33
- emb|AQ841805|AQ841805 T134055 Soybean RFLP probe Glycine max gen... 140 2e-32
- emb|AW736648|AW736648 EST333140 KV3 Medicago truncatula cDNA clo... 138 1e-31
- 25 emb|AV418629|AV418629 AV418629 Lotus japonicus young plants (two... 130 3e-29
- emb|AW442349|AW442349 EST311745 tomato fruit red ripe, TAMU Lyco... 130 3e-29
- emb|AW738564|AW738564 EST339991 tomato flower buds, anthesis, Co... 104 7e-29
- emb|AW561095|AW561095 EST316143 DSIR Medicago truncatula cDNA cl... 126 6e-28
- emb|AW234791|AW234791 sf19c06.y1 Gm-c1028 Glycine max cDNA clone... 124 2e-27
- 30 gb|U31932|NSU31932 Nicotiana sylvestris amino acid permease 1 (N... 61 3e-27
- emb|AI441371|AI441371 sa64f02.y1 Gm-c1004 Glycine max cDNA clone... 72 2e-26
- emb|AW438003|AW438003 ST83D04 Pine TriplEx shoot tip library Pin... 111 2e-23
- emb|AW056573|AW056573 ST52G03 Pine TriplEx shoot tip library Pin... 109 8e-23
- emb|AW923686|AW923686 DG1\_57\_F07.g1\_A002 Dark Grown 1 (DG1) Sorg... 107 3e-22
- 35 emb|AW924285|AW924285 WS1\_52\_F10.b1\_A002 Water-stressed 1 (WS1) ... 106 5e-22
- emb|AJ238635|CPR238635 Chlorella protothecoides partial mRNA for... 75 4e-20
- emb|AW102174|AW102174 sd84c08.y1 Gm-c1009 Glycine max cDNA clone... 100 6e-20
- emb|AW102244|AW102244 sd85c02.y1 Gm-c1009 Glycine max cDNA clone... 92 1e-17
- emb|AW620352|AW620352 sj04b02.y1 Gm-c1032 Glycine max cDNA clone... 92 1e-17
- 40 emb|AW288077|AW288077 N100921e rootphos(-) Medicago truncatula c... 84 2e-15
- emb|AW396191|AW396191 sh02e09.y1 Gm-c1026 Glycine max cDNA clone... 57 2e-14
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- emb|AF014810|AF014810 Lycopersicon esculentum proline transporte... 54 9e-12
- 45 emb|AI728355|AI728355 BNLGHi10544 Six-day Cotton fiber Gossypium... 70 4e-11
- emb|AW780460|AW780460 sl71b05.y1 Gm-c1027 Glycine max cDNA clone... 70 6e-11
- emb|AF014808|AF014808 Lycopersicon esculentum proline transporte... 55 5e-09
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- 50 emb|AW563318|AW563318 LG1\_228\_A07.g1\_A002 Light Grown 1 (LG1) So... 48 2e-07
- gb|U64823|NSU64823 Nicotiana sylvestris amino acid permease (nsa... 37 2e-06
- emb|AI489487|AI489487 EST247826 tomato ovary, TAMU Lycopersicon ... 52 1e-05
- emb|AV417239|AV417239 AV417239 Lotus japonicus young plants (two... 52 1e-05
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- 55 gb|BE023644|BE023644 sm83e05.y1 Gm-c1015 Glycine max cDNA clone ... 51 2e-05
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- 60 emb|AV409658|AV409658 AV409658 Lotus japonicus young plants (two... 47 4e-04
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30	emb X12739 NTPRRMAJ N. tabacum mRNA for pathogenesis-related pro...	201	4e-99
	emb AF003007 AF003007 Vitis vinifera thaumatin-like protein VVTL...	214	7e-98
	emb X15223 NTE2TLP Tobacco E2 gene for a thaumatin-like protein.	195	2e-97
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	emb AW684755 AW684755 NF021G01NR1F1000 Nodulated root Medicago t...	348	3e-95
35	emb AV428977 AV428977 AV428977 Lotus japonicus young plants (two...	343	7e-94
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	emb AF199508 AF199508 Fragaria x ananassa osmotin-like protein (...)	220	1e-89
	emb X72928 SC13OLP S.commersonii (pOSML13) gene for osmotin-like...	200	1e-88
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45	emb X95308 NTOSPR N.tabacum osmotin gene.	195	8e-87
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20 emb|AI895910|AI895910 EST265353 tomato callus, TAMU Lycopersicon... 177 3e-80  
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Database: plantfungal  
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	emb AB010434 AB010434	Brassica rapa PEC-2 mRNA for Thioredoxin, ...	192 9e-49
	emb AW255457 AW255457	ML480 peppermint glandular trichome Mentha...	190 3e-48
20	emb AW569018 AW569018	si74e02.y1 Gm-c1031 Glycine max cDNA clone...	185 1e-46
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	emb AW924685 AW924685	WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ...	181 2e-45
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	emb AW671668 AW671668	LG1_349_G02.b1_A002 Light Grown 1 (LG1) So...	181 2e-45
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 (1896 letters)

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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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 Sequences producing significant alignments: (bits) Value

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25 emb|AI166806|AI166806 xylem.est.601 Poplar xylem Lambda ZAPII li... 84 9e-20  
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emb|AW038769|AW038769 EST280630 tomato mixed elicitor, BTI Lycop... 56 9e-07  
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Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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	emb AB024006 AB024006 Hordeum vulgare naat-B and naat-A genes fo...	184	3e-78
15	emb AW760137 AW760137 sl58e07.y1 Gm-c1027 Glycine max cDNA clone...	270	1e-72
	emb AW508844 AW508844 si41a10.y1 Gm-r1030 Glycine max cDNA clone...	191	7e-61
	emb AW348839 AW348839 GM210003B11G12R Gm-r1021 Glycine max cDNA ...	233	2e-60
	emb AW832427 AW832427 sm10c03.y1 Gm-c1027 Glycine max cDNA clone...	233	3e-60
20	emb AW760284 AW760284 sl48d01.y1 Gm-c1027 Glycine max cDNA clone...	206	6e-55
	emb AW620771 AW620771 sj09d03.y1 Gm-c1032 Glycine max cDNA clone...	209	5e-53
	emb AW568831 AW568831 si61g09.y1 Gm-r1030 Glycine max cDNA clone...	199	5e-50
	emb AW030722 AW030722 EST273977 tomato callus, TAMU Lycopersicon...	198	9e-50
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25	emb AW459166 AW459166 sh21e03.y1 Gm-c1016 Glycine max cDNA clone...	170	3e-41
	emb AW030650 AW030650 EST273905 tomato callus, TAMU Lycopersicon...	96	4e-38
	emb AW202348 AW202348 sf14a04.y1 Gm-c1027 Glycine max cDNA clone...	96	1e-33
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	gb BE020273 BE020273 sm42g02.y1 Gm-c1028 Glycine max cDNA clone ...	91	3e-31
30	gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine aminotransf...	97	1e-26
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Database: plantfungal  
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	emb AI777064 AI777064	EST252031	tomato callus, TAMU Lycopersicon... 261 3e-69
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5 emb|AW928514|AW928514 EST337302 tomato flower buds 8 mm to pre-a... 95 5e-41  
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this gene. [arabidopsis thaliana]" /blast\_score 0 /ec\_number /family  
50 kinase /chip nova /gb\_link  
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000132|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000132|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000132|/ncgi)  
<http://www.ncgr.org/cgi-bin/ff?ac000132>  
(2766 letters)

55 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

60 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like...	333	2e-91
	emb AW036763 AW036763 EST252152 tomato ovary, TAMU Lycopersicon ...	175	3e-77
5	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon ...	173	3e-76
	gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe...	198	1e-70
	emb A57130 A57130 Sequence 1 from Patent WO9531564.	198	1e-70
	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	198	1e-70
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	198	1e-70
10	emb AF053998 AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ...	194	3e-68
	emb A67434 A67434 Sequence 7 from Patent WO9743429.	194	3e-68
	gb U77888 INU77888 Ipomoea nil receptor-like protein kinase (inr...	174	2e-66
	emb AF053995 AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ...	195	1e-65
	emb AF053993 AF053993 Lycopersicon esculentum disease resistance...	198	2e-65
15	emb A67429 A67429 Sequence 2 from Patent WO9743429.	198	2e-65
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	198	2e-65
	emb AI485090 AI485090 EST243394 tomato ovary, TAMU Lycopersicon ...	177	9e-64
	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	180	8e-62
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20	emb AF053994 AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ...	180	1e-61
	emb AI486438 AI486438 EST244759 tomato ovary, TAMU Lycopersicon ...	230	1e-61
	emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ...	183	1e-61
	emb A67432 A67432 Sequence 5 from Patent WO9743429.	183	1e-61
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25	emb AF197947 AF197947 Glycine max receptor protein kinase-like p...	144	2e-59
	emb AI771841 AI771841 EST252941 tomato ovary, TAMU Lycopersicon ...	177	6e-57
	emb AW726024 AW726024 GA_Ea0020G24 Gossypium arboreum 7-10 dpa ...	193	2e-55
	emb AI485862 AI485862 EST244183 tomato ovary, TAMU Lycopersicon ...	177	3e-54
	emb AW224642 AW224642 EST303085 tomato root, plants pre-anthesis...	123	6e-54
30	emb AI495469 AI495469 sa98d06.y1 Gm-c1004 Glycine max cDNA clone...	209	1e-52
	emb AF197946 AF197946 Glycine max receptor protein kinase-like p...	146	2e-52
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	emb AI442177 AI442177 sa58c02.y1 Gm-c1004 Glycine max cDNA clone...	158	3e-45
	emb AW727470 AW727470 GA_Ea0012H16 Gossypium arboreum 7-10 dpa ...	86	5e-41
35	emb AW979740 AW979740 EST341365 tomato root deficiency, Cornell ...	151	2e-39
	emb AW010219 AW010219 ST03E03 Pine TriplEx shoot tip library Pin...	164	2e-39
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	emb Z73295 CRPK1 C.roseus mRNA for receptor-like protein kinase.	125	2e-32
	emb AW618736 AW618736 EST320722 L. pennellii trichome, Cornell U...	141	2e-32
50	emb AA557073 AA557073 915 Loblolly pine N Pinus taeda cDNA clone...	85	6e-32
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	emb AI495862 AI495862 sb17b07.y1 Gm-c1004 Glycine max cDNA clone...	138	2e-31
	emb AW156187 AW156187 se20f08.y1 Gm-c1015 Glycine max cDNA clone...	137	5e-31
	emb AI967314 AI967314 Ljirmp00-017 Ljirmp Lambda HybriZap two...	88	9e-31
55	emb AW034426 AW034426 EST277997 tomato callus, TAMU Lycopersicon...	119	1e-30
	emb AW224303 AW224303 EST301030 tomato fruit red ripe, TAMU Lyco...	128	1e-30
	emb AW035394 AW035394 EST281132 tomato callus, TAMU Lycopersicon...	136	1e-30
	emb AW930866 AW930866 EST356709 tomato fruit mature green, TAMU ...	84	1e-30
	emb AW932515 AW932515 EST358358 tomato fruit mature green, TAMU ...	78	1e-30
60	emb AI166936 AI166936 xylem.est.719 Poplar xylem Lambda ZAPII li...	85	1e-30
	emb AV419736 AV419736 AV419736 Lotus japonicus young plants (two...	135	1e-30



- gb|BE054944|BE054944 GA\_Ea0032D07f Gossypium arboreum 7-10 dpa ... 91 2e-30  
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 5 gb|BE060551|BE060551 HVSMEg0012J19f Hordeum vulgare pre-anthesis... 88 1e-29  
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 emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 89 4e-29  
 10 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 129 8e-29  
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 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 85 2e-28  
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 25 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 73 2e-27  
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 35 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 77 5e-27  
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50 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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55 Score E  
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60 gb|U22147|HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1)... 279 e-123  
 emb|AJ133470|HBR133470 Hevea brasiliensis mRNA for beta-1,3-gluc... 276 e-123  
 emb|A26453|A26453 Recombinant soya beta-1,3-glucanase plasmid. 259 e-117  
 emb|A26449|A26449 Soya mutant beta-1,3-glucanase cDNA. 259 e-117



- emb|A26447|A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f... 259 e-117  
 emb|A26451|A26451 Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin... 259 e-117  
 emb|X53129|PV13BDGL P. vulgaris mRNA for 1,3-beta-D-glucanase. 244 e-111  
 emb|X89717|PVB13GLUC P.vulgaris beta-1,3-glucanase gene. 247 e-110  
 5 emb|X07280|NPGLUCB Nicotiana plumbaginifolia mRNA for beta-glucanase... 245 e-108  
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 gb|L02212|PEABETAGLU Pea beta-1,3-glucanase gene, complete cds. 246 e-106  
 gb|S51479|S51479 beta-1,3-glucanase [Pisum sativum=peas, cultiva... 246 e-106  
 10 gb|U27179|MSU27179 Medicago sativa acidic glucanase mRNA, comple... 232 e-104  
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 gb|U01901|U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan... 235 1e-96  
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 gb|M60402|TOBGLA13B Nicotiana tabacum glucan beta-1,3-glucanase ... 240 6e-95  
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 20 emb|AF004838|AF004838 Musa acuminata beta-1,3-glucanase mRNA, pa... 205 8e-95  
 gb|M60403|TOBGLB13B Nicotiana tabacum glucan-beta-1,3-glucosidas... 238 2e-94  
 emb|AF034117|AF034117 Glycine max beta-1,3-glucanase 12 (SGlu12)... 180 3e-94  
 gb|M59442|TOBGLUCA N.tabacum basic-1,3-glucanase gene, complete cds. 236 7e-94  
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 25 gb|M59443|TOBGLUCB N.tabacum acidic beta-1,3-glucanase gene, com... 150 2e-92  
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 30 gb|U49454|PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene... 211 2e-89  
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 emb|AF034106|AF034106 Glycine max beta-1,3-glucanase 1 (SGlu1) g... 221 2e-88  
 emb|AF141654|AF141654 Nicotiana tabacum beta-1,3-glucanase (GGL4... 139 3e-88  
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 35 gb|M20620|TOBGLUBC N.tabacum beta-1,3-glucanase mRNA, clone pGL43. 238 4e-88  
 emb|AF034113|AF034113 Glycine max beta-1,3-glucanase 8 (SGlu8) g... 222 1e-87  
 emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 136 6e-87  
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 40 emb|AJ000081|CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 113 2e-86  
 emb|X81560|NTSP41AGN N.tabacum Sp41a gene. 136 4e-86  
 emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 135 8e-86  
 dbj|E03985|E03985 DNA encoding beta-1,3-endoglucanase. 167 3e-84  
 dbj|E02108|E02108 cDNA sequence coding for beta-1,3-endoglucanase. 167 3e-84  
 45 gb|M37753|SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... 167 3e-84  
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 gb|U41323|GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c... 169 3e-82  
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 50 gb|M80604|TOMB13GLUA Lycopersicon esculentum beta-1,3-glucanase ... 142 5e-82  
 emb|X74905|LEQA L.esculentum TomQ'a mRNA for beta(1,3)glucanase. 128 4e-79  
 emb|AI896001|AI896001 EST265444 tomato callus, TAMU Lycopersicon... 175 9e-79  
 emb|AW034584|AW034584 EST278268 tomato callus, TAMU Lycopersicon... 226 9e-79  
 emb|X54456|NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana... 127 2e-78  
 55 emb|AJ012751|CAR012751 Cicer arietinum mRNA for glucan endo-beta... 126 2e-78  
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 emb|AW031078|AW031078 EST274385 tomato callus, TAMU Lycopersicon... 169 4e-77  
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 5 gb|M63634|TOBGCBREG Nicotiana plumbaginifolia beta(1,3)-glucanas... 250 9e-73  
 emb|AW032644|AW032644 EST276203 tomato callus, TAMU Lycopersicon... 189 1e-71  
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 gb|M20618|TOBGLUBA N.tabacum beta-1,3-glucanase mRNA, clones pGL... 238 3e-71  
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 20 emb|AW032444|AW032444 EST276003 tomato callus, TAMU Lycopersicon... 142 6e-69  
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 emb|AJ011769|CIN011769 Cichorium intybus X Cichorium endivia sub... 97 1e-68  
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 gb|M13237|BLYGLUCB Barley beta glucanase mRNA. 158 7e-68  
 25 emb|Z15131|ASBGLUCAN A.sativa mRNA for beta glucanase. 158 9e-68  
 emb|AI896042|AI896042 EST265485 tomato callus, TAMU Lycopersicon... 237 1e-67  
 gb|M62740|BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan... 158 2e-67  
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 30 emb|AW032451|AW032451 EST276010 tomato callus, TAMU Lycopersicon... 136 3e-67  
 emb|AW031353|AW031353 EST274807 tomato callus, TAMU Lycopersicon... 136 3e-67  
 emb|AI895981|AI895981 EST265424 tomato callus, TAMU Lycopersicon... 136 3e-67  
 gb|U73709|VVU73709 Vitis vinifera beta-1,3-glucanase mRNA, parti... 244 3e-67  
 emb|Z22874|TABETGLUB T.aestivum (1,3;1,4) beta glucanase mRNA, c... 160 3e-67  
 35 emb|AF034114|AF034114 Glycine max beta-1,3-glucanase 9 (SGlu9) p... 119 7e-67

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 (939 letters)

Database: plantfungal

45 661,018 sequences; 426,114,510 total letters

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50 Score E  
 Sequences producing significant alignments: (bits) Value

emb|AW730233|AW730233 GA\_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98  
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 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77  
 55 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75  
 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72  
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70  
 emb|Z21642|CHASTRNAA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67  
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59  
 60 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58  
 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56

- emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53  
emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49  
dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49  
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5 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47  
dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46  
emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46  
dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45  
gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43  
10 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42  
emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42  
emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38  
emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38  
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15 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycopersicon... 138 5e-32  
emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30  
emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26  
emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21  
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20 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17  
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emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10  
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30 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08  
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emb|AV390244|AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla... 49 4e-05  
emb|AW616467|AW616467 EST322878 L. hirsutum trichome, Cornell Un... 48 7e-05  
35 emb|AL354022|P761R Leishmania major Friedlin PAC P761 right end-... 44 0.002  
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gb|U12630|ENU12630 Emericella nidulans R153 core histone H3 (H3)... 34 1.3  
45 emb|AI007494|AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3  
emb|AA787433|AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3  
emb|X55548|ANH3GENE A.nidulans gene for core histone for H3. 34 1.3  
emb|AQ396426|AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P... 34 1.6  
emb|AF262997|AF262997 Ricinus communis NADP-dependent malic prot... 34 1.6  
50 gb|M19025|CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c... 34 1.6  
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emb|Y18012|TVE18012 Trametes versicolor mRNA for laccase. 33 2.3  
55 emb|AQ500614|AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc... 33 2.5  
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60 emb|AW187537|AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ... 33 3.1  
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 5 gb|BE028433|BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag... 32 5.9  
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 15 emb|Z69381|SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom... 32 6.5  
 emb|Z71509|SCYNL233W S.cerevisiae chromosome XIV reading frame O... 32 6.5  
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 30 emb|X77895|CPGPRNL28 G.pyrenaica chloroplast trnL gene intron. 32 8.1

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 35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z97339|/ncgi)  
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40 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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45 Score E  
 Sequences producing significant alignments: (bits) Value

emb|AW685774|AW685774 NF035A03NR1F1000 Nodulated root Medicago t... 123 6e-28  
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 50 emb|AW687794|AW687794 NF013E08RT1F1066 Developing root Medicago ... 89 3e-23  
 emb|AW310121|AW310121 sf31d07.x1 Gm-c1028 Glycine max cDNA clone... 68 3e-19  
 emb|AW704640|AW704640 sk54f05.y1 Gm-c1019 Glycine max cDNA clone... 68 3e-19  
 emb|AW395252|AW395252 sh45g06.y1 Gm-c1017 Glycine max cDNA clone... 68 3e-19  
 emb|AW704612|AW704612 sk54c11.y1 Gm-c1019 Glycine max cDNA clone... 68 3e-19  
 55 emb|AT000508|AT000508 AT000508 Brassica rapa guard cell Brassica... 50 2e-18  
 emb|AW704218|AW704218 sk17c12.y1 Gm-c1028 Glycine max cDNA clone... 63 3e-17  
 emb|AW423428|AW423428 sh66f08.y1 Gm-c1015 Glycine max cDNA clone... 63 1e-16  
 emb|AW687188|AW687188 NF006H09RT1F1079 Developing root Medicago ... 82 3e-15  
 emb|AW684973|AW684973 NF023G04NR1F1000 Nodulated root Medicago t... 68 1e-13  
 60 emb|AW233878|AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone... 69 3e-13  
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5	gb BE033951 BE033951 MG02E05 MG Mesembryanthemum crystallinum cD...	44	3e-10
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	emb AI930953 AI930953 sb45c07.y1 Gm-cl015 Glycine max cDNA clone...	48	4e-08
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10	emb AW284126 AW284126 LG1_262_A05.g1_A002 Light Grown 1 (LG1) So...	55	3e-07
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	emb AW299176 AW299176 EST305986 KV2 Medicago truncatula cDNA clo...	38	0.036
	emb AW220014 AW220014 EST302497 tomato root during/after fruit s...	38	0.050
	gb C96140 C96140 C96140 Marchantia polymorpha immature sex organ...	38	0.050
30	emb AW625648 AW625648 EST319555 tomato radicle, 5 d post-imbibit...	38	0.050
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35	emb AW725520 AW725520 GA_Ea0018G22 Gossypium arboreum 7-10 dpa ...	35	0.46
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	emb AW310120 AW310120 sf31d06.x1 Gm-cl028 Glycine max cDNA clone...	35	0.46
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 5 dbj|E06816|E06816 DNA encoding alcohol acetyltransferase 1. 33 1.2  
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 10 emb|X01777|HVB3HORD Barley mRNA fragment for B3-hordein. 33 1.6  
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 emb|AE001274|AE001274 Leishmania major chromosome 1, complete se... 30 2.2  
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 gb|B67221|B67221 CpG0036A CpIOWAgDNA1 Cryptosporidium parvum gen... 32 3.1  
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 emb|AL122012|LMFL8342 Leishmania major Friedlin chromosome 23 co... 31 4.2  
 25 emb|X60772|GMOLEOA G.max mRNA for 24 kDa oleosin isoform (partia... 31 4.2

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(592 letters)

Database: plantfungal  
 35 661,018 sequences; 426,114,510 total letters

Searching.....done

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 45 emb|AI487510|AI487510 EST245832 tomato ovary, TAMU Lycopersicon ... 327 5e-89  
 emb|AI486784|AI486784 EST245106 tomato ovary, TAMU Lycopersicon ... 327 5e-89  
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	emb AW649016 AW649016 EST327470 tomato germinating seedlings, TA...	265 2e-70
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 emb|AI729618|AI729618 BNLGHi13779 Six-day Cotton fiber Gossypium... 105 3e-44  
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(940 letters)

Database: plantfungal

30 661,018 sequences; 426,114,510 total letters

Searching.....done

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 40 emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIA (or... 125 7e-38  
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(940 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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 Sequences producing significant alignments: (bits) Value

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	emb AV424084 AV424084 AV424084 Lotus japonicus young plants (two...	68 7e-17
	emb AV413163 AV413163 AV413163 Lotus japonicus young plants (two...	68 7e-17
45	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	54 3e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	70 3e-16
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50	emb AI736394 AI736394 sb28a06.y1 Gm-c1009 Glycine max cDNA clone...	64 7e-16
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	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon...	54 2e-15
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60	emb AV419425 AV419425 AV419425 Lotus japonicus young plants (two...	62 4e-15
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	emb AW738399 AW738399 EST339826 tomato flower buds, anthesis, Co...	62	5e-14
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	emb AW223703 AW223703 EST300514 tomato fruit red ripe, TAMU Lyco...	244	3e-64
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30	gb BE124622 BE124622 EST393657 GVN Medicago truncatula cDNA clon...	243	5e-64
	emb AW747419 AW747419 WS1_68_E10.b1_A002 Water-stressed 1 (WS1) ...	242	1e-63
	gb BE033541 BE033541 MF02E10 MF Mesembryanthemum crystallinum cD...	242	1e-63
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35	emb AI960575 AI960575 sc86c01.y1 Gm-c1018 Glycine max cDNA clone...	240	4e-63
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	emb AW568285 AW568285 si69g11.y1 Gm-r1030 Glycine max cDNA clone...	240	5e-63
	emb AW186193 AW186193 se64g04.y1 Gm-c1019 Glycine max cDNA clone...	240	5e-63
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40	emb AW981480 AW981480 EST392633 DSIL Medicago truncatula cDNA cl...	239	1e-62
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	emb AI443884 AI443884 sa44f06.y1 Gm-c1004 Glycine max cDNA clone...	237	5e-62
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60	emb AI026521 AI026521 TENU0733 T. cruzi epimastigote normalized ...	124	3e-31
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5 emb|X59720|SCCHRIII S.cerevisiae chromosome III complete DNA seq... 80 8e-25  
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10 emb|AW222638|AW222638 EST299449 tomato fruit red ripe, TAMU Lyco... 89 2e-22  
emb|AW094164|AW094164 EST287344 tomato mixed elicitor, BTI Lycop... 89 2e-22  
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20 emb|AW220746|AW220746 EST297215 tomato fruit mature green, TAMU ... 89 2e-17  
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25 emb|AT000681|AT000681 AT000681 Brassica rapa guard cell Brassica... 61 3e-12  
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30 emb|AZ215418|AZ215418 Sheared DNA-79B7.TF Sheared DNA Trypanosom... 54 2e-09  
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gb|U14566|SCU14566 Saccharomyces cerevisiae formylglycinamide ri... 35 0.23  
35 emb|Z72847|SCYGR062C S.cerevisiae chromosome VII reading frame O... 35 0.23  
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40 emb|AQ945483|AQ945483 Sheared DNA-44G3.TR Sheared DNA Trypanosom... 32 2.1  
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emb|AW030467|AW030467 EST273722 tomato callus, TAMU Lycopersicon... 31 4.0  
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50 gb|U73817|CRU73817 Chlamydomonas reinhardtii LRG5 mRNA, complete... 30 7.6  
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments:

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	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	334	e-148
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	333	e-147
	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450; ...	309	e-145
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P...	227	e-136
15	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P...	227	e-135
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 ...	236	7e-85
	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro...	299	3e-80
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	272	4e-72
	emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone...	264	1e-69
20	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	261	1e-68
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25	emb AW171738 AW171738 N100632e rootphos(-) Medicago truncatula c...	245	6e-64
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	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium...	183	4e-58
	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium...	182	1e-57
	emb AW257188 AW257188 EST305325 KV2 Medicago truncatula cDNA clo...	189	1e-56
30	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	220	2e-56
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 emb|AW617605|AW617605 EST324016 *L. hirsutum* trichome, Cornell Un... 138 1e-42  
 5 emb|Y10492|GMC450CP5 *G.max* mRNA for putative cytochrome P450, cl... 105 2e-42  
 emb|AF195809|AF195809 *Vigna radiata* isoflavone synthase 4 (ifs4)... 100 3e-42  
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 10 emb|AW616809|AW616809 EST323220 *L. hirsutum* trichome, Cornell Un... 137 4e-42  
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 20 emb|Y10491|GMC450CP4 *G.max* mRNA for putative cytochrome P450, cl... 144 8e-42  
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 45 emb|AF195804|AF195804 *Lens culinaris* isoflavone synthase 1 (ifs1... 96 6e-40  
 emb|AF195816|AF195816 *Beta vulgaris* isoflavone synthase 1 (ifs1)... 99 6e-40  
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- Database: plantfungal  
 60 661,018 sequences; 426,114,510 total letters



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5	emb AJ277945 LES277945	Lycopersicon esculentum mRNA for putative...	125 3e-72
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	gb U21801 LEU21801	Lycopersicon esculentum alcohol dehydrogenase...	111 1e-64
	emb AW729170 AW729170	GA_Ea0024E17 Gossypium arboreum 7-10 dpa ...	126 3e-59
10	emb AW625848 AW625848	EST319755 tomato radicle, 5 d post-imbibit...	125 2e-54
	emb AW096560 AW096560	EST289740 tomato mixed elicitor, BTI Lycop...	117 5e-52
	emb AI494929 AI494929	sa92g06.y1 Gm-c1004 Glycine max cDNA clone...	203 1e-51
	emb AB018559 AB018559	Citrullus lanatus mRNA for wts2L, complete...	74 1e-50
	emb AF053638 AF053638	Pisum sativum short-chain alcohol dehydrog...	103 3e-50
15	emb AF097651 AF097651	Pisum sativum short-chain alcohol dehydrog...	103 8e-50
	emb AF053639 AF053639	Pisum sativum short-chain alcohol dehydrog...	103 2e-49
	emb AW092874 AW092874	EST286054 tomato mixed elicitor, BTI Lycop...	112 3e-49
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	gb U53827 SLU53827	Silene latifolia ssp. alba STA1-2 (STA1-2) mR...	140 2e-46
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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 (1216 letters)

50 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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30 emb|AW030038|AW030038 EST273293 tomato callus, TAMU Lycopersicon... 293 2e-78  
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emb|AJ010829|TSP010829 *Triticum* sp. mRNA for GRAB1 protein. 195 2e-69  
35 emb|A82384|A82384 Sequence 9 from Patent WO9856811. 195 2e-69  
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emb|AI900247|AI900247 sc03a01.y1 Gm-c1012 *Glycine max* cDNA clone... 251 1e-65  
emb|AW617735|AW617735 EST324146 *L. hirsutum* trichome, Cornell Un... 250 1e-65  
40 emb|AI777446|AI777446 EST258325 tomato susceptible, Cornell Lyco... 248 6e-65  
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45 emb|AI487038|AI487038 EST245360 tomato ovary, TAMU Lycopersicon ... 206 7e-64  
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50 emb|AW727788|AW727788 GA\_Ea0028C07 *Gossypium arboreum* 7-10 dpa ... 200 2e-62  
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emb|AW035978|AW035978 EST282837 tomato callus, TAMU Lycopersicon... 176 9e-61  
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55 emb|AV410710|AV410710 AV410710 *Lotus japonicus* young plants (two... 185 2e-59  
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20 emb|AI484813|AI484813 EST243074 tomato ovary, TAMU Lycopersicon ... 150 2e-54  
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30 emb|AI897257|AI897257 EST266616 tomato ovary, TAMU Lycopersicon ... 160 4e-52  
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35 emb|AW099384|AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone... 137 4e-51  
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Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical...	115	1e-24	
60 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago ...	88	2e-16	
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 emb|AL136326|LMFL377 Leishmania major Friedlin chromosome 23 cos... 34 3.1  
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 15 emb|AJ001925|PAAJ1925 Picea abies cad7 gene. 33 4.3  
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 20 emb|AC006281|AC006281 Plasmodium falciparum chromosome 12 clone ... 33 7.7  
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 25 emb|AW221805|AW221805 EST298616 tomato fruit red ripe, TAMU Lyco... 32 8.1  
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 (2403 letters)

40 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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45 Score E  
 Sequences producing significant alignments: (bits) Value

emb|AJ006378|LES6378 Lycopersicon esculentum sbt1 gene. 240 e-157  
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 50 emb|Y18932|LES18932 Lycopersicon esculentum p69F gene. 142 e-152  
 emb|Y17278|LES17278 Lycopersicon esculentum p69d gene, complete ... 141 e-146  
 emb|AJ005173|LEAJ5173 Lycopersicon esculentum p69f gene, complet... 141 e-146  
 emb|AJ005172|LEAJ5172 Lycopersicon esculentum p69e gene, complet... 142 e-146  
 emb|Y18931|LES18931 Lycopersicon esculentum p69E gene. 144 e-144  
 55 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142  
 emb|X98930|LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142  
 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136  
 emb|AJ005171|LEAJ517 Lycopersicon esculentum p69c gene, complete... 142 e-136  
 emb|Y17276|LES17276 Lycopersicon esculentum p69b gene, complete ... 138 e-130  
 60 emb|Y10149|LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130  
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- emb|X95270|LESUBENDO *L.esculentum* mRNA for subtilisin-like endop... 138 e-126  
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 5 emb|AW218382|AW218382 EST303565 tomato radicle, 5 d post-imbibit... 322 6e-87  
 dbj|D86598|D86598 Norway spruce mRNA for antifreeze-like protein... 135 6e-77  
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 10 emb|AJ006376|LES6376 *Lycopersicon esculentum* mRNA for serine pro... 102 3e-68  
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 emb|AJ006481|LES6481 *Lycopersicon esculentum* sbt4c gene. 138 2e-66  
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 20 emb|AJ012164|CGL012164 *Casuarina glauca* mRNA for cg12 gene fragm... 114 4e-62  
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 25 emb|AW695319|AW695319 NF093H12ST1F1103 Developing stem *Medicago* ... 105 2e-57  
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 30 emb|AW668484|AW668484 GA\_Ea0014C06 *Gossypium arboreum* 7-10 dpa ... 188 4e-56  
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 55 emb|AW704701|AW704701 sk39d09.y1 Gm-c1028 Glycine max cDNA clone... 124 2e-47  
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 60 gb|BE053648|BE053648 GA\_Ea0001B22f *Gossypium arboreum* 7-10 dpa ... 81 9e-46  
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 25 emb|AW692289|AW692289 NF054B05ST1F1000 Developing stem Medicago ... 128 2e-38  
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 (2403 letters)

35 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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 Sequences producing significant alignments: (bits) Value

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 5 emb|AJ006376|LES6376 Lycopersicon esculentum mRNA for serine pro... 102 3e-68  
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 30 (2002 letters)

Database: plantfungal  
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	gb U45243 NTU45243 Nicotiana tabacum diphenol oxidase mRNA, part...	232	e-124
	emb Y13769 PTY13769 Populus trichocarpa mRNA for laccase, lac1 g...	237	e-121
45	emb AW774748 AW774748 EST333899 KV3 Medicago truncatula cDNA clo...	419	e-116
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	gb U43542 NTU43542 Nicotiana tabacum diphenol oxidase mRNA, comp...	379	e-104
	gb U73103 LTU73103 Liriodendron tulipifera high-pI laccase (LAC2...	363	e-103
	gb U12757 APU12757 Acer pseudoplatanus laccase mRNA, complete cds.	368	e-100
50	gb U73104 LTU73104 Liriodendron tulipifera high-pI laccase (LAC2...	353	3e-99
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	emb AW688902 AW688902 NF013A07ST1F1000 Developing stem Medicago ...	360	2e-98
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55	emb Y13771 PTY13771 Populus trichocarpa mRNA for laccase, lac3 g...	257	1e-88
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5 emb|AW625159|AW625159 EST319066 tomato radicle, 5 d post-imbibit... 247 3e-64  
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35 emb|AI167003|AI167003 xylem.est.78 Poplar xylem Lambda ZAPII lib... 204 3e-51  
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Database: plantfungal

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|    | emb X94943 LECEVI16G L.esculentum mRNA for peroxidase.              | 212 | e-100        |
|    | emb AB027753 AB027753 Nicotiana tabacum mRNA for peroxidase, com... | 191 | 1e-94        |
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15 emb|AJ242742|IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... 82 5e-50  
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20 emb|X56011|TAPERO Wheat mRNA for peroxidase. 102 2e-48  
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25 gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 100 2e-47  
gb|M60729|HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge... 78 3e-47  
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emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 109 5e-47  
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30 emb|AW035207|AW035207 EST280469 tomato callus, TAMU Lycopersicon... 188 8e-47  
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50 gb|L36111|SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 77 3e-43  
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60 gb|L07554|LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA... 92 3e-42  
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- emb|AI778513|AI778513 EST259392 tomato susceptible, Cornell Lyco... 170 1e-41  
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 10 emb|Y10469|SOPR XR8 S.oleracea mRNA for peroxidase, clone PC55. 111 4e-41  
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 emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 86 6e-41  
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 15 gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 107 1e-40

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[post/entrez/query?db=n&form=6&dopt=g&uid=gb|af163823|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af163823|/ncgi)  
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25 Database: plantfungal  
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Searching.....done

30 Score E  
 Sequences producing significant alignments: (bits) Value

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10 emb|AW218862|AW218862 EST301344 tomato root during/after fruit s... 354 5e-97  
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30 emb|AI489962|AI489962 EST248301 tomato ovary, TAMU Lycopersicon ... 341 4e-93  
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5 dbj|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85  
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(1025 letters)

20 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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25 Score E  
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 40 emb|AW687253|AW687253 NF007F05RT1F1046 Developing root Medicago ... 292 1e-88  
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 45 emb|AW038999|AW038999 EST280972 tomato mixed elicitor, BTI Lycop... 303 3e-88  
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 50 emb|AI496348|AI496348 sb05e11.y1 Gm-cl004 Glycine max cDNA clone... 320 8e-87  
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 55 emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85  
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 emb|AI729066|AI729066 BNLGHi12528 Six-day Cotton fiber Gossypium... 315 4e-85  
 dbj|D16456|TOMEXT3 Tomato mRNA for endo-xyloglucan transferase, ... 295 4e-85  
 dbj|E06971|E06971 DNA encoding xyloglucan endotransferase. 295 4e-85  
 60 dbj|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85  
 dbj|E06961|E06961 Anti-sense DNA of xyloglucan endotransferase g... 295 4e-85

emb|AW934469|AW934469 EST353373 tomato flower buds 0-3 mm, Corne... 314 7e-85  
 emb|AW185234|AW185234 se88f12.y1 Gm-c1023 Glycine max cDNA clone... 314 1e-84  
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 emb|AW216790|AW216790 EST295504 tomato callus, TAMU Lycopersicon... 312 3e-84  
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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	emb AW980547 AW980547	EST391700	GVN Medicago truncatula cDNA clo... 95 2e-22
	emb AW685869 AW685869	NF031B09NR1F1000	Nodulated root Medicago t... 95 2e-22
25	gb BE124445 BE124445	EST393480	GVN Medicago truncatula cDNA clon... 95 2e-22
	gb BE124752 BE124752	EST393787	GVN Medicago truncatula cDNA clon... 95 2e-22
	emb AW684629 AW684629	NF019B05NR1F1000	Nodulated root Medicago t... 95 2e-22
	emb AW329233 AW329233	N200445e	rootphos(-) Medicago truncatula c... 95 2e-22
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30	emb AW125962 AW125962	N100157e	rootphos(-) Medicago truncatula c... 92 2e-21
	emb AW622601 AW622601	EST313401	tomato root during/after fruit s... 101 2e-21
	emb AW624937 AW624937	EST313766	tomato radicle, 5 d post-imbibit... 101 2e-21
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	emb AW035571 AW035571	EST281309	tomato callus, TAMU Lycopersicon... 98 1e-20
	emb AW217082 AW217082	EST295796	tomato callus, TAMU Lycopersicon... 98 1e-20
	emb AW032764 AW032764	EST276323	tomato callus, TAMU Lycopersicon... 98 1e-20
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55	emb AW725519 AW725519	GA_Ea0018G20	Gossypium arboreum 7-10 dpa ... 94 4e-19
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60	emb AV413531 AV413531	AV413531	Lotus japonicus young plants (two... 93 1e-18
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15	emb AW306872 AW306872 sf49g05.y1 Gm-c1009 Glycine max cDNA clone...	62	3e-15
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 (1579 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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emb AW672225 AW672225 LG1_358_C11.b1_A002 Light Grown 1 (LG1) So...	192	6e-48	
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Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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	emb AF025857 AF025857 Aegilops caudata RAPD marker generated by ...	36	0.18
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	emb AF242188 AF242188 Plasmodium falciparum membrane protein Pfl...	34	0.89
	gb M28889 PFAMEM12A P.falciparum membrane protein Pfl2 gene, com...	34	0.89
	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom...	33	1.2
15	gb U47092 U47092 DCU47092 Carrot somatic embryos Daucus carota c...	33	1.2
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	emb AQ849793 AQ849793 LMAJFV1_lm49f04.x1 Leishmania major FV1 ra...	33	1.2
	gb U91982 SHU91982 Stylosanthes hamata EREBP-3 homolog mRNA, com...	33	1.7
20	emb AW727560 AW727560 GA_Ea0012P04 Gossypium arboreum 7-10 dpa ...	33	1.7
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	emb AL136236 SPAPJ696 S.pombe chromosome I PCR product p696.	32	2.3
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25	emb AW728870 AW728870 GA_Ea0028O24 Gossypium arboreum 7-10 dpa ...	32	2.3
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	emb AC068564 AC068564 Filobasidiella neoformans var. neoformans,...	32	3.2
30	emb Z38058 LMCLPB L.major (MHOM/SU/5ASKH) DNA for 100 kDa heat s...	32	3.2
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35	emb X95256 HVXYLISOG H.vulgare xylose isomerase gene.	32	3.2
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	emb X62675 TRMINEX5S T.rangeli DNA for mini-exon and 5S rRNA.	29	3.5
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50	emb AW307483 AW307483 sf57e09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4
	emb AW307220 AW307220 sf54c09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4
	emb AI437852 AI437852 sa40e07.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4
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60	emb AI494951 AI494951 sa93a10.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4
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	dbj D87895 D87895 Aspergillus nidulans chiA gene for chitinase, ...	30	8.3
	emb AQ162420 AQ162420 mgxb0012N11r CUGI Rice Blast BAC Library P...	30	8.3
	gb BE036961 BE036961 MP09G07 MP Mesembryanthemum crystallinum cD...	30	8.3
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	emb AW980894 AW980894 EST392047 GVN Medicago truncatula cDNA clo...	30	8.3
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	gb BE053868 BE053868 GA__Ea0013O20f Gossypium arboreum 7-10 dpa ...	27	8.9
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35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x99923|/ncgi)  
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(1710 letters)

40 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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	emb AF149917 AF149917 Simmondsia chinensis acyl CoA reductase mR...	158	e-144	
	emb X99922 BNMS2PROT B.napus mRNA for male sterility protein 2.	137	2e-74	
50	emb A45743 A45743 Sequence 22 from Patent WO9520668.	137	2e-74	
	emb AW615992 AW615992 EST325442 tomato flower buds 0-3 mm, Corne...	277	2e-73	
	emb AI730540 AI730540 BNLGHi7015 Six-day Cotton fiber Gossypium ...	153	4e-59	
	emb AW738637 AW738637 EST340064 tomato flower buds, anthesis, Co...	158	3e-51	
	emb AW931162 AW931162 EST357005 tomato fruit mature green, TAMU ...	201	1e-50	
55	emb AW616784 AW616784 EST323195 L. hirsutum trichome, Cornell Un...	200	3e-50	
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	emb AW278653 AW278653 sf63e03.y1 Gm-c1013 Glycine max cDNA clone...	110	1e-46	
	emb AI727421 AI727421 BNLGHi7945 Six-day Cotton fiber Gossypium ...	106	3e-46	
	emb AI901240 AI901240 sc22e07.y1 Gm-c1013 Glycine max cDNA clone...	166	3e-40	
60	emb AW306151 AW306151 se46e08.y1 Gm-c1017 Glycine max cDNA clone...	145	2e-39	
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	emb AW648210 AW648210 EST326664 tomato germinating seedlings, TA...	107	1e-37
	emb AW279265 AW279265 sf68h11.y1 Gm-c1013 Glycine max cDNA clone...	123	3e-37
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	emb AW688474 AW688474 NF008A09ST1F1000 Developing stem Medicago ...	106	5e-31
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	emb AW622996 AW622996 EST320941 tomato flower buds 3-8 mm, Corne...	128	1e-28
	emb AI055562 AI055562 coau0004F11 Cotton Boll Abscission Zone cD...	98	1e-27
10	emb AW287082 AW287082 LG1_265_C07.b2_A002 Light Grown 1 (LG1) So...	119	7e-26
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	emb AW649410 AW649410 EST327864 tomato germinating seedlings, TA...	115	1e-24
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	emb AW217787 AW217787 EST296501 tomato flower buds 8 mm to pre-a...	91	3e-17
	emb AW928598 AW928598 EST337386 tomato flower buds 8 mm to pre-a...	86	1e-16
	emb Z11889 MITTARRNG T.aestivum mitochondrion rm26 gene for rRN...	88	2e-16
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	emb AF076792 AF076792 Irvingia gabonensis clone BM35, genomic su...	51	2e-08
	emb AW056631 AW056631 ST53H08 Pine TriplEx shoot tip library Pin...	36	7e-05
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	emb Y13967 PCLYS2 Penicillium chrysogenum lys2 gene.	41	0.021
	emb AW929360 AW929360 EST338148 tomato flower buds 8 mm to pre-a...	40	0.074
35	emb AW564691 AW564691 LG1_300_C05.b1_A002 Light Grown 1 (LG1) So...	37	0.50
	emb AF114171 AF114171 Sorghum bicolor BAC clone 25.M18, complete...	37	0.50
	gb BE033566 BE033566 MF03E04 MF Mesembryanthemum crystallinum cD...	36	0.69
	emb AI488290 AI488290 EST246612 tomato ovary, TAMU Lycopersicon ...	36	0.94
	emb AW932683 AW932683 EST358526 tomato fruit mature green, TAMU ...	36	0.94
40	emb AW932440 AW932440 EST358283 tomato fruit mature green, TAMU ...	36	0.94
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 10 gb|U58133|CAU58133 Candida albicans alpha-aminoadipate reductase... 26 6.1  
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 15 emb|AW618444|AW618444 EST320430 L. pennellii trichome, Cornell U... 33 6.3  
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 emb|AF072272|AF072272 Lactuca sativa resistance protein candidat... 33 6.3  
 20 emb|AB012945|AB012945 Aspergillus oryzae gene for amyRp, complet... 33 8.7  
 emb|AF180560|AF180560 Emericella nidulans sgdA gene, partial seq... 33 8.7  
 dbj|D29761|YSACSH Candida maltosa gene for chitin synthase 2, p... 33 8.7  
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 25 dbj|D50617|YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp... 33 8.7

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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031804|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031804|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031804|/ncgi)  
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 (1467 letters)

35 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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| Sequences producing significant alignments:                            | (bits) | Value |
| emb AI894665 AI894665 EST264108 tomato callus, TAMU Lycopersicon...    | 341    | 6e-93 |
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| emb AW035000 AW035000 EST279229 tomato callus, TAMU Lycopersicon...    | 297    | 2e-79 |
| emb AI896184 AI896184 EST265627 tomato callus, TAMU Lycopersicon...    | 282    | 5e-75 |
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| 60 emb AT000492 AT000492 AT000492 Brassica rapa guard cell Brassica... | 92     | 6e-28 |
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5 emb|AW685452|AW685452 NF029F12NR1F1000 Nodulated root Medicago t... 104 2e-21  
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15 emb|AW934333|AW934333 EST360176 tomato fruit mature green, TAMU ... 84 4e-15  
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Score E  
 Sequences producing significant alignments: (bits) Value

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Database: plantfungal

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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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 gb|L13654|TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN... 204 e-118  
 emb|Y16776|SOY16776 Spinacia oleracea mRNA for peroxidase, prx10... 210 e-113  
 60 emb|Z22920|SPPEROXDS S.polyrrhiza mRNA for peroxidase. 183 5e-90  
 emb|AI495190|AI495190 sa89c07.y1 Gm-c1004 Glycine max cDNA clone... 325 6e-88

- emb|AW219258|AW219258 EST301740 tomato root during/after fruit s... 212 5e-85  
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5 emb|AW622057|AW622057 EST312855 tomato root during/after fruit s... 182 2e-83  
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40 emb|AW621545|AW621545 EST312343 tomato root during/after fruit s... 166 8e-65  
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gb|M37637|ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... 100 2e-63  
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45 emb|X94943|LECEVI16G L.esculentum mRNA for peroxidase. 104 4e-63  
emb|AI487546|AI487546 EST245868 tomato ovary, TAMU Lycopersicon ... 150 5e-63  
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50 emb|AW218589|AW218589 EST303772 tomato radicle, 5 d post-imbibit... 147 6e-62  
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55 emb|AW621885|AW621885 EST312683 tomato root during/after fruit s... 145 2e-61  
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 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi)  
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	emb AW224727 AW224727 EST303170 tomato root, plants pre-anthesis...	77 1e-28
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30 emb|AW443955|AW443955 EST308885 tomato mixed elicitor, BTI Lycop... 75 5e-25  
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Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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emb AF135127 AF135127 Betula pendula isoflavone reductase homolo...	534	e-151
55 emb AF242491 AF242491 Forsythia x intermedia clone 1 phenylcouma...	527	e-149
emb AF242492 AF242492 Forsythia x intermedia clone 2 phenylcouma...	512	e-144
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- emb|AJ003245|GMAJ3245 Glycine max mRNA for putative NADPH:isofla... 311 2e-99
- emb|AW306732|AW306732 sf47f07.y1 Gm-c1009 Glycine max cDNA clone... 222 2e-99
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- emb|AW560880|AW560880 EST315928 DSIR Medicago truncatula cDNA cl... 335 3e-91
- emb|X60755|CANADPHIO C.arietinum mRNA for NADPH:isoflavone oxido... 302 2e-90
- 25 emb|AW308968|AW308968 sf92d11.y1 Gm-c1019 Glycine max cDNA clone... 331 5e-90
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- 45 emb|AF242504|AF242504 Thuja plicata clone 2 pinoresinol-laricire... 160 7e-76
- emb|AF242503|AF242503 Thuja plicata clone 1 pinoresinol-laricire... 120 7e-76
- emb|AW623613|AW623613 EST321558 tomato flower buds 3-8 mm, Come... 199 3e-75
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- emb|AW719567|AW719567 LjNEST6f2r Lotus japonicus nodule library,... 281 8e-75
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40 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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45 Score E  
 Sequences producing significant alignments: (bits) Value

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 emb|AI490296|AI490296 EST248622 tomato ovary, TAMU Lycopersicon ... 122 4e-27  
 emb|AI486929|AI486929 EST245251 tomato ovary, TAMU Lycopersicon ... 122 4e-27  
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 (378 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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	gb M74102 TOBCPII Nicotiana sylvestris serine proteinase inhibit...	52 6e-09
35	emb AW622766 AW622766 EST306752 tomato flower buds 3-8 mm, Come...	46 1e-08
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	emb AI563140 AI563140 EST00264 watermelon lambda zap library Cit...	58 3e-08
	emb AI723907 AI723907 RHIZ1_32_B07.y1_A001 Rhizome1 Sorghum hale...	57 5e-08
	emb AI724626 AI724626 RHIZ1_11_A01.y1_A001 Rhizome1 Sorghum hale...	57 5e-08
40	emb AJ250663 HVU250663 Hordeum vulgare partial mRNA for putative...	57 5e-08
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	gb L06985 POTPIN1A Solanum tuberosum proteinase inhibitor I mRNA...	43 1e-07
45	gb M13938 TOMWIPIG Tomato (L.esculentum) wound-inducible protein...	42 2e-07
	emb AI771798 AI771798 EST252898 tomato ovary, TAMU Lycopersicon ...	42 2e-07
	emb AI490242 AI490242 EST248568 tomato ovary, TAMU Lycopersicon ...	42 2e-07
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50	gb K03290 TOMWIPI Tomato leaf wound-induced proteinase inhibitor...	42 2e-07
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 15 emb|AW092125|AW092125 EST285221 tomato mixed elicitor, BTI Lycop... 35 5e-06  
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 20 emb|AI938012|AI938012 sc40a06.x1 Gm-cl014 Glycine max cDNA clone... 51 5e-06  
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 (2247 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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emb Z49320 SCYJL045W S.cerevisiae chromosome X reading frame ORF...	403	0.0
gb M86909 YSCSDH1A Saccharomyces cerevisiae succinate dehydrogen...	408	0.0
45 gb M94874 YSCSDH1B Saccharomyces cerevisiae succinate dehydrogen...	408	0.0
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gb M86746 YSCSDHA Saccharomyces cerevisiae succinate dehydrogena...	408	0.0
dbj D86573 D86573 Plasmodium falciparum DNA for flavoprotein sub...	676	0.0
emb AB031741 AB031741 Trypanosoma cruzi mRNA for succinate dehyd...	456	0.0
50 dbj D89263 D89263 Schizosaccharomyces pombe mRNA, partial cds, c...	637	0.0
emb Y10377 CATOP2 C.albicans TOP2 gene.	635	0.0
emb AI771965 AI771965 EST253065 tomato resistant, Cornell Lycops...	495	e-139
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55 emb AI727777 AI727777 BNLGHi9047 Six-day Cotton fiber Gossypium ...	391	e-114
emb AW775119 AW775119 EST334270 KV3 Medicago truncatula cDNA clo...	407	e-112
emb AL110721 CNS018RU Botrytis cinerea strain T4 cDNA library un...	323	e-110
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emb AW687411 AW687411 NF009C11RT1F1085 Developing root Medicago ...	208	2e-85
60 emb AW180257 AW180257 MgA0347fMgA Library Mycosphaerella gramin...	309	4e-83
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5 emb|AW350842|AW350842 GM210009B10E8R Gm-r1021 Glycine max cDNA 3... 293 3e-78  
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10 emb|AW667947|AW667947 GA\_Ea0012A06 Gossypium arboreum 7-10 dpa ... 250 4e-65  
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40 emb|AW991033|AW991033 SsS0224 Suaeda salsa ZAP cDNA library Suae... 95 9e-28  
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55 gb|L36344|YSCTGGMS Saccharomyces cerevisiae tRNA-Met, tRNA-Ser, ... 47 1e-06  
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 10 emb|AA785876|AA785876 h8g02a1.r1 Aspergillus nidulans 24hr asexu... 40 0.053  
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 (2008 letters).

30 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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35 Score E  
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45 emb|AI728047|AI728047 BNLGHi9685 Six-day Cotton fiber Gossypium ... 51 4e-05  
emb|AI771145|AI771145 EST252341 tomato ovary, TAMU Lycopersicon ... 51 4e-05  
emb|AI939275|AI939275 sc69f06.y1 Gm-cl016 Glycine max cDNA clone... 50 5e-05  
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60 emb|AW677101|AW677101 DG1\_4\_D08.b1\_A002 Dark Grown 1 (DG1) Sorgh... 47 5e-04  
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5 emb|AL035475|PFMAI4P2 Plasmodium falciparum MAL4P2, complete seq... 46 0.001  
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10 emb|AI060327|AI060327 Mpc6 Ice plant seedlings, RT-PCR, pCRII M... 42 0.002  
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25 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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	emb AW329378 AW329378 N200608e rootphos(-) Medicago truncatula c...	386	e-107
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40	emb AI966343 AI966343 sc37e08.y1 Gm-cl014 Glycine max cDNA clone...	260	6e-97
	emb AW442228 AW442228 EST311624 tomato fruit red ripe, TAMU Lyco...	308	5e-95
	emb AW255529 AW255529 ML562 peppermint glandular trichome Mentha...	319	3e-93
	emb AW221896 AW221896 EST298707 tomato fruit red ripe, TAMU Lyco...	215	2e-78
	emb AW678275 AW678275 WS1_14_A02.b1_A002 Water-stressed 1 (WS1) ...	157	1e-77
45	emb AW668498 AW668498 GA_Ea0014E02 Gossypium arboreum 7-10 dpa ...	259	3e-75
	emb AI730573 AI730573 BNLGH7295 Six-day Cotton fiber Gossypium ...	272	3e-72
	emb AW219191 AW219191 EST301673 tomato root during/after fruit s...	211	5e-54
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50	emb AA231842 AA231842 CDO920.R cDNA from oat Avena sativa cDNA c...	175	9e-46
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55	emb AW684174 AW684174 NF013F01NR1F1000 Nodulated root Medicago t...	112	3e-24
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60	emb AE001381 AE001381 Plasmodium falciparum chromosome 2, sectio...	57	2e-07
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	emb AW508088 AW508088 si50f10.y1 Gm-r1030 Glycine max cDNA clone...	156	4e-60
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35	emb AW774738 AW774738 EST333889 KV3 Medicago truncatula cDNA clo...	157	1e-37
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Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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55 emb|AW687497|AW687497 NF010C03RT1F1020 Developing root Medicago ... 53 6e-12  
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40	emb AI822355 AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre...	123	7e-42
	emb AI822907 AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr...	123	7e-42
	emb AW687233 AW687233 NF007D09RT1F1077 Developing root Medicago ...	84	8e-42
	emb Y14600 SBRLK1 Sorghum bicolor mRNA for protein serine/threon...	73	1e-41
	emb AB041504 AB041504 Populus nigra PnPK2 mRNA for protein kinas...	73	1e-41
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	emb AF220603 AF220603 Lycopersicon esculentum VFNT Cherry Pto lo...	68	1e-39
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(1953 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 330 e-134

gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 224 e-107

gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 215 e-105

gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 297 e-104

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dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 285 e-103

emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 287 e-103

gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 304 e-102

emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 289 e-102

emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 292 e-102

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emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 291 e-101

emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 303 e-101

emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 299 e-101

gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 294 e-101

emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 301 e-101

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emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 302 e-101

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emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 303 e-100

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gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 290 2e-99

emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 270 3e-93

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emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 126 2e-74

emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 119 3e-74

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(1947 letters)

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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10	gb M58362 DARBFRUC <i>D.carota</i> cell wall beta-fructosidase mRNA, co...	239 0.0
	emb X81792 CRCIN1 <i>C.rubrum</i> CIN1 mRNA for extracellular invertase.	181 0.0
	emb X81834 NTMRNABDF <i>N.tabacum</i> mRNA for beta-fructosidase.	205 0.0
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	emb Y11176 CIFRUCTOS <i>C.intybus</i> mRNA for fructosidase.	144 0.0
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	emb AJ272305 LPE272305 <i>Lycopersicon pennellii</i> mRNA for beta-fruc...	190 e-170
	emb X85327 PSRNABFRU <i>P.sativum</i> mRNA for beta-fructofuranosidase.	398 e-169
	emb AF063246 AF063246 <i>Pisum sativum</i> cell wall invertase (bfructl...	398 e-169
	emb AJ272304 LES272304 <i>Lycopersicon esculentum</i> mRNA for beta-fru...	190 e-169
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	emb AF000520 AF000520 <i>Fragaria x ananassa</i> cell wall invertase (I...	210 e-164
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	emb X75352 DCRNAABF <i>D.carota</i> (Nantaise) mRNA for soluble acid be...	203 e-119
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50	emb X67163 DCSBFRU <i>D.carota</i> mRNA for soluble beta-fructosidase.	140 e-107
	gb L29099 POTBFRUASE <i>Solanum tuberosum</i> beta-fructosidase mRNA, c...	198 e-107
	dbj E07108 E07108 cDNA encoding acid invertase.	198 e-106
	dbj D11350 TOMBFSO <i>Tomato</i> mRNA for beta-fructosidase, complete cds.	198 e-106
	emb Z12026 LPBFRUCM <i>L.pimpinellifolium</i> beta-fructosidase mRNA fo...	198 e-106
55	emb Z12025 LEBFRUCM <i>L.esculentum</i> beta-fructosidase mRNA for vacu...	198 e-106
	gb M81081 TOMACIN <i>Tomato</i> acid invertase (TIV1) mRNA, complete cds.	198 e-106
	gb S70040 S70040 acid invertase [ <i>Lycopersicon esculentum</i> =tomatoe...	198 e-106
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	dbj E08976 E08976 cDNA encoding tomato invertase.	198 e-106
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	emb Y11124 CIPINVERT <i>C.intybus</i> mRNA for putative invertase.	138 e-102

	emb X97642 TGINV5GEN T.gesneriana mRNA for invertase 5.	180 6e-97
	emb X95651 TGINV11GN T.gesneriana mRNA for invertase.	186 7e-96
	emb X97643 TGINV6GEN T.gesneriana mRNA for invertase 6.	186 2e-94
	emb Y18706 DCA18706 Daucus carota Inv*Dc5 gene.	130 2e-93
5	emb Y18707 DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge...	161 2e-93
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	gb U84398 CIU84398 Cichorium intybus fructan-fructan 1-fructosyl...	161 5e-88
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15	emb Z12027 LEBFRUCG L.esculentum gene for vacuolar invertase.	157 6e-88
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20	emb X91392 LELIN8 L.esculentum mRNA for invertase (LIN8).	133 2e-82
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60	emb AF000521 AF000521 Fragaria x ananassa cell wall invertase pr... 413 0.0	



- emb|Z35163|VFCWINV2 V.faba VFCWINV2 mRNA for cell wall invertase... 418 0.0  
gb|M58362|DARBFRUC D.carota cell wall beta-fructosidase mRNA, co... 239 0.0  
emb|X81792|CRCIN1 C.rubrum CIN1 mRNA for extracellular invertase. 181 0.0  
emb|X81834|NTMRNABDF N.tabacum mRNA for beta-fructosidase. 205 0.0  
5 emb|AF030420|AF030420 Triticum aestivum cell wall invertase (IVR... 240 0.0  
emb|Y11176|CIFRUCTOS C.intybus mRNA for fructosidase. 144 0.0  
emb|Z21486|STBETFRUA S.tuberosum mRNA for invertase gene encodin... 196 e-180  
emb|AJ272305|LPE272305 Lycopersicon pennellii mRNA for beta-fruc... 190 e-170  
emb|X85327|PSRNABFRU P.sativum mRNA for beta-fructofuranosidase. 398 e-169  
10 emb|AF063246|AF063246 Pisum sativum cell wall invertase (bfruct1... 398 e-169  
emb|AJ272304|LES272304 Lycopersicon esculentum mRNA for beta-fru... 190 e-169  
emb|Z22645|STBETFRCA S.tuberosum invertase gene encoding beta-fr... 204 e-166  
emb|AF000520|AF000520 Fragaria x ananassa cell wall invertase (I... 210 e-164  
emb|AB004558|AB004558 Lycopersicon esculentum mRNA for acid inve... 200 e-164  
15 emb|X69321|DCBFRUCT D.carota (Queen Anne's Lace) Inv\*Dc1 gene. 178 e-145  
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emb|Z35162|VFCWINV1 V.faba VFCWINV1 mRNA for cell wall invertase I. 207 e-132  
emb|AF030421|AF030421 Triticum aestivum cell wall invertase (IVR... 138 e-130  
emb|AJ133765|STU133765 Solanum tuberosum invGE and invGF genes. 148 e-128  
20 gb|U87849|CAU87849 Capsicum annuum acid beta-fructosidase mRNA, ... 200 e-126  
emb|AJ006067|ACE6067 Allium cepa mRNA for invertase. 210 e-126  
emb|A94218|A94218 Sequence 1 from Patent EP0952222. 176 e-122  
emb|AF002656|AF002656 Asparagus officinalis acid invertase mRNA,... 198 e-120  
gb|U81520|CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl... 173 e-120  
25 emb|X75351|DCRNABF D.carota (Nantaise) mRNA for soluble acid bet... 202 e-120  
emb|X75353|DCRNASABF D.carota (Nantaise) mRNA for soluble acid b... 203 e-120  
emb|AJ272307|LPE272307 Lycopersicon pennellii lin 5 gene for bet... 145 e-119  
emb|X75352|DCRNAABF D.carota (Nantaise) mRNA for soluble acid be... 203 e-119  
emb|X78423|DCINUC1 D.carota (Queen Anne's Lace) Inv\*Dc3 gene, 44... 160 e-118  
30 emb|A94222|A94222 Sequence 5 from Patent EP0952222. 173 e-117  
emb|Y09662|CSSSIFT C.scolymus mRNA for sucrose sucrose 1-fructos... 170 e-117  
emb|A86530|A86530 Sequence 1 from Patent WO9839460. 170 e-117  
emb|AJ272306|LES272306 Lycopersicon esculentum lin 5 gene for be... 145 e-116  
emb|AJ250634|TOF250634 Taraxacum officinale mRNA for sucrose:suc... 169 e-116  
35 emb|Z49831|VFVCINVMR V.faba VFVCINV mRNA for invertase (beta-fru... 199 e-115  
gb|U92438|PVU92438 Phaseolus vulgaris soluble acid invertase mRN... 198 e-114  
emb|AW686881|AW686881 NF003E07RT1F1000 Developing root Medicago ... 413 e-114  
dbj|D10265|VIRINVA Vigna radiata mRNA for invertase, complete cds. 194 e-114  
emb|AJ009757|HTU9757 Helianthus tuberosus sst-1 gene. 171 e-113  
40 emb|A52468|A52468 Sequence 1 from Patent WO9621023. 171 e-113  
emb|X70368|STPAIN1A S.tuberosum PAIN-1 mRNA for beta-fructofuran... 200 e-108  
emb|X67163|DCSBFRU D.carota mRNA for soluble beta-fructosidase. 140 e-107  
gb|L29099|POTBFRUASE Solanum tuberosum beta-fructosidase mRNA, c... 198 e-107  
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45 dbj|D11350|TOMBFSO Tomato mRNA for beta-fructosidase, complete cds. 198 e-106  
emb|Z12026|LPBFRUCM L.pimpinellifolium beta-fructosidase mRNA fo... 198 e-106  
emb|Z12025|LEBFRUCM L.esculentum beta-fructosidase mRNA for vacu... 198 e-106  
gb|M81081|TOMACIN Tomato acid invertase (TIV1) mRNA, complete cds. 198 e-106  
gb|S70040|S70040 acid invertase [Lycopersicon esculentum=tomatoe... 198 e-106  
50 dbj|E16293|E16293 cDNA encoding invertase. 198 e-106  
dbj|E08976|E08976 cDNA encoding tomato invertase. 198 e-106  
emb|AF017082|AF017082 Ipomoea batatas beta-fructofuranosidase (S... 141 e-103  
emb|Y11124|CIPINVERT C.intybus mRNA for putative invertase. 138 e-102  
emb|X97642|TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97  
55 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96  
emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94  
emb|Y18706|DCA18706 Daucus carota Inv\*Dc5 gene. 130 2e-93  
emb|Y18707|DCA18707 Daucus carota Inv\*Dc4, Inv\*Dc4' (partial) ge... 161 2e-93  
emb|AF062735|AF062735 Saccharum officinarum soluble acid inverta... 129 1e-91  
60 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91  
emb|AF091549|AF091549 Hamamelis virginiana clone 7 beta-fructofu... 331 9e-90

	emb AJ000481 CSFF1FRUC Cynara scolymus mRNA for fructan fructan ...	162	3e-89
	emb AF091550 AF091550 Hamamelis virginiana clone C beta-fructofu...	330	3e-89
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	emb AF091548 AF091548 Hamamelis virginiana clone 3 beta-fructofu...	327	1e-88
5	gb U84398 CIU84398 Cichorium intybus fructan-fructan 1-fructosyl...	161	5e-88
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	emb Z12027 LEBFRUCG L.esculentum gene for vacuolar invertase.	157	6e-88
	emb AJ009756 HTU9756 Helianthus tuberosus fft-1 gene.	161	2e-87
	emb A52470 A52470 Sequence 3 from Patent WO9621023.	161	2e-87
10	emb X81795 BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver...	265	5e-86
	gb BE055183 BE055183 GA_Ea0035H23f Gossypium arboreum 7-10 dpa ...	203	4e-83
	emb X91392 LELIN8 L.esculentum mRNA for invertase (LIN8).	133	2e-82
	emb AF091547 AF091547 Hamamelis virginiana clone 1 beta-fructofu...	295	3e-81
	emb X81793 CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase.	135	2e-80
15	emb X91389 LELIN5 L.esculentum mRNA for invertase (LIN5).	129	1e-78
	emb X91391 LELIN7 L.esculentum mRNA for invertase (LIN7).	133	5e-78
	emb Y07838 ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl...	156	2e-77
	emb X81796 BVBIN44 B.vulgaris BIN44 mRNA for intracellular inver...	149	5e-77
20	emb AF014925 AF014925 Citrus unshiu acid invertase (CUAI1) gene,...	138	4e-76
	emb AJ006066 ACE6066 Allium cepa mRNA for sucrose sucrose 1-fruc...	132	2e-75
	emb AF091545 AF091545 Hamamelis virginiana clone 4 beta-fructofu...	196	2e-75
	emb A48282 A48282 Sequence 3 from Patent WO9601904.	152	4e-75
	emb AW685050 AW685050 NF024F09NR1F1000 Nodulated root Medicago t...	248	5e-75
	emb Z83339 PSZ83339 P.sativum mRNA for cell wall invertase II.	280	2e-74
25	emb AF091546 AF091546 Hamamelis virginiana clone 6 beta-fructofu...	193	3e-74
	emb AV407850 AV407850 AV407850 Lotus japonicus young plants (two...	267	2e-70
	emb A48284 A48284 Sequence 5 from Patent WO9601904.	130	1e-69
	emb AW666614 AW666614 GA_Ea0005C10 Gossypium arboreum 7-10 dpa ...	207	3e-69
	emb AW730389 AW730389 GA_Ea0023K22 Gossypium arboreum 7-10 dpa ...	141	2e-68
30	emb A48280 A48280 Sequence 1 from Patent WO9601904.	82	2e-68
	emb X83233 HVSF6FT Hordeum vulgare mRNA for sucrose:fructan 6-fr...	82	2e-68
	emb AF069309 AF069309 Triticum aestivum vacuolar invertase (WIVR...	127	5e-67
	emb AW350139 AW350139 GM210007B20F11R Gm-r1021 Glycine max cDNA ...	112	4e-66
	emb AW618261 AW618261 EST314311 L. pennellii trichome, Cornell U...	248	1e-64
35	emb AW738685 AW738685 EST340112 tomato flower buds, anthesis, Co...	189	3e-64
	emb X91390 LELIN6 L.esculentum mRNA for invertase (LIN6).	133	5e-64
	emb AI522941 AI522941 sa92d01.y1 Gm-c1004 Glycine max cDNA clone...	201	1e-63
	emb AW441409 AW441409 EST310805 tomato fruit red ripe, TAMU Lyco...	114	4e-62
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45	Database: plantfungal 661,018 sequences; 426,114,510 total letters  Searching.....done		
50	Score E Sequences producing significant alignments: (bits) Value		
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	emb Z48179 SC9302X S.cerevisiae chromosome IV cosmid 9302.	185	e-114
55	gb L35237 YSCYCF1MRP Saccharomyces cerevisiae metal resistance p...	184	e-114
	gb U33010 SPU33010 Schizosaccharomyces pombe cosmids 359, 1198 a...	291	e-112
	emb AL356012 SPBC359 Schizosaccharomyces pombe cosmid c359.	291	e-112
	emb AW278374 AW278374 sf43c10.y1 Gm-c1009 Glycine max cDNA clone...	383	e-105
	dbj D89231 D89231 Schizosaccharomyces pombe mRNA, partial cds, c...	308	e-105
60	emb AI781883 AI781883 EST262762 tomato susceptible, Cornell Lyco...	370	e-101
	emb X91488 SCCEN12RG S.cerevisiae DNA from CEN12 region includin...	159	1e-94

- emb|X97560|SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome ... 159 1e-94  
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5 emb|AW441253|AW441253 EST310649 tomato fruit red ripe, TAMU Lyco... 308 2e-82  
emb|AW686402|AW686402 NF037F01NR1F1000 Nodulated root *Medicago t...* 244 7e-78  
emb|AW217265|AW217265 EST295979 tomato callus, TAMU Lycopersicon... 291 3e-77  
emb|AW223995|AW223995 EST300806 tomato fruit red ripe, TAMU Lyco... 290 7e-77  
emb|AW222948|AW222948 EST299759 tomato fruit red ripe, TAMU Lyco... 285 2e-75  
10 emb|AI437711|AI437711 sa38f05.y1 *Gm-c1004* Glycine max cDNA clone... 276 7e-73  
emb|AW476771|AW476771 ga37g03.y1 Moss EST library PPU Physcomitr... 275 1e-72  
emb|AW100468|AW100468 sd55e07.y1 *Gm-c1016* Glycine max cDNA clone... 272 2e-71  
emb|AI487304|AI487304 EST245626 tomato ovary, TAMU Lycopersicon ... 268 2e-70  
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15 emb|AW100453|AW100453 sd55c07.y1 *Gm-c1016* Glycine max cDNA clone... 266 1e-69  
emb|AW034253|AW034253 EST277824 tomato callus, TAMU Lycopersicon... 265 2e-69  
emb|AW216929|AW216929 EST295643 tomato callus, TAMU Lycopersicon... 259 1e-67  
emb|AW759237|AW759237 sl38f09.y1 *Gm-c1027* Glycine max cDNA clone... 259 1e-67  
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20 emb|Z73066|SCYGR281W *S.cerevisiae* chromosome VII reading frame O... 171 2e-67  
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emb|AW092564|AW092564 EST285744 tomato mixed elicitor, BTI Lycop... 249 1e-64  
emb|AF110027|AF110027 *Candida albicans* ATP-dependent transporter... 150 5e-64  
emb|AI779714|AI779714 EST260593 tomato susceptible, Cornell Lyco... 246 9e-64  
25 emb|AI900368|AI900368 sc04g04.y1 *Gm-c1012* Glycine max cDNA clone... 243 6e-63  
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emb|AF110147|AF110147 *Cryptosporidium parvum* ATP-binding cassett... 242 2e-62  
emb|Z73153|SCYLL048C *S.cerevisiae* chromosome XII reading frame O... 142 4e-62  
emb|AL114698|CNS01BUA *Botrytis cinerea* strain T4 cDNA library un... 238 7e-62  
30 emb|Z28329|SCYKR104W *S.cerevisiae* chromosome XI reading frame OR... 129 7e-61  
emb|AI895676|AI895676 EST265119 tomato callus, TAMU Lycopersicon... 234 4e-60  
emb|AL115672|CNS01CLC *Botrytis cinerea* strain T4 cDNA library un... 185 1e-58  
emb|AW737284|AW737284 EST338711 tomato flower buds, anthesis, Co... 229 2e-58  
emb|X17154|LTHCPG *Leishmania tarentolae* H circle borne ltpgpA ge... 197 2e-57  
35 gb|L29484|LEIPGLYA *Leishmania tarentolae* P-glycoprotein related ... 181 2e-57  
emb|AI729186|AI729186 BNLGHi12864 Six-day Cotton fiber *Gossypium*... 210 3e-57  
gb|U11583|YSCH9196 *Saccharomyces cerevisiae* chromosome VIII cosm... 136 6e-57  
gb|L29485|LEIPGLYB *Leishmania tarentolae* P-glycoprotein related ... 171 6e-57  
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40 emb|AL135898|LMFL673 *Leishmania major* Friedlin chromosome 23 cos... 176 2e-56  
emb|AW459613|AW459613 sh89d10.y1 *Gm-c1016* Glycine max cDNA clone... 219 1e-55  
emb|AB009972|AB009972 *Aspergillus oryzae* gene for beta-1,4-xylos... 122 2e-53  
emb|AW757110|AW757110 sl29c06.y1 *Gm-c1027* Glycine max cDNA clone... 208 3e-52  
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emb|AW761593|AW761593 sl69g02.y1 *Gm-c1027* Glycine max cDNA clone... 205 2e-51  
45 emb|Z99262|SPAC9E9 *S.pombe* chromosome I cosmid c9E9. 129 2e-51  
emb|Y09354|SPABC1 *S.pombe* ABC1 gene. 129 2e-51  
emb|AL136538|SPAC30 *S.pombe* chromosome I cosmid c30. 144 1e-48  
emb|AI974480|AI974480 T110430e KV0 *Medicago truncatula* cDNA clon... 196 1e-48  
50 emb|AI495498|AI495498 sa98g09.y1 *Gm-c1004* Glycine max cDNA clone... 194 4e-48  
emb|AW736468|AW736468 EST332482 KV3 *Medicago truncatula* cDNA clo... 191 3e-47  
emb|AW677202|AW677202 DG1\_6\_D10.b1\_A002 Dark Grown 1 (DG1) *Sorgh...* 191 5e-47  
gb|BE022474|BE022474 sm74d06.y1 *Gm-c1015* Glycine max cDNA clone ... 188 3e-46  
emb|Z49222|TCPGP2 *T.cruzi* gene for P-glycoprotein. 140 9e-45  
55 emb|AI437929|AI437929 sa41e03.y1 *Gm-c1004* Glycine max cDNA clone... 153 2e-44  
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gb|U95956|TCU95956 *Trypanosoma cruzi* P-glycoprotein (tcpgp1A) ge... 130 9e-42  
emb|AW830202|AW830202 sm24a04.y1 *Gm-c1028* Glycine max cDNA clone... 172 2e-41  
emb|AL113101|CNS01ALX *Botrytis cinerea* strain T4 cDNA library un... 138 4e-41  
60 emb|AW155943|AW155943 ga22b09.y1 Moss EST library PPU Physcomitr... 167 7e-40  
emb|AW202254|AW202254 sf12h06.y1 *Gm-c1027* Glycine max cDNA clone... 166 9e-40



- emb|AW759534|AW759534 sl44f02.y1 Gm-c1027 Glycine max cDNA clone... 166 9e-40  
 emb|AW223508|AW223508 EST300319 tomato fruit red ripe, TAMU Lyco... 165 2e-39  
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 emb|AW775340|AW775340 EST334405 DSIL Medicago truncatula cDNA cl... 161 3e-38  
 5 emb|Z28328|SCYKR103W S.cerevisiae chromosome XI reading frame OR... 122 6e-38  
 emb|AW039256|AW039256 EST281513 tomato mixed elicitor, BTI Lycop... 159 2e-37  
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 emb|AQ849029|AQ849029 LMAJFV1\_lm45c02.x1 Leishmania major FV1 ra... 112 2e-37  
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 10 emb|AW350529|AW350529 GM210009A10F6R Gm-r1021 Glycine max cDNA 3... 157 7e-37  
 emb|AQ950989|AQ950989 Sheared DNA-52G21.TF Sheared DNA Trypanoso... 154 5e-36  
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 emb|AW775084|AW775084 EST334235 KV3 Medicago truncatula cDNA clo... 153 1e-35  
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 15 emb|AW781305|AW781305 sk68b06.y1 Gm-c1016 Glycine max cDNA clone... 152 2e-35  
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 20 emb|AB013851|AB013851 Aspergillus oryzae gene for beta-xylosidas... 122 5e-35  
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 emb|AJ278038|BFU278038 Botryotinia fuckeliana BcatrG gene for MR... 148 4e-34  
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 25 emb|AQ646228|AQ646228 RPCI93-DpnII-30J14.TV RPCI93-DpnII Trypano... 141 5e-32  
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 emb|AI676508|AI676508 etmEST0269 EtH1 Eimeria tenella cDNA clone... 135 2e-30  
 emb|AQ640396|AQ640396 927P1-5E2.TP 927P1 Trypanosoma brucei geno... 105 4e-30  
 30 emb|AI782195|AI782195 EST263074 tomato susceptible, Cornell Lyco... 134 4e-30  
 emb|AW033521|AW033521 EST277092 tomato callus, TAMU Lycopersicon... 134 6e-30

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(2055 letters)

Database: plantfungal

- 40 661,018 sequences; 426,114,510 total letters

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- emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 356 e-115  
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 318 e-100  
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 322 e-99  
 50 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 312 9e-99  
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 313 1e-97  
 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 315 2e-97  
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 323 3e-97  
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 55 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 308 1e-93  
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 313 2e-93  
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 312 1e-92  
 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 310 3e-92  
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 309 7e-92  
 60 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 266 1e-90  
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 182 6e-90

- dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 260 1e-89  
 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 286 2e-89  
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 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 258 3e-87  
 5 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 197 4e-84  
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 10 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 232 1e-80  
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 15 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 107 2e-68  
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 20 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 105 5e-64  
 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 105 7e-64  
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 25 emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 202 1e-62  
 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 109 2e-62  
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 30 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 99 7e-61  
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 35 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 215 7e-55  
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 40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 166 5e-53  
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 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 119 1e-51  
 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 104 1e-51  
 emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 119 4e-51  
 45 emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 161 7e-51  
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 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 157 9e-50  
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 50 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 106 2e-49  
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 55 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 119 3e-48  
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 60 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 118 8e-47  
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emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 109 1e-45  
5 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 2e-45  
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10 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 65 7e-44  
emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 178 1e-43  
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15 emb|AW706972|AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone... 174 2e-42  
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emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 173 5e-42  
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emb|AW775756|AW775756 EST334821 DSIL Medicago truncatula cDNA cl... 137 5e-41  
20 emb|AF085168|AF085168 Triticum aestivum receptor-like protein ki... 68 6e-41  
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emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycop... 127 2e-40  
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gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 96 2e-40  
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gb|U82975|CSU82975 Citrus sinensis pectinesterase (PECS-2.1) gen... 421 e-116  
45 emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 208 e-111  
emb|AF229849|AF229849 Vigna radiata pectin methylesterase isoform... 208 e-107  
gb|U49330|SLU49330 Solanum lycopersicum pectin methylesterase (P... 205 e-106  
emb|Z71752|NPPME2MR N.plumbaginifolia mRNA for pectin methyleste... 177 e-104  
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50 emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. 175 e-100  
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emb|AF056493|AF056493 Pisum sativum pectin methylesterase mRNA, ... 163 3e-95  
emb|AF152171|AF152171 Solanum tuberosum cultivar Desiree pectin ... 190 2e-94  
emb|AJ249786|NTA249786 Nicotiana tabacum partial mRNA for pectin... 192 4e-94  
55 emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 190 5e-94  
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emb|X74639|LEPEC2 L.esculentum mRNA for pectin esterase clone. 188 3e-93  
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60 gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 190 8e-93  
emb|X07910|LEPECES Tomato mRNA for pectin esterase. 190 1e-92



- emb|A15983|A15983 *L. esculentum* mRNA for pectin esterase. 190 1e-92  
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 emb|Z71754|NPPME4MR *N. plumbaginifolia* mRNA for pectin methyleste... 177 2e-92  
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 5 emb|A24196|A24196 *L. esculentum* pectin esterase clone pPE1. 188 7e-92  
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 10 emb|AB029461|AB029461 *Salix gilgiana* SgPME1 mRNA for pectin meth... 144 1e-82  
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 30 emb|AW760550|AW760550 sl51g07.y1 Gm-c1027 Glycine max cDNA clone... 155 2e-67  
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 40 emb|AW774519|AW774519 EST333670 KV3 *Medicago truncatula* cDNA clo... 137 3e-63  
 emb|AW706153|AW706153 sj52e04.y1 Gm-c1033 Glycine max cDNA clone... 242 5e-63  
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 45 emb|AW758821|AW758821 NXNV\_091\_A04\_F Nsf Xylem Normal wood Verti... 160 8e-62  
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 55 emb|AW620942|AW620942 sj95g05.y1 Gm-c1023 Glycine max cDNA clone... 164 1e-58  
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 60 emb|AW041247|AW041247 EST284111 tomato mixed elicitor, BTI Lycop... 135 7e-58  
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emb|X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 156 6e-55  
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45 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 227 5e-91  
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 5 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 156 7e-75  
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 20 emb|AW922776|AW922776 DG1\_46\_C01.g1\_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65  
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 25 emb|AI055037|AI055037 coau0002N18 Cotton Boll Abscission Zone cD... 111 3e-60  
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 gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59  
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 30 emb|AW922735|AW922735 DG1\_45\_B06.g1\_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58  
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 35 emb|Z78202|PACHII Persea americana mRNA for endochitinase. 118 4e-57  
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 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56  
 emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56  
 40 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56  
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 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 105 4e-55  
 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 109 6e-55  
 45 emb|AW745819|AW745819 WS1\_37\_H11.g1\_A002 Water-stressed 1 (WS1) ... 214 7e-55  
 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54  
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54  
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54  
 emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54  
 50 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54  
 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53  
 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 105 1e-53  
 emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53  
 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53  
 55 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53  
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 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53  
 emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52  
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 60 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51  
 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51



emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 108 2e-51  
 emb|AF043248|AF043248 Solanum tuberosum class I chitinase (ChtC2... 100 3e-51  
 gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 112 4e-51  
 gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 112 4e-51  
 5 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 102 7e-51  
 gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50  
 emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase I (p... 107 2e-50  
 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50  
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50  
 10 emb|X63899|PSCHITIN P.sativum mRNA for chitinase. 94 1e-49  
 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49  
 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48  
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48  
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48  
 15 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48

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 20 /blast\_score 1.00e-166 /ec\_number /family /chip\_nova /gb\_link /ncgi

(825 letters)

Database: plantfungal  
 25 661,018 sequences; 426,114,510 total letters

Searching.....done

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	(bits)	Value	
30	Sequences producing significant alignments:		
	emb X57187 PVCHITIN P.vulgaris mRNA for chitinase.	238 e-123	
	gb U97522 VVU97522 Vitis vinifera class IV endochitinase (VvChi4...	248 e-112	
	emb X88803 VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p...	201 e-107	
35	gb U97521 VVU97521 Vitis vinifera class IV endochitinase (VvChi4...	247 1e-97	
	dbj D45183 D45183 Chenopodium amaranticolor mRNA for chitinase, ...	197 8e-96	
	dbj D45182 D45182 Chenopodium amaranticolor mRNA for chitinase, ...	136 6e-95	
	dbj D45181 D45181 Chenopodium amaranticolor mRNA for chitinase, ...	136 4e-94	
	emb AF112966 AF112966 Triticum aestivum chitinase IV precursor (...)	227 5e-91	
40	gb U52845 DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP...	143 5e-91	
	emb AI897733 AI897733 EST267176 tomato ovary, TAMU Lycopersicon ...	164 1e-90	
	gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3...	137 3e-90	
	gb U52846 DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP...	142 4e-90	
	emb AI897843 AI897843 EST267286 tomato ovary, TAMU Lycopersicon ...	158 2e-89	
45	gb U52847 DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP...	133 4e-89	
	emb X61488 BNCHITIN B.napus mRNA for chitinase.	181 5e-85	
	emb Z46948 SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re...	166 2e-84	
	emb AI897217 AI897217 EST266756 tomato ovary, TAMU Lycopersicon ...	164 2e-84	
	gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds.	185 9e-83	
50	emb X75945 BVCH4RNA B.vulgaris Ch4 mRNA for chitinase.	127 8e-80	
	emb A23392 A23392 B.vulgaris mRNA for chitinase 4 (B15).	127 8e-80	
	emb AI898279 AI898279 EST267722 tomato ovary, TAMU Lycopersicon ...	126 2e-78	
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55	emb AW691007 AW691007 NF036E09ST1F1000 Developing stem Medicago ...	131 5e-78	
	emb AW030814 AW030814 EST274069 tomato callus, TAMU Lycopersicon...	126 1e-77	
	emb AW035013 AW035013 EST279284 tomato callus, TAMU Lycopersicon...	126 2e-77	
	emb AI485982 AI485982 EST244303 tomato ovary, TAMU Lycopersicon ...	126 2e-77	
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	dbj D45184 D45184 Chenopodium amaranticolor mRNA for chitinase, ...	136 2e-76	
60	gb BE034975 BE034975 ML07H10 ML Mesembryanthemum crystallinum cD...	156 7e-75	
	emb AF090336 AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA...	215 1e-74	

- gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 160 1e-74  
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emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 139 1e-74  
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5 gb|L42467|PLACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74  
emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72  
emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71  
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70  
gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68  
10 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68  
gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67  
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emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66  
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15 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64  
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emb|AW680953|AW680953 WS1\_9\_A06.b1\_A002 Water-stressed 1 (WS1) S... 224 7e-63  
emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 121 1e-61  
emb|AI055037|AI055037 coau0002N18 Cotton Boll Abscission Zone cD... 111 3e-60  
20 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60  
gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59  
emb|AW924422|AW924422 WS1\_69\_C06.b1\_A002 Water-stressed 1 (WS1) ... 171 4e-59  
emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58  
emb|AW922735|AW922735 DG1\_45\_B06.g1\_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58  
25 emb|AW746695|AW746695 WS1\_54\_E02.g1\_A002 Water-stressed 1 (WS1) ... 224 6e-58  
gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57  
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57  
emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57  
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30 emb|AW746018|AW746018 WS1\_38\_H11.g1\_A002 Water-stressed 1 (WS1) ... 221 4e-57  
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56  
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56  
emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56  
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35 emb|AW924229|AW924229 WS1\_51\_H04.b1\_A002 Water-stressed 1 (WS1) ... 215 3e-55  
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emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 105 4e-55  
emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 109 6e-55  
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40 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54  
emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54  
gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54  
emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54  
gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54  
45 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53  
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emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53  
gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53  
gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53  
50 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53  
emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53  
emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52  
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55 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51  
emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 108 2e-51  
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gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 112 4e-51  
60 emb|Z54234|VVCHITIMR V.vinifera mRNA for chitinase. 102 7e-51  
gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50

emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 107 2e-50  
 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50  
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50  
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 5 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49  
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 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48  
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48  
 10 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48

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 gb|aaa32738.1| (m92353) anthranilate synthase alpha subunit  
 [arabidopsis thaliana] /blast\_score 0 /ec\_number /family /chip nova  
 15 /gb\_link /ncgi  
 (1788 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters  
 20

Searching.....done

	Score	E
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emb AL031966 SPCC1442 S.pombe chromosome III cosmid c1442.	209	6e-69
emb AW651095 AW651095 EST329549 tomato germinating seedlings, TA...	222	2e-64
dbj D89256 D89256 Schizosaccharomyces pombe mRNA, partial cds, c...	205	5e-64
emb AW982499 AW982499 HVSMEg0003G22f Hordeum vulgare pre-anthesi...	215	2e-58
35 emb AW460005 AW460005 si07d11.y1 Gm-c1029 Glycine max cDNA clone...	116	1e-57
gb U18839 SCE9747 Saccharomyces cerevisiae chromosome V cosmids ...	123	4e-48
emb X68327 SCTRP2 S.cerevisiae TRP2 gene for anthranilate syntha...	123	4e-48
emb AW719463 AW719463 LjNEST5b1r Lotus japonicus nodule library,...	184	1e-45
emb AI736775 AI736775 sb33d01.y1 Gm-c1012 Glycine max cDNA clone...	104	2e-40
40 gb K01388 YSCTRP2 Yeast (S.cerevisiae) TRP2 gene coding for anth...	122	4e-38
emb AL032684 SPBP8B7 S.pombe chromosome II p1 p8B7.	95	6e-25
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45 emb AF119554 AF119554 Plasmodium falciparum para-aminobenzoic ac...	67	6e-10
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	emb AW680905 AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S...	35	1.4
	emb AW679666 AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ...	35	1.4
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20	emb AI959816 AI959816 sc94f02.y1 Gm-c1019 Glycine max cDNA clone...	35	1.9
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	emb AW696796 AW696796 NF109A07ST1F1052 Developing stem Medicago ...	35	1.9
	emb AW396753 AW396753 sf37c11.x1 Gm-c1028 Glycine max cDNA clone...	35	2.6
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	emb AW348617 AW348617 GM210002B22G1R Gm-r1021 Glycine max cDNA 3...	35	2.6
	emb AW310362 AW310362 sf35a09.x1 Gm-c1028 Glycine max cDNA clone...	35	2.6
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30	gb BE023927 BE023927 sm94c05.y1 Gm-c1015 Glycine max cDNA clone ...	35	2.6
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	emb AW309356 AW309356 sf16d02.x1 Gm-c1028 Glycine max cDNA clone...	35	2.6
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	emb AW222457 AW222457 EST299268 tomato fruit red ripe, TAMU Lyco...	33	9.2
	emb AB012116 AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl...	33	9.2
	emb AW725836 AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa ...	33	9.2
60	emb AQ324451 AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P...	33	9.2
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN...	33	9.2

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 emb|AI166186|AI166186 a032p32u Hybrid aspen plasmid library Popu... 33 9.2  
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 (1342 letters)

Database: plantfungal  
 15 661,018 sequences; 426,114,510 total letters

Searching.....done

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20	Sequences producing significant alignments:			
	emb AI729480 AI729480 BNLGHi13474 Six-day Cotton fiber Gossypium...	365	e-116	
	emb AW032260 AW032260 EST275714 tomato callus, TAMU Lycopersicon...	336	2e-91	
	emb AW719468 AW719468 LjNEST5c2r Lotus japonicus nodule library,...	297	2e-79	
25	emb AW729492 AW729492 GA__Ea0025C18 Gossypium arboreum 7-10 dpa ...	291	8e-78	
	emb AW924000 AW924000 WS1_32_E10.b1_A002 Water-stressed 1 (WS1) ...	277	1e-73	
	emb AW042762 AW042762 ST25B02 Pine TriplEx shoot tip library Pin...	268	2e-72	
	emb AW755778 AW755778 sl09c05.y1 Gm-cl036 Glycine max cDNA clone...	248	1e-64	
	emb AW737762 AW737762 EST339189 tomato flower buds, anthesis, Co...	169	1e-60	
30	emb AW621695 AW621695 EST312493 tomato root during/after fruit s...	206	3e-52	
	emb AW350933 AW350933 GM210010B10D11R Gm-r1021 Glycine max cDNA ...	203	3e-51	
	emb AI166669 AI166669 xylem.est.479 Poplar xylem Lambda ZAPII li...	144	3e-50	
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35	emb AI774565 AI774565 EST255665 tomato resistant, Cornell Lycope...	192	7e-48	
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	emb AW034075 AW034075 EST277570 tomato callus, TAMU Lycopersicon...	150	2e-35	
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	gb L20634 POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb...	36	1e-04
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	emb AI487017 AI487017 EST245339 tomato ovary, TAMU Lycopersicon ...	36	1e-04
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60	emb AF083814 AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR...	39	0.11
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(1752 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|A92838|A92838 Sequence 12 from Patent WO9804586. 258 e-123

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emb|AW934153|AW934153 EST359996 tomato fruit mature green, TAMU... 235 4e-74

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emb|AI054629|AI054629 coau0001J02 Cotton Boll Abscission Zone cD... 133 2e-44

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emb|AV426381|AV426381 AV426381 Lotus japonicus young plants (two... 145 3e-43

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 60 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi)  
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(1125 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb Y11485 TAESERPIN T.aestivum mRNA for serpin WZS2.	116	2e-62
15	emb Z49890 TAWZCISPIN T.aestivum WZCI mRNA for serpin.	109	3e-60
	emb X95277 HVSEH H.vulgare mRNA for serpin.	98	6e-58
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45	emb AI210660 AI210660 k0b03a1.r1 Aspergillus nidulans 24hr asexu...	53 1e-07
	emb AA785435 AA785435 g7d04a1.r1 Aspergillus nidulans 24hr asexu...	54 2e-07
	emb AA787768 AA787768 r1d06a1.r1 Aspergillus nidulans 24hr asexu...	46 2e-06
	emb AA784794 AA784794 g2d07a1.r1 Aspergillus nidulans 24hr asexu...	43 2e-06
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	gb U60806 CIU60806 Coccidioides immitis complement-fixation chit...	44 5e-06
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	emb X07127 KLK1P Kluyveromyces lactis killer plasmid k1 DNA.	39 1e-04

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40	emb AW145916 AW145916 ga35g12.y1 Moss EST library PPN Physcomitr...	34	5.5
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60	emb Y08926 PFAARP1PR P.falciparum mRNA for AARP1 protein, partial.	33	7.6
	emb AV410224 AV410224 AV410224 Lotus japonicus young plants (two...	33	7.6

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 emb|AQ944606|AQ944606 Sheared DNA-48P15.TR Sheared DNA Trypanoso... 28 8.4  
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10

(864 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

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 emb|AB000451|AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com... 74 5e-29  
 emb|AW685937|AW685937 NF031H10NR1F1000 Nodulated root Medicago t... 76 9e-29  
 emb|AB006599|AB006599 Petunia x hybrida mRNA for ZPT2-12, comple... 77 1e-28  
 emb|AB006601|AB006601 Petunia x hybrida mRNA for ZPT2-14, comple... 72 2e-26  
 25 emb|AI898309|AI898309 EST267752 tomato ovary, TAMU Lycopersicon ... 68 3e-26  
 emb|AI485362|AI485362 EST243683 tomato ovary, TAMU Lycopersicon ... 67 1e-25  
 emb|AI483886|AI483886 EST249757 tomato ovary, TAMU Lycopersicon ... 68 1e-25  
 emb|AW030869|AW030869 EST274159 tomato callus, TAMU Lycopersicon... 68 5e-24  
 emb|AI966235|AI966235 sc35g05.y1 Gm-c1014 Glycine max cDNA clone... 72 3e-23  
 30 emb|AB006603|AB006603 Petunia x hybrida mRNA for ZPT2-8, complet... 65 1e-22  
 emb|AI486627|AI486627 EST244948 tomato ovary, TAMU Lycopersicon ... 61 1e-22  
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5 (1890 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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15	emb AJ224518 CAR224518 Cicer arietinum mRNA for LEA protein (clo...	126	2e-28
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	emb AW395529 AW395529 sg72c09.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24
	emb AW507599 AW507599 si53h08.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW318205 AW318205 sg62d04.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24
20	emb AW568476 AW568476 si59c06.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW567816 AW567816-si66b10.y1-Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW706800 AW706800 sk03e03.y1 Gm-c1023 Glycine max cDNA clone...	88	1e-23
	emb AW509384 AW509384 si22d10.y1 Gm-c1029 Glycine max cDNA clone...	86	2e-23
	emb AW746690 AW746690 WS1_54_F07.g1_A002 Water-stressed 1 (WS1) ...	106	2e-22
25	emb AW096396 AW096396 EST289576 tomato mixed elicitor, BTI Lycop...	103	1e-21
	emb X78205 HVVHVA1 H.vulgare (Himalaya) HVA1 gene.	77	1e-20
	emb X13498 HVABAIP Barley pHVA1 mRNA for an ABA-inducible protein.	77	1e-20
	gb M36000 BLYABA Barley abscisic acid (ABA) mRNA, complete cds.	77	1e-20
	emb AW680076 AW680076 WS1_3_C03.g1_A002 Water-stressed 1 (WS1) S...	100	2e-20
30	emb AW397921 AW397921 sg69h06.y1 Gm-c1007 Glycine max cDNA clone...	57	3e-20
	emb AW747095 AW747095 WS1_65_C09.g1_A002 Water-stressed 1 (WS1) ...	95	4e-19
	gb BE034388 BE034388 MH04B06 MH Mesembryanthemum crystallinum cD...	73	1e-18
	emb X13201 GHLEA7 Cotton set 5A Lea gene for seed protein D-7.	61	1e-18
	emb X15086 GHLEA29R Cotton set 5A Lea mRNA for seed protein D-29.	61	1e-18
35	emb X56882 TA3LEA Wheat mRNA for a group 3 late embryogenesis ab...	75	1e-18
	emb AW746385 AW746385 WS1_49_G03.g1_A002 Water-stressed 1 (WS1) ...	93	2e-18
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	emb AF255052 AF255052 Triticum aestivum cold-responsive LEA/RAB-...	85	6e-17
	emb AF139915 AF139915 Triticum aestivum ABA-inducible protein WR...	85	6e-17
40	emb AW164114 AW164114 Ljirnp20-575-b9 Ljirnp Lambda HybriZap ...	88	7e-17
	emb Y10779 SSY10779 S.stapfianus pSD.42 mRNA.	86	3e-16
	emb AW569002 AW569002 si62c03.y1 Gm-r1030 Glycine max cDNA clone...	62	4e-16
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	gb M80664 SOYLEAB Soybean late embryogenesis abundant (LEA) prot...	58	9e-08
60	emb AF166485 AF166485 Glycine max maturation protein pPM32 (PM32...	57	2e-07
	gb M19388 COTSPG G.hirsutum (cotton) storage protein (late embry...	57	2e-07



	gb U47096 DCU47096 <i>Daucus carota</i> LEA protein mRNA, somatic embry...	57	2e-07
	gb U02966 GMU02966 <i>Glycine max</i> Shi-shi 51 kDa seed maturation pr...	56	3e-07
	emb Z49715 PMDORORF8 <i>P.menziesii</i> mRNA (open reading frame) (DF77D).	56	4e-07
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	emb X92955 BOPC15 <i>B.oleracea</i> mRNA for pollen coat protein.	51	1e-05
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	emb AW678045 AW678045 WS1_13_A03.b1_A002 Water-stressed 1 (WS1) ...	50	2e-05
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	emb AJ000100 HVAJ100 <i>Hordeum vulgare</i> mRNA for cold-regulated pro...	39	4e-05
25	emb AJ130888 FSY130888 <i>Fagus sylvatica</i> mRNA for ABA-inducible pr...	49	4e-05
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55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708|/ncgi)  
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(885 letters)

60 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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	emb AI486681 AI486681	EST245003	tomato ovary, TAMU Lycopersicon ...	414 e-115
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	emb AW564397 AW564397	LG1_292_F08.b1_A002	Light Grown 1 (LG1) So...	275 2e-73
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15	emb AW309188 AW309188	sg05d07.y1	Gm-c1019 Glycine max cDNA clone...	274 8e-73
	emb AW329561 AW329561	N200812e	rootphos(-) Medicago truncatula c...	204 3e-69
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	emb AI898201 AI898201	EST267644	tomato ovary, TAMU Lycopersicon ...	118 1e-51
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	emb AW622515 AW622515	EST313315	tomato root during/after fruit s...	189 3e-47
	emb AW933718 AW933718	EST359561	tomato fruit mature green, TAMU ...	188 7e-47
	emb AI897919 AI897919	EST267362	tomato ovary, TAMU Lycopersicon ...	102 6e-45
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55	emb Z49259 SC9582X	S.cerevisiae chromosome XIII cosmid 9582.		55 9e-08
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 (2633 letters)

55 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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Database: plantfungal

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20	emb Z29537 NTPROTINH N.tabacum (Samsun NN) gene for proteinase i...	32	9.4
	emb AF155848 AF155848 Lysinema ciliatum chloroplast atpB-rbcL in...	32	9.4
	gb U38804 PPU38804 Porphyra purpurea chloroplast, complete genome.	32	9.4
	emb AW333913 AW333913 S27H9 AGS-1 Pneumocystis carinii f. sp. ca...	32	9.4
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25	emb AF102653 AF102653 Podranea ricasoliana ribulose 1,5-bisphosp...	32	9.4
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments: (bits) Value

45	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	375	e-120
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	332	e-105
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	339	e-105
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	330	e-105
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	333	e-104
50	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	332	e-104
	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	328	e-103
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	329	e-100
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	321	1e-99
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	316	2e-98
55	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	323	2e-98
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	324	4e-98
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	195	4e-97
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	312	4e-95
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	314	4e-95
60	emb AW620957 AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone...	285	3e-94
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 35 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 231 2e-59  
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 20 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 177 2e-43  
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 30 http://www.ncgr.org/cgi-bin/ff?ac002392  
 (2631 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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	emb AW774582 AW774582	EST333733 KV3 Medicago truncatula cDNA clo...	204 5e-74
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	emb Z73295 CRPK1	C. roseus mRNA for receptor-like protein kinase.	146 5e-56
	emb AF220602 AF220602	Lycopersicon pimpinellifolium Rio Grande 7...	112 7e-54
45	gb U59317 LPU59317	Lycopersicon pimpinellifolium serine/threonin...	108 7e-54
	gb U13923 LEU13923	Lycopersicon pimpinellifolium serine/threonin...	108 7e-54
	emb AW222552 AW222552	EST299363 tomato fruit-red ripe, TAMU Lyco...	210 3e-53
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50	emb AW200786 AW200786	se93e06.y1 Gm-c1027 Glycine max cDNA clone...	206 5e-52
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	emb AF108892 AF108892	AF108892 Capsicum annuum root 1st-branched...	194 3e-48
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	gb U59315 LPU59315	Lycopersicon pimpinellifolium serine/threonin...	103 1e-47
60	gb U02271 LEU02271	Lycopersicon pimpinellifolium Rio Grande-PtoR...	103 1e-47
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5 emb|AF053127|AF053127 Malus domestica leucine-rich receptor-like... 130 4e-46  
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10 emb|AI736063|AI736063 sb22d04.y1 Gm-c1007 Glycine max cDNA clone... 147 6e-46  
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 (1008 letters)

25 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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30 Score E  
 Sequences producing significant alignments: (bits) Value

- emb|AF135130|AF135130 Arabis holboellii from Denmark class I chi... 438 0.0  
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 35 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 494 e-158  
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 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 493 e-158  
 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 541 e-153  
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 40 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 482 e-151  
 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 442 e-150  
 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 443 e-150  
 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 442 e-149  
 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 440 e-148  
 45 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 467 e-148  
 gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 310 e-146  
 gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 310 e-146  
 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 309 e-146  
 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 472 e-146  
 50 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 463 e-146  
 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 286 e-145  
 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 305 e-144  
 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 466 e-144  
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 332 e-144  
 55 emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 333 e-144  
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 469 e-144  
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 435 e-143  
 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 284 e-143  
 emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 296 e-143  
 60 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 459 e-141  
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 455 e-140



- gb|M94105|ALCCHITIN *Allium sativum* chitinase mRNA, 3' end. 448 e-140  
 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 286 e-139  
 emb|AF000964|AF000964 *Poa pratensis* chitinase (Chi1) gene, compl... 408 e-139  
 gb|L34211|BLYCHI33A *Hordeum vulgare* chitinase (CHI33) gene, comp... 448 e-138  
 5 gb|U02608|STU02608 *Solanum tuberosum* chitinase (chtB4) mRNA, par... 408 e-137  
 emb|X63899|PSCHITIN *P. sativum* mRNA for chitinase. 270 e-135  
 emb|AF061805|AF061805 *Elaeagnus umbellata* acidic chitinase mRNA,... 430 e-134  
 emb|AF202731|AF202731 *Glycine max* endochitinase homolog (Chn1) m... 273 e-134  
 gb|L34210|BLYCHI26A *Hordeum vulgare* chitinase (CHI26) gene, comp... 475 e-133  
 10 emb|A37990|A37990 Sequence 9 from Patent EP0616035. 475 e-133  
 gb|M62904|BLYCHI H.vulgare L. 26kD chitinase mRNA, complete cds. 475 e-133  
 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 265 e-132  
 gb|U30324|TCU30324 *Theobroma cacao* class I chitinase gene, compl... 238 e-131  
 emb|X95610|CSHITB *C. sativa* mRNA for chitinase Ib. 259 e-130  
 15 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 259 e-130  
 emb|AF141372|AF141372 *Petroselinum crispum* chitinase precursor (... 463 e-130  
 emb|AF135137|AF135137 *Arabis fecunda* country USA class I chitina... 459 e-128  
 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 297 e-128  
 emb|AB023464|AB023464 *Arabis gemmifera* ChiB gene for basic endoc... 455 e-127  
 20 emb|AF135152|AF135152 *Arabis parishii* country USA class I chitin... 455 e-127  
 emb|AF135141|AF135141 *Arabis gunnisoniana* class I chitinase gene... 455 e-127  
 emb|AF135135|AF135135 *Arabis drummondii* class I chitinase gene, ... 455 e-127  
 emb|AF135143|AF135143 *Arabis lemmonii* country USA class I chitin... 452 e-126  
 emb|X67693|STMREN *S. tuberosum* mRNA for endochitinase. 452 e-126  
 25 emb|AF135132|AF135132 *Arabis gunnisoniana* from USA class I chiti... 452 e-126  
 emb|AF135144|AF135144 *Arabis lemmonii* country USA class I chitin... 451 e-126  
 emb|AF135140|AF135140 *Arabis glabra* country USA class I chitinas... 449 e-125  
 gb|U30465|LEU30465 *Lycopersicon esculentum* class II chitinase (C... 447 e-125  
 emb|AF135153|AF135153 *Arabis parishii* country USA class I chitin... 445 e-124  
 30 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (pHS2) mRNA, compl... 295 e-124  
 emb|AF135148|AF135148 *Arabis lyallii* class I chitinase gene, par... 444 e-124  
 emb|AF135151|AF135151 *Arabis microphylla* country USA class I chi... 444 e-124  
 emb|AF135150|AF135150 *Arabis microphylla* country USA class I chi... 443 e-124  
 emb|AF135147|AF135147 *Arabis lignifera* country USA class I chiti... 443 e-124  
 35 emb|AF135136|AF135136 *Arabis fecunda* country USA class I chitina... 443 e-124  
 emb|AF135145|AF135145 *Arabis lignifera* country USA class I chiti... 443 e-123  
 emb|AF135146|AF135146 *Arabis lignifera* country USA class I chiti... 441 e-123  
 emb|AF135149|AF135149 *Arabis microphylla* class I chitinase gene,... 441 e-123  
 emb|AF043247|AF043247 *Solanum tuberosum* class I chitinase (ChtC1... 431 e-122  
 40 emb|AF043248|AF043248 *Solanum tuberosum* class I chitinase (ChtC2... 431 e-122  
 emb|Z15138|LECHI14 *L. esculentum* mRNA for chitinase (partial). 439 e-122  
 emb|AF135142|AF135142 *Halimolobos perplexa* var. *perplexa* class I... 435 e-121  
 emb|AF135134|AF135134 *Arabis blepharophylla* class I chitinase ge... 434 e-121  
 gb|U01660|U01660 *Populus trichocarpa* x *Populus deltoides* acidic ... 207 e-121  
 45 emb|AF135138|AF135138 *Arabis glabra* country USA class I chitinas... 431 e-120  
 emb|AF135133|AF135133 *Arabis blepharophylla* country USA class I ... 423 e-118  
 gb|M95835|BNACH25A *Brassica napus* (clone BnCh25) endochitinase g... 422 e-117  
 emb|AW034530|AW034530 EST278146 tomato callus, TAMU *Lycopersicon*... 418 e-116  
 emb|AW560048|AW560048 EST315096 DSIR *Medicago truncatula* cDNA cl... 350 e-112  
 50 emb|AW687771|AW687771 NF013C08RT1F1065 Developing root *Medicago* ... 311 e-111  
 emb|AW033115|AW033115 EST276674 tomato callus, TAMU *Lycopersicon*... 391 e-108  
 emb|AW034645|AW034645 EST278376 tomato callus, TAMU *Lycopersicon*... 366 e-106  
 emb|AF082713|AF082713 AF082713 *Capsicum annuum* leaf mRNA *Capsicu*... 364 e-106  
 emb|AW738053|AW738053 EST339480 tomato flower buds, anthesis, Co... 379 e-104  
 55 emb|AF141373|AF141373 *Petroselinum crispum* chitinase precursor (... 237 e-104  
 emb|Z70032|CSACHIT2 *C. sinensis* mRNA for class II acidic chitinase. 197 e-104  
 emb|AW030745|AW030745 EST274000 tomato callus, TAMU *Lycopersicon*... 360 e-104  
 emb|AF141374|AF141374 *Petroselinum crispum* chitinase precursor (... 237 e-104  
 emb|AW033034|AW033034 EST276593 tomato callus, TAMU *Lycopersicon*... 367 e-103  
 60 emb|AW216454|AW216454 EST295084 tomato callus, TAMU *Lycopersicon*... 373 e-102  
 emb|AW267781|AW267781 EST305909 DSIR *Medicago truncatula* cDNA cl... 316 e-102

emb|AW033757|AW033757 EST277328 tomato callus, TAMU Lycopersicon... 285 e-101  
 emb|AW037673|AW037673 EST279276 tomato mixed elicitor, BTI Lycop... 281 e-100  
 emb|AW216787|AW216787 EST295501 tomato callus, TAMU Lycopersicon... 364 e-100  
 emb|AI771248|AI771248 EST252264 tomato ovary, TAMU Lycopersicon ... 363 1e-99  
 5 emb|AW031102|AW031102 EST274409 tomato callus, TAMU Lycopersicon... 275 1e-98  
 emb|X15349|HVENDCHT Barley (H. vulgare) mRNA for endochitinase. 359 2e-98  
 emb|AW622028|AW622028 EST312826 tomato root during/after fruit s... 269 9e-97  
 emb|Z15139|LECHI17 L. esculentum mRNA for chitinase. 242 2e-96  
 emb|AW032161|AW032161 EST275615 tomato callus, TAMU Lycopersicon... 334 2e-96  
 10 emb|AW560177|AW560177 EST315225 DSIR Medicago truncatula cDNA cl... 295 1e-95

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 [arabidopsis thaliana] /blast\_score 0 /ec\_number /family /chip nova  
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 (1881 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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	Score	E	(bits)	Value
25	Sequences producing significant alignments:			
	gb U79958 PSU79958	Pisum sativum BP-80 vacuolar sorting receptor...	810	0.0
	emb AB006809 AB006809	Cucurbita sp. mRNA for PV72, complete cds.	780	0.0
	emb AW267745 AW267745	EST305873 DSIR Medicago truncatula cDNA cl...	453	e-126
	emb AW931583 AW931583	EST357426 tomato fruit mature green, TAMU ...	308	e-112
30	emb AW309187 AW309187	sg05d06.y1 Gm-cl019 Glycine max cDNA clone...	405	e-112
	gb BE054150 BE054150	GA_Ea0034H17f Gossypium arboreum 7-10 dpa ...	398	e-110
	emb AW622833 AW622833	EST306903 tomato flower buds 3-8 mm, Corne...	387	e-106
	emb AW689392 AW689392	NF018F12ST1F1000 Developing stem Medicago ...	371	e-102
	emb AW737948 AW737948	EST339375 tomato flower buds, anthesis, Co...	342	3e-94
35	emb AW774434 AW774434	EST333585 KV3 Medicago truncatula cDNA clo...	263	2e-90
	emb AW932529 AW932529	EST358372 tomato fruit mature green, TAMU ...	326	3e-88
	emb AW615949 AW615949	EST325315 tomato flower buds 0-3 mm, Corne...	216	1e-87
	emb AI728635 AI728635	BNLGH11276 Six-day Cotton fiber Gossypium...	281	8e-84
	emb AI782787 AI782787	EST263666 tomato susceptible, Cornell Lyco...	307	2e-82
40	emb AI443067 AI443067	sa47a01.y1 Gm-cl1004 Glycine max cDNA clone...	305	6e-82
	emb AW747297 AW747297	WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ...	292	8e-78
	emb AI727826 AI727826	BNLGH19195 Six-day Cotton fiber Gossypium ...	280	1e-77
	emb AI484571 AI484571	EST242801 tomato ovary, TAMU Lycopersicon ...	284	1e-75
	emb AW685785 AW685785	NF030C07NR1F1000 Nodulated root Medicago t...	166	1e-71
45	emb AV406766 AV406766	AV406766 Lotus japonicus young plants (two...	260	2e-68
	emb AW509740 AW509740	ga63h11.y1 Moss EST library PPU Physcomitr...	232	1e-65
	emb AV428420 AV428420	AV428420 Lotus japonicus young plants (two...	249	4e-65
	emb AW695542 AW695542	NF096C05ST1F1037 Developing stem Medicago ...	124	1e-58
	emb AW289687 AW289687	NXNV004E04F Nsf Xylem Normal wood Vertical...	226	4e-58
50	emb AW064744 AW064744	ST35C06 Pine TriplEx shoot tip library Pin...	198	2e-56
	emb AW309191 AW309191	sg05d10.y1 Gm-cl019 Glycine max cDNA clone...	171	3e-52
	emb AW096632 AW096632	EST289812 tomato mixed elicitor, BTI Lycop...	165	7e-52
	emb AW568619 AW568619	si60a11.y1 Gm-r1030 Glycine max cDNA clone...	205	1e-51
	emb AF209910 AF209910	Prunus dulcis vacuolar sorting receptor pr...	160	5e-51
55	emb AW623959 AW623959	EST321904 tomato flower buds 3-8 mm, Corne...	75	1e-50
	emb AW397829 AW397829	sg68h03.y1 Gm-cl1007 Glycine max cDNA clone...	201	2e-50
	emb AW256542 AW256542	EST304679 KV2 Medicago truncatula cDNA clo...	151	2e-50
	emb AI967865 AI967865	Ljimp14-100-E3 Ljimp Lambda HybriZap ...	197	3e-49
	emb AW680054 AW680054	WS1_3_A01.g1_A002 Water-stressed 1 (WS1) S...	150	6e-47
60	emb AA660289 AA660289	00158 MtRHE Medicago truncatula cDNA 5', m...	107	9e-44
	emb AW056624 AW056624	ST53G07 Pine TriplEx shoot tip library Pin...	178	1e-43

- emb|AW690002|AW690002 NF026G04ST1F1000 Developing stem Medicago ... 109 2e-43  
 emb|AW290400|AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical... 177 3e-43  
 emb|AI162330|AI162330 A016P01U Hybrid aspen plasmid library Popu... 131 2e-39  
 emb|AI161766|AI161766 A006P54U Hybrid aspen plasmid library Popu... 93 3e-38  
 5 emb|AW737369|AW737369 EST338892 tomato flower buds, anthesis, Co... 149 5e-35  
 gb|BE125908|BE125908 DG1\_59\_E01.b1\_A002 Dark Grown 1 (DG1) Sorgh... 149 5e-35  
 emb|AW201441|AW201441 sf03b09.y1 Gm-c1027 Glycine max cDNA clone... 113 1e-34  
 emb|AW398931|AW398931 EST309431 L. pennellii trichome, Cornell U... 95 2e-34  
 gb|BE049814|BE049814 NXNV\_144\_F04\_F Nsf Xylem Normal wood Vertic... 143 6e-33  
 10 emb|AW126100|AW126100 N100297e rootphos(-) Medicago truncatula c... 100 5e-30  
 emb|AW508719|AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone... 125 1e-27  
 gb|L38113|L38113 BNAF0628E Mustard flower buds Brassica rapa cDN... 117 4e-26  
 emb|AW317388|AW317388 sg48g10.y1 Gm-c1025 Glycine max cDNA clone... 80 1e-25  
 emb|AW706755|AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone... 118 2e-25  
 15 emb|AA660955|AA660955 00852 MtRHE Medicago truncatula cDNA 5' si... 74 7e-25  
 emb|AW616461|AW616461 EST322872 L. hirsutum trichome, Cornell Un... 69 2e-24  
 emb|AW348825|AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3... 68 8e-24  
 emb|AW932524|AW932524 EST358367 tomato fruit mature green, TAMU ... 80 1e-23  
 emb|AW774190|AW774190 EST333273 KV3 Medicago truncatula cDNA clo... 101 2e-20  
 20 emb|AW125944|AW125944 N100139e rootphos(-) Medicago truncatula c... 66 6e-20  
 emb|AW093844|AW093844 EST287024 tomato mixed elicitor, BTI Lycop... 96 7e-19  
 emb|AW906386|AW906386 EST342508 potato stolon, Cornell Universit... 67 2e-16  
 gb|BE060808|BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis... 87 4e-16  
 emb|AW620693|AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone... 76 1e-15  
 25 emb|AW256398|AW256398 EST304465 KV2 Medicago truncatula cDNA clo... 74 6e-14  
 emb|AW037563|AW037563 EST278890 tomato mixed elicitor, BTI Lycop... 79 8e-14  
 emb|AW691052|AW691052 NF037B05ST1F1000 Developing stem Medicago ... 72 4e-13  
 emb|AW686287|AW686287 NF040A08NR1F1000 Nodulated root Medicago t... 77 4e-13  
 emb|AW685952|AW685952 NF036G09NR1F1000 Nodulated root Medicago t... 46 2e-11  
 30 emb|AW760128|AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone... 58 1e-10  
 emb|AW119909|AW119909 sd54d08.y1 Gm-c1016 Glycine max cDNA clone... 66 8e-10  
 emb|AI794754|AI794754 sb68f11.y1 Gm-c1019 Glycine max cDNA clone... 64 4e-09  
 emb|AW774852|AW774852 EST334003 KV3 Medicago truncatula cDNA clo... 64 4e-09  
 emb|AW127457|AW127457 M110648 DSIL Medicago truncatula cDNA clon... 58 3e-07  
 35 emb|AW443352|AW443352 EST308282 tomato mixed elicitor, BTI Lycop... 56 1e-06  
 emb|AW747372|AW747372 WS1\_67\_G06.g1\_A002 Water-stressed 1 (WS1) ... 55 2e-06  
 emb|AI939286|AI939286 sc69h02.y1 Gm-c1016 Glycine max cDNA clone... 46 0.001  
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 40 gb|BE035779|BE035779 MO16H05 MO Mesembryanthemum crystallinum cD... 36 0.025  
 emb|AI822869|AI822869 L30-712T3 Ice plant Lambda Uni-Zap XR expr... 36 0.025  
 emb|AI822754|AI822754 L0-1287T3 Ice plant Lambda Uni-Zap XR expr... 36 0.025  
 emb|AI756736|AI756736 EtESTea24h07.y1 Eimeria S5-2 Sporozoite st... 34 0.035  
 gb|M36941|BLYHORDCA Hordeum vulgare C-hordein gene, complete cds. 33 0.079  
 45 emb|AU036628|AU036628 Schizosaccharomyces pombe genomic clone ha... 40 0.083  
 emb|AA948752|AA948752 L0-271M13R Ice plant Lambda Uni-Zap XR exp... 35 0.086  
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 55 gb|BE036036|BE036036 MO18H02 MO Mesembryanthemum crystallinum cD... 36 0.76  
 gb|C95899|C95899 C95899 Marchantia polymorpha immature sex organ... 36 1.0  
 emb|AA966307|AA966307 v8c01a1.r1 Aspergillus nidulans 24hr asexu... 36 1.0  
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 gb|U11583|YSCH9196 Saccharomyces cerevisiae chromosome VIII cosm... 35 1.4  
 60 emb|AQ639257|AQ639257 927P1-10E12.TV 927P1 Trypanosoma brucei ge... 35 1.4  
 emb|AQ943504|AQ943504 Sheared DNA-43F22.TF Sheared DNA Trypanoso... 35 1.4



emb|AW623282|AW623282 EST321227 tomato flower buds 3-8 mm, Corne... 35 1.4  
 dbj|D85226|D85226 Brassica campestris DNA for S glycoprotein, pa... 28 1.6  
 emb|AF001525|AF001525 Musa acuminata ripening-associated protein... 35 2.0

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 gb|aaal7993.1| (m91192) phenylalanine ammonia-lyase [trifolium  
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(1962 letters)

10

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

15

Score E

Sequences producing significant alignments:

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20 gb|L11747|POPPALGA Populus tricarpa X Populus deltoides (hybri... 354 0.0  
 emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 352 0.0  
 emb|X58180|MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase. 351 0.0  
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 25 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 349 0.0  
 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 349 0.0  
 emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 349 0.0  
 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 348 0.0  
 30 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 348 0.0  
 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 348 0.0  
 emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 347 0.0  
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 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 344 0.0  
 35 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 343 0.0  
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 40 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 330 0.0  
 dbj|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 349 0.0  
 emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 353 0.0  
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 45 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0  
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 50 gb|M84466|TOBTPA1A Tobacco phenylalanine ammonia-lyase (tpal) gen... 352 0.0  
 emb|AB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 352 0.0  
 dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 347 0.0  
 emb|X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 355 0.0  
 emb|X99705|TAPALGEN1 T.aestivum PAL gene. 342 0.0  
 55 gb|M91192|TFRPAL1X Trifolium subterraneum phenylalanine ammonia-... 345 0.0  
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 emb|Y07654|PCPAL1 P.crispum pal1 gene. 350 0.0  
 emb|X16772|PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo... 350 0.0  
 60 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 336 0.0  
 gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 353 0.0

- emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 318 0.0  
 dbj|D30657|POPPALB Populus kitakamiensis gene for phenylalanine ... 333 0.0  
 dbj|D43802|POPPALG2BA Populus kitakamiensis gene for phenylalani... 336 0.0  
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 5 dbj|D10002|PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0  
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 emb|X63104|STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon... 353 0.0  
 gb|U39792|PTU39792 Pinus taeda phenylalanine ammonia-lyase (lpPA... 311 0.0  
 gb|M11939|PHVPAL Phaseolus vulgaris L. phenylalanine ammonia-lya... 354 0.0  
 10 dbj|E04043|E04043 cDNA sequence coding for kidney bean phenylala... 354 0.0  
 emb|AB015871|AB015871 Vitis vinifera gene for phenylalanine ammo... 350 0.0  
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 emb|Z49146|HVPAL3MR H.vulgare partial PAL mRNA for phenylalanine... 311 0.0  
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 15 gb|S46988|S46988 phenylalanine ammonia-lyase [soybeans, mRNA, 14... 344 0.0  
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 emb|AW218834|AW218834 EST301314 tomato root during/after fruit s... 347 e-134  
 20 emb|AW031612|AW031612 EST275066 tomato callus, TAMU Lycopersicon... 327 e-132  
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 25 emb|AI166817|AI166817 xylem.est.611 Poplar xylem Lambda ZAPII li... 251 e-117  
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 30 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 247 e-105  
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 35 emb|AW734312|AW734312 sk81e07.y1 Gm-c1016 Glycine max cDNA clone... 324 6e-98  
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 40 emb|AW443181|AW443181 EST308111 tomato mixed elicitor, BTI Lycop... 329 6e-89  
 emb|AW781748|AW781748 sl90e11.y1 Gm-c1037 Glycine max cDNA clone... 326 3e-88  
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 45 emb|AF218454|AF218454 Coffea arabica clone 430.4 phenylalanine a... 243 6e-85  
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 (1554 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

10	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k... 251 1e-65
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	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 230 2e-59
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 227 1e-58
15	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 226 4e-58
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds. 225 7e-58
	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 225 7e-58
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 224 1e-57
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20	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds. 222 6e-57
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	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 221 2e-56
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25	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 218 8e-56
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5 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 97 3e-40  
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20 dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 100 2e-34  
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35 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor... 76 2e-32  
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55 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E  
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55	emb AW096584 AW096584 EST289764 tomato mixed elicitor, BTI Lycop...	181 1e-44
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60	emb AW559359 AW559359 EST314407 DSIR Medicago truncatula cDNA cl...	178 9e-44
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 emb|AQ911427|AQ911427 LMAJFV1\_ln04f02.x1 Leishmania major FV1 ra... 69 1e-21  
 30 emb|AW042912|AW042912 ST27A02 Pine TriplEx shoot tip library Pin... 92 7e-21  
 emb|AT000037|AT000037 AT000037 Apple young fruit cDNA library Ma... 101 1e-20  
 gb|BE049708|BE049708 NXNV\_142\_E09\_F Nsf Xylem Normal wood Vertic... 100 3e-20  
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 35 emb|AW278733|AW278733 sf96f12.y1 Gm-c1019 Glycine max cDNA clone... 95 8e-19  
 emb|AW495793|AW495793 NXNV\_065\_E02\_FF Nsf Xylem Normal wood Vert... 94 2e-18  
 emb|AW568805|AW568805 si61d03.y1 Gm-r1030 Glycine max cDNA clone... 89 7e-17  
 emb|AQ948883|AQ948883 Sheared DNA-46E23.TF Sheared DNA Trypanoso... 69 1e-16  
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 40 emb|AW255631|AW255631 ML690 peppermint glandular trichome Mentha... 86 7e-16  
 emb|AW102109|AW102109 sd83c02.y1 Gm-c1009 Glycine max cDNA clone... 83 6e-15  
 emb|X68950|TRUROCAN T.repens gene for urocanase. 58 5e-14

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 45 0 /ec\_number /family /chip nova /gb\_link /ncgi  
 (1347 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E  
 Sequences producing significant alignments: (bits) Value

55 emb|AB012932|AB012932 Vigna radiata mRNA for Ca<sup>2+</sup>/H<sup>+</sup> exchanger, ... 324 e-141  
 emb|AW119450|AW119450 sd47b12.y1 Gm-c1016 Glycine max cDNA clone... 328 7e-89  
 emb|AW395054|AW395054 sh38h04.y1 Gm-c1017 Glycine max cDNA clone... 323 2e-87  
 emb|AI748459|AI748459 sb53b12.y1 Gm-c1016 Glycine max cDNA clone... 321 6e-87  
 60 emb|AB018526|AB018526 Ipomoea nil mRNA for H<sup>+</sup>/Ca<sup>2+</sup> exchanger 2, ... 262 4e-86  
 emb|AW132719|AW132719 se09c07.y1 Gm-c1013 Glycine max cDNA clone... 293 2e-78



- gb|BE059799|BE059799 sn37c09.y1 Gm-c1016 Glycine max cDNA clone ... 270 1e-71  
emb|AW424368|AW424368 sh64g04.y1 Gm-c1015 Glycine max cDNA clone... 221 6e-70  
emb|AW283631|AW283631 LG1\_242\_D12.g1\_A002 Light Grown 1 (LG1) So... 243 2e-63  
emb|AW668567|AW668567 GA\_Ea0014K15 Gossypium arboreum 7-10 dpa ... 141 1e-61  
5 emb|AW648038|AW648038 EST326492 tomato germinating seedlings, TA... 230 2e-59  
emb|AW132572|AW132572 se05h06.y1 Gm-c1013 Glycine max cDNA clone... 151 3e-52  
emb|AW399625|AW399625 EST310125 L. pennellii trichome, Cornell U... 154 4e-49  
gb|U18944|SCU18944 Saccharomyces cerevisiae putative transmembra... 195 5e-49  
gb|U36603|SCU36603 Saccharomyces cerevisiae vacuolar H<sup>+</sup>/Ca<sup>2+</sup> exc... 195 5e-49  
10 emb|Z74176|SCYDL128W S.cerevisiae chromosome IV reading frame OR... 195 5e-49  
emb|AJ001273|SCMNR1W30 Saccharomyces cerevisiae MNR1 gene, strai... 194 1e-48  
emb|AW737408|AW737408 EST338751 tomato flower buds, anthesis, Co... 149 5e-48  
emb|AJ001272|SCMNR1MNR Saccharomyces cerevisiae mmr1 gene, strai... 191 1e-47  
emb|AI896399|AI896399 EST265830 tomato callus, TAMU Lycopersicon... 190 2e-47  
15 emb|AF053229|AF053229 Neurospora crassa calcium/proton exchanger... 167 3e-46  
emb|AW329785|AW329785 N201056e rootphos(-) Medicago truncatula c... 168 4e-46  
emb|AW471762|AW471762 si15e11.y1 Gm-c1029 Glycine max cDNA clone... 99 8e-43  
emb|AW133119|AW133119 se14e12.y1 Gm-c1013 Glycine max cDNA clone... 173 3e-42  
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20 emb|AL022598|SPCC1795 S.pombe chromosome III cosmid c1795. 150 1e-39  
emb|AL035247|SPCC895 S.pombe chromosome III cosmid c895. 150 1e-39  
emb|AW934664|AW934664 EST353556 tomato flower buds 0-3 mm, Corne... 120 1e-39  
emb|AW508855|AW508855 si41b10.y1 Gm-r1030 Glycine max cDNA clone... 136 3e-39  
emb|AW034341|AW034341 EST277912 tomato callus, TAMU Lycopersicon... 159 4e-38  
25 emb|AI484823|AI484823 EST243084 tomato ovary, TAMU Lycopersicon ... 106 2e-35  
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30 emb|AW737653|AW737653 EST339080 tomato flower buds, anthesis, Co... 140 3e-32  
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emb|AW695100|AW695100 NF091E10ST1F1082 Developing stem Medicago ... 98 1e-30  
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35 emb|AI899610|AI899610 EST269053 tomato susceptible, Cornell Lyco... 121 7e-30  
emb|AW688561|AW688561 NF009A06ST1F1000 Developing stem Medicago ... 80 2e-29  
emb|AW929865|AW929865 EST354135 tomato flower buds 8 mm to pre-a... 88 9e-29  
emb|AI780101|AI780101 EST260980 tomato susceptible, Cornell Lyco... 88 8e-28  
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40 emb|AW691346|AW691346 NF043G04ST1F1000 Developing stem Medicago ... 85 4e-27  
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45 emb|AW394839|AW394839 sh36a06.y1 Gm-c1017 Glycine max cDNA clone... 118 1e-25  
emb|AW119664|AW119664 sd50f07.y1 Gm-c1016 Glycine max cDNA clone... 117 1e-25  
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50 emb|AI211368|AI211368 o6g04a1.fl Aspergillus nidulans 24hr asexu... 111 9e-24  
emb|AW692971|AW692971 NF057G06ST1F1000 Developing stem Medicago ... 85 1e-23  
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emb|AW690067|AW690067 NF027E05ST1F1000 Developing stem Medicago ... 58 8e-22  
55 emb|AW218225|AW218225 EST303406 tomato radicle, 5 d post-imbibit... 105 1e-21  
emb|AW696232|AW696232 NF104B05ST1F1044 Developing stem Medicago ... 61 1e-19  
emb|AW041446|AW041446 EST284310 tomato mixed elicitor, BTI Lycop... 95 9e-19  
emb|AW041435|AW041435 EST284299 tomato mixed elicitor, BTI Lycop... 95 9e-19  
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60 emb|AW432234|AW432234 sh70h05.y1 Gm-c1015 Glycine max cDNA clone... 93 6e-18  
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- emb|AW310634|AW310634 sg22e01.x1 Gm-c1024 Glycine max cDNA clone... 82 1e-14  
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 5 emb|AW923051|AW923051 DG1\_48\_G08.g1\_A002 Dark Grown 1 (DG1) Sorg... 74 2e-12  
 emb|AW695860|AW695860 NF099D07ST1F1061 Developing stem Medicago ... 74 3e-12  
 emb|AW704472|AW704472 sk53e05.y1 Gm-c1019 Glycine max cDNA clone... 74 3e-12  
 emb|AA901983|AA901983 NCM5F6T7 Mycelial Neurospora crassa cDNA c... 72 9e-12  
 gb|BE022406|BE022406 sm85d09.y1 Gm-c1015 Glycine max cDNA clone ... 72 9e-12  
 10 emb|AW694605|AW694605 NF078B03ST1F1027 Developing stem Medicago ... 58 4e-11  
 emb|AI756356|AI756356 EtESTea42h07.y1 Eimeria S5-2 Sporozoite st... 67 3e-10  
 emb|AW875004|AW875004 00125 leafy spurge Lambda HybriZAP 2.1 two... 47 6e-10  
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 15 emb|AW694277|AW694277 NF074D01ST1F1012 Developing stem Medicago ... 58 1e-07  
 emb|AI812387|AI812387 1G6 Pine Lambda Zap Xylem library Pinus ta... 54 3e-06  
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 20 emb|AI043540|AI043540 L30-547T3 Ice plant Lambda Uni-Zap XR expr... 48 2e-04  
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 25 emb|AV424693|AV424693 AV424693 Lotus japonicus young plants (two... 46 7e-04  
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 emb|AV425896|AV425896 AV425896 Lotus japonicus young plants (two... 46 7e-04  
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 30 emb|AQ855371|AQ855371 CpG1905B CpIOWAgDNA1 Cryptosporidium parvu... 40 0.030  
 emb|AW038228|AW038228 EST279885 tomato mixed elicitor, BTI Lycop... 40 0.030  
 emb|AL114296|CNS01BJ4 Botrytis cinerea strain T4 cDNA library un... 40 0.057  
 emb|AW285641|AW285641 LG1\_319\_E05.g1\_A002 Light Grown 1 (LG1) So... 39 0.079
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- emb|Z71753|NPPME3MR N.plumbaginifolia mRNA for pectin methyleste... 142 3e-34  
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 55 emb|AW429110|AW429110 EST306566 tomato flower buds 0-3 mm, Corne... 135 5e-32  
 emb|AW429158|AW429158 EST306614 tomato flower buds 0-3 mm, Corne... 135 5e-32  
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 emb|AI780635|AI780635 EST261610 tomato susceptible, Cornell Lyco... 135 5e-32  
 gb|U49330|SLU49330 Solanum lycopersicum pectin methylesterase (P... 135 5e-32  
 60 emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 134 1e-31  
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- emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. 133 2e-31  
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 emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 132 3e-31  
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 5 emb|AI494978|AI494978 sa93d09.y1 Gm-c1004 Glycine max cDNA clone... 132 3e-31  
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 emb|AW623150|AW623150 EST321095 tomato flower buds 3-8 mm, Corne... 131 6e-31  
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 10 emb|X97762|STBPE1 S.tuberosum mRNA BPE1 for pectin methylesterase. 131 7e-31  
 emb|X67425|PSPMEAG Pisum sativum pmeA gene for pectinesterase. 131 1e-30  
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 emb|AF081457|AF081457 Pisum sativum pectin methylesterase (rcpme... 131 1e-30  
 emb|AW329215|AW329215 N200427e rootphos(-) Medicago truncatula c... 130 2e-30  
 15 emb|AW257345|AW257345 EST305482 KV2 Medicago truncatula cDNA clo... 130 2e-30  
 emb|AI781140|AI781140 EST262019 tomato susceptible, Cornell Lyco... 129 3e-30  
 emb|AI441604|AI441604 sa68e03.y1 Gm-c1004 Glycine max cDNA clone... 129 3e-30  
 emb|AI166540|AI166540 xylem.est.362 Poplar xylem Lambda ZAPII li... 129 4e-30  
 emb|X68029|PVVPE2 P.vulgaris PvVPE2 mRNA for pectin esterase. 128 8e-30  
 20 emb|AW784073|AW784073 NXNV\_117\_D06\_F Nsf Xylem Normal wood Verti... 126 2e-29  
 emb|AW429112|AW429112 EST306568 tomato flower buds 0-3 mm, Corne... 126 3e-29  
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 25 emb|A17010|A17010 tomato fruit pectin esterase seq ID no1. 121 1e-27  
 emb|AW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 121 1e-27  
 emb|AW934244|AW934244 EST360087 tomato fruit mature green, TAMU ... 121 1e-27  
 emb|AW930330|AW930330 EST340883 tomato fruit mature green, TAMU ... 121 1e-27  
 gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 121 1e-27  
 30 emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 121 1e-27  
 emb|AW221863|AW221863 EST298674 tomato fruit red ripe, TAMU Lyco... 121 1e-27  
 emb|X74638|LEPEC1 L.esculentum mRNA for pectin esterase. 121 1e-27  
 emb|AW696177|AW696177 NF103C11ST1F1085 Developing stem Medicago ... 121 1e-27  
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 35 emb|AW289642|AW289642 NXNV003F09F Nsf Xylem Normal wood Vertical... 119 3e-27  
 gb|U50986|SLU50986 Solanum lycopersicum pectin methylesterase PM... 119 4e-27  
 gb|U70675|LEU70675 Lycopersicon esculentum fruit-specific pectin... 118 6e-27  
 gb|U70676|LEU70676 Lycopersicon esculentum pectin methylesteras... 118 6e-27  
 emb|Z71751|NPPME1MR N.plumbaginifolia mRNA for pectin methyleste... 118 8e-27  
 40 emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 118 8e-27  
 emb|AF229849|AF229849 Vigna radiata pectin methylesterase isoform... 118 8e-27  
 gb|U70677|LEU70677 Lycopersicon esculentum (LePME1) gene, partia... 118 8e-27  
 gb|U82974|CSU82974 Citrus sinensis pectinesterase (PECS-1.2) gen... 117 1e-26  
 emb|AI897776|AI897776 EST267219 tomato ovary, TAMU Lycopersicon ... 117 2e-26  
 45 gb|U50985|SLU50985 Solanum lycopersicum pectin methylesterase PM... 116 3e-26  
 emb|AW758821|AW758821 NXNV\_091\_A04\_F Nsf Xylem Normal wood Verti... 116 3e-26  
 emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 116 3e-26  
 emb|X74639|LEPEC2 L.esculentum mRNA for pectin esterase clone. 116 3e-26  
 emb|X07910|LEPECES Tomato mRNA for pectin esterase. 116 3e-26  
 50 emb|A15983|A15983 L.esculentum mRNA for pectin esterase. 116 3e-26  
 emb|AW623570|AW623570 EST321515 tomato flower buds 3-8 mm, Corne... 116 3e-26  
 emb|AW221834|AW221834 EST298645 tomato fruit red ripe, TAMU Lyco... 115 5e-26  
 emb|X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 115 5e-26  
 emb|A24196|A24196 L.esculentum pectin esterase clone pPE1. 113 2e-25  
 55 emb|AW687047|AW687047 NF005D06RT1F1057 Developing root Medicago ... 113 2e-25  
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 emb|AW398532|AW398532 EST309032 L. pennellii trichome, Cornell U... 111 8e-25  
 emb|AW666622|AW666622 GA\_Ea0005C20 Gossypium arboreum 7-10 dpa ... 110 2e-24  
 emb|AW163926|AW163926 Ljirmp17-358-e10 Ljirmp Lambda HybriZap... 110 2e-24  
 60 emb|AW620942|AW620942 sj95g05.y1 Gm-c1023 Glycine max cDNA clone... 108 5e-24  
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gb|U82977|CSU82977 Citrus sinensis pectinesterase mRNA, complete... 84 2e-23  
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5 gb|U82975|CSU82975 Citrus sinensis pectinesterase (PECS-2.1) gen... 81 7e-23  
gb|BE123534|BE123534 NXNV\_149\_D04\_F Nsf Xylem Normal wood Vertic... 103 2e-22  
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emb|AB029461|AB029461 Salix gilgiana SgPME1 mRNA for pectin meth... 102 4e-22  
emb|AW647968|AW647968 EST326422 tomato germinating seedlings, TA... 100 3e-21  
emb|AW617630|AW617630 EST324041 L. hirsutum trichome, Cornell Un... 97 2e-20  
10 emb|Y07899|CPSPE1 C.papaya mRNA for pectinesterase. 97 3e-20  
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emb|X95991|PPPECESTR P.persica mRNA for pectin esterase. 85 1e-18  
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20 emb|AA556385|AA556385 240 Loblolly pine C Pinus taeda cDNA clone... 71 1e-12  
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emb|AW220222|AW220222 EST302705 tomato root during/after fruit s... 62 4e-10  
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/gb\_link http://www3.ncbi.nlm.nih.gov/htbin-  
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30 http://www.ncgr.org/cgi-bin/ff?al079344  
(1386 letters)  
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emb|AL034352|SPBC725 S.pombe chromosome II cosmid c725. 87 6e-42  
gb|C96280|C96280 C96280 Marchantia polymorpha immature sex organ... 89 9e-37  
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emb|AW306350|AW306350 se49e12.y1 Gm-c1017 Glycine max cDNA clone... 116 2e-33  
50 emb|AV409781|AV409781 AV409781 Lotus japonicus young plants (two... 140 2e-32  
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emb|X59720|SCCHRIII S.cerevisiae chromosome III complete DNA seq... 68 2e-13  
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55 emb|AQ397058|AQ397058 mgxb0003P19f CUGI Rice Blast BAC Library P... 40 7e-06  
emb|AV427570|AV427570 AV427570 Lotus japonicus young plants (two... 52 8e-06  
gb|H74550|H74550 501 Random-primed Brassica napus cDNA clone RRM... 49 1e-04  
emb|AW186036|AW186036 se62g09.y1 Gm-c1019 Glycine max cDNA clone... 46 5e-04  
emb|AW832253|AW832253 sm21f10.y1 Gm-c1027 Glycine max cDNA clone... 46 5e-04  
60 emb|AW596708|AW596708 sj15g06.y1 Gm-c1032 Glycine max cDNA clone... 46 5e-04  
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	emb AW349789 AW349789 GM210006B10E8R Gm-r1021 Glycine max cDNA 3...	37	0.29
	emb AW703931 AW703931 sk25h05.yl Gm-c1028 Glycine max cDNA clone...	37	0.29
	emb AW733463 AW733463 sk73h10.yl Gm-c1016 Glycine max cDNA clone...	28	0.38
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15	emb AW599349 AW599349 gb13g12.yl Moss EST library PPN Physcomitr...	36	0.54
	emb Z73136 SCYLL031C S.cerevisiae chromosome XII reading frame O...	29	0.61
	emb AA898221 AA898221 NCC2C5T7 Conidial Neurospora crassa cDNA c...	35	1.0
	emb AF130334 AF130334 Bruguiera cylindrica internal transcribed ...	35	1.9
	gb B13384 B13384 jd152 Trypanosome Shotgun M13 genomic Trypanoso...	34	2.7
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	emb AW102097 AW102097 sd83a09.yl Gm-c1009 Glycine max cDNA clone...	34	2.7
	emb AW334235 AW334235 S32B4 AGS-1 Pneumocystis carinii f. sp. ca...	34	3.6
	emb AW648115 AW648115 EST326569 tomato germinating seedlings, TA...	34	3.6
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	gb M55447 BLYRCAA2 Hordeum vulgare rubisco activase (RcaA2) mRNA...	34	3.6
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30	emb AW109433 AW109433 gate0004K24f Gossypium arboreum 7-10 dpa f...	33	5.0
	emb AW666951 AW666951 GA_Ea0006H12 Gossypium arboreum 7-10 dpa ...	33	5.0
	emb AW661478 AW661478 833006F08.yl C. reinhardtii CC-125 -S, Lam...	33	5.0
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	emb AL353822 NC15E6 Neurospora crassa DNA linkage group V Cosmid...	33	6.9
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50	emb AV393427 AV393427 AV393427 Chlamydomonas reinhardtii C9 Chla...	33	6.9
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	gb U30821 CPU30821 Cyanophora paradoxa cyanelle, complete genome.	32	9.4
	emb AQ449508 AQ449508 500001C11.x1 CplOWAM13mpl18gDNA1 Cryptospor...	32	9.4
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60	emb AQ641373 AQ641373 RPCI93-DpnII-28A9.TV RPCI93-DpnII Trypanos...	32	9.4
	emb AW695807 AW695807 NF098G11ST1F1087 Developing stem Medicago ...	32	9.4

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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	gb L47866 L47866 BNAF1507 Mustard flower buds Brassica rapa cDNA...	94	6e-20
	emb X94986 MEBGLA M.esculenta bglA gene.	94	6e-20
	emb AW257154 AW257154 EST305291 KV2 Medicago truncatula cDNA clo...	93	8e-20
	gb U39228 PAU39228 Prunus avium beta-glucosidase mRNA, partial cds.	93	8e-20
25	emb AI729894 AI729894 BNLGHi5504 Six-day Cotton fiber Gossypium ...	93	8e-20
	gb U95298 MEU95298 Manihot esculenta linamarase (pLIN-GEN) gene,...	93	8e-20
	gb S35175 S35175 linamarase=beta-glucosidase [Manihot esculenta=...	92	2e-19
	emb AF072736 AF072736 Pinus contorta beta-glucosidase mRNA, comp...	92	2e-19
30	emb AW568866 AW568866 si73c03.y1 Gm-c1031 Glycine max cDNA clone...	91	4e-19
	gb U50201 PSU50201 Prunus serotina prunasin hydrolase precursor ...	90	5e-19
	emb AW560545 AW560545 EST315593 DSIR Medicago truncatula cDNA cl...	90	7e-19
	emb AI900802 AI900802 sb93e10.y1 Gm-c1017 Glycine max cDNA clone...	89	2e-18
	gb BE058816 BE058816 sn21c08.y1 Gm-c1016 Glycine max cDNA clone ...	89	2e-18
35	emb AW597982 AW597982 sj40c05.y1 Gm-c1008 Glycine max cDNA clone...	89	2e-18
	emb AW395210 AW395210 sh45c06.y1 Gm-c1017 Glycine max cDNA clone...	89	2e-18
	emb AW570004 AW570004 si85e02.y1 Gm-c1031 Glycine max cDNA clone...	89	2e-18
	emb AW733524 AW733524 sk74g01.y1 Gm-c1016 Glycine max cDNA clone...	89	2e-18
	emb AW423986 AW423986 sh59a09.y1 Gm-c1015 Glycine max cDNA clone...	89	2e-18
40	emb AW423387 AW423387 sh65b01.y1 Gm-c1015 Glycine max cDNA clone...	89	2e-18
	emb AW597368 AW597368 si91h08.y1 Gm-c1031 Glycine max cDNA clone...	88	3e-18
	emb AW569966 AW569966 si83h05.y1 Gm-c1031 Glycine max cDNA clone...	88	3e-18
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45	emb AW317654 AW317654 sg55e02.y1 Gm-c1025 Glycine max cDNA clone...	87	5e-18
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	emb AW309715 AW309715 sf23f08.x1 Gm-c1028 Glycine max cDNA clone...	87	7e-18
	emb AF221526 AF221526 Prunus serotina prunasin hydrolase isoform...	86	9e-18
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50	emb AW279169 AW279169 sf67c06.y1 Gm-c1013 Glycine max cDNA clone...	85	2e-17
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55	emb AI774009 AI774009 EST255109 tomato resistant, Cornell Lycopen...	63	2e-16
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	emb AW101162 AW101162 sd74h08.y1 Gm-c1008 Glycine max cDNA clone...	81	4e-16



- emb|AW132549|AW132549 se05f01.y1 Gm-c1013 Glycine max cDNA clone... 80 6e-16  
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emb|AB003110|AB003110 Trichoderma reesei bgl2 gene for bete-gluc... 80 8e-16  
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5 emb|AJ005950|AJ005950 AJ005950 chickpea mRNA CAP-4 Cicer arietin... 79 1e-15  
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10 emb|AW311377|AW311377 sg38b12.y1 Gm-c1025 Glycine max cDNA clone... 63 5e-15  
emb|AW677220|AW677220 DG1\_6\_D11.g1\_A002 Dark Grown 1 (DG1) Sorgh... 77 7e-15  
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20 emb|AB003109|AB003109 Humicola grisea var. thermoidea bgl4 gene ... 76 1e-14  
emb|AI723853|AI723853 RHIZ1\_28\_C08.y1\_A001 Rhizome1 Sorghum hale... 76 1e-14  
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emb|X67838|BNDNAM B.napus DNA for myrosinase. 66 1e-11  
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50 emb|AW284341|AW284341 LG1\_275\_C12.g1\_A002 Light Grown 1 (LG1) So... 66 1e-11  
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emb|X56733|TRBG104 T.repens mRNA for cyanogenic beta-glucosidase... 52 2e-11  
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55 emb|X59881|SAMYRMB1 S.alba thioglucoside glucosylhydrolase (myrosin... 63 7e-11  
emb|AW927073|AW927073 HVSMEg0009H02 Hordeum vulgare pre-anthesis... 57 1e-10  
gb|L11258|BNAMYROS Brassica campestris myrosinase gene, complete... 62 2e-10

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(1374 letters)

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Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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Searching.....done

15

Score E  
Sequences producing significant alignments: (bits) Value

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30 emb|AW310471|AW310471 sf36e11.x1 Gm-cl028 Glycine max cDNA clone... 105 6e-22  
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emb|AW907159|AW907159 EST343282 potato stolon, Cornell Universit... 60 2e-14  
40 emb|AW565825|AW565825 LG1\_352\_B09.g1\_A002 Light Grown 1 (LG1) So... 57 8e-14  
emb|AW625736|AW625736 EST319643 tomato radicle, 5 d post-imbibit... 56 8e-14  
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gb|BE060164|BE060164 HVSMEg0011B20f Hordeum vulgare pre-anthesis... 76 5e-13  
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45 emb|AW398760|AW398760 EST309260 L. pennellii trichome, Cornell U... 54 2e-12  
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emb|AW697758|AW697758 Str1-D8 Sugar Beet germination cDNA librar... 46 5e-11  
emb|AW030302|AW030302 EST273557 tomato callus, TAMU Lycopersicon... 53 7e-11  
emb|AW982668|AW982668 HVSMEg0003O06f Hordeum vulgare pre-anthesi... 48 2e-10  
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- emb|AT000645|AT000645 AT000645 Brassica rapa guard cell Brassica... 56 6e-07  
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 5 emb|AW154916|AW154916 EST290281 tomato root deficiency, Cornell ... 40 6e-05  
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 10 emb|AW564044|AW564044 LG1\_281\_A09.b1\_A002 Light Grown 1 (LG1) So... 47 4e-04  
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 60 (1512 letters)



Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

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 30 emb|A85491|A85491 Sequence 150 from Patent EP0866129. 34 4.0  
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 35 emb|AW617216|AW617216 EST323627 L. hirsutum trichome, Cornell Un... 33 5.5  
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 (1488 letters)

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

50

Score E

Sequences producing significant alignments: (bits) Value

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 emb|AW560118|AW560118 EST315166 DSIR Medicago truncatula cDNA cl... 166 3e-64  
 emb|AW394771|AW394771 sh35b02.y1 Gm-c1017 Glycine max cDNA clone... 213 3e-54  
 60 emb|AW622568|AW622568 EST313368 tomato root during/after fruit s... 181 5e-51  
 emb|AW737712|AW737712 EST339139 tomato flower buds, anthesis, Co... 162 1e-45

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	emb AL111744 CNS019K8 Botrytis cinerea strain T4 cDNA library un...	123	3e-37
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	emb Z49211 SC9711X S.cerevisiae chromosome XIII cosmid 9711.	113	3e-36
	gb U34636 SCU34636 Saccharomyces cerevisiae cytochrome P450 gene...	113	3e-36
10	emb AW928489 AW928489 EST337277 tomato flower buds 8 mm to pre-a...	149	5e-35
	emb AL033396 CAC35A5 C.albicans cosmid Ca35A5.	117	2e-34
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25	emb AA556134 AA556134 TENF0475 T.cruzi epimastigote normalized c...	61	2e-08
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	emb AW706535 AW706535 sj57g05.y1 Gm-c1033 Glycine max cDNA clone...	49	1e-04
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40 (417 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters

45 Searching.....done

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55	emb AW458973 AW458973 sh17e01.y1 Gm-c1016 Glycine max cDNA clone...	61	3e-12
	emb AW132527 AW132527 se05c02.y1 Gm-c1013 Glycine max cDNA clone...	61	3e-12
	emb AW102493 AW102493 sd88h04.y1 Gm-c1009 Glycine max cDNA clone...	61	4e-12
	emb AV421249 AV421249 AV421249 Lotus japonicus young plants (two...	62	2e-09
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	emb AW278066 AW278066 sf39c09.y1 Gm-c1009 Glycine max cDNA clone...	40	0.007
40	emb AW318239 AW318239 sg62g03.y1 Gm-c1007 Glycine max cDNA clone...	40	0.007
	emb AW706818 AW706818 sk03g11.y1 Gm-c1023 Glycine max cDNA clone...	40	0.009
	emb AI166481 AI166481 xylem.est.309 Poplar xylem Lambda ZAPII li...	40	0.013
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	emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl...	39	0.018
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25 emb|AI895984|AI895984 EST265427 tomato callus, TAMU Lycopersicon... 38 0.046  
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35 (1161 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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45	emb AW185155 AW185155 se87e11.y1 Gm-c1023 Glycine max cDNA clone...	134	2e-30
	emb AW278569 AW278569 sf46b12.y1 Gm-c1009 Glycine max cDNA clone...	131	1e-29
	emb AW683973 AW683973 NF004E08NR1F1000 Nodulated root Medicago t...	97	2e-19
	emb AI055338 AI055338 coau0003L11 Cotton Boll Abscission Zone cD...	56	2e-07
	emb AW693058 AW693058 NF059E03ST1F1021 Developing stem Medicago ...	49	9e-05
50	emb AW686062 AW686062 NF033A11NR1F1000 Nodulated root Medicago t...	49	9e-05
	gb BE060490 BE060490 HVSMEg0012H04f Hordeum vulgare pre-anthesis...	37	0.22
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	emb AV425088 AV425088 AV425088 Lotus japonicus young plants (two...	34	1.5
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60	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai...	33	2.8
	emb AF108883 AF108883 Capsicum annuum small GTP-binding protein ...	28	3.6

- emb|X75082|STCITS *S.tuberosum* mRNA for mitochondrial citrate-syn... 33 3.9  
 emb|A46545|A46545 Sequence 1 from Patent WO9524487. 33 3.9  
 emb|X07693|SPNUC2 Fission yeast nuc2 gene encoding nuclear scaff... 33 3.9  
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 5 emb|AF143971|AF143971 *Pinus taeda* microsatellite PtTX3026 sequence. 33 3.9  
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 10 emb|AW761626|AW761626 gb27h09.y1 Moss EST library PPN *Physcomitr...* 32 6.9  
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 25 emb|AW735860|AW735860 EST336628 tomato flower buds 0-3 mm, Corne... 32 9.4  
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 (999 letters)

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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- emb|AI727718|AI727718 BNLGHi8830 Six-day Cotton fiber *Gossypium* ... 405 e-112  
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 emb|AW091566|AW091566 EST284842 tomato mixed elicitor, BTI *Lycop...* 364 e-100  
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 50 emb|AW038822|AW038822 EST280778 tomato mixed elicitor, BTI *Lycop...* 282 3e-75  
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 emb|AW508528|AW508528 si33a06.y1 *Gm-r1030* Glycine max cDNA clone... 177 8e-60  
 emb|AW201152|AW201152 se98d11.y1 *Gm-c1027* Glycine max cDNA clone... 137 1e-49  
 emb|AW011518|AW011518 ST21G07 Pine TriplEx shoot tip library Pin... 178 5e-44  
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 60 emb|AW459302|AW459302 sh23c04.y1 *Gm-c1016* Glycine max cDNA clone... 166 3e-40  
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	emb AW428965 AW428965 EST306505 tomato flower buds 0-3 mm, Come...	35	1.3
	emb X79743 SCBPPS <i>S.cerevisiae</i> BET1, PAN1 PRI1 and STS1 genes.	35	1.3
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30	emb AF106079 AF106079 <i>Chlamydomonas reinhardtii</i> dynein heavy cha...	34	1.8
	gb M80437 YSCSEQ <i>Saccharomyces cerevisiae</i> gene, complete cds.	34	2.5
	gb J05603 YSCCTR <i>Saccharocyces cerevisiae</i> choline transport prot...	34	2.5
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35	emb Z71519 SCYNL243W <i>S.cerevisiae</i> chromosome XIV reading frame O...	33	3.4
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	emb Z22811 SCSLA2PA <i>S.cerevisiae</i> of Sla2p gene.	33	3.4
	emb Z69381 SCCXIV39K <i>S.cerevisiae</i> 38,855 bp segment of chromosom...	33	3.4
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	emb AQ649183 AQ649183 Sheared DNA-6F2.TR Sheared DNA Trypanosoma...	33	4.7
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45	dbj D90206 CRECAH1G <i>C. reinhardtii</i> CAH1 gene for carbonic anhydr...	33	4.7
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 10 emb|X54488|CRCAH2 Chlamydomonas reinhardtii CAH2 gene for carbon... 32 8.9  
 emb|A85864|A85864 Sequence 523 from Patent EP0866129. 32 8.9  
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 emb|AW184970|AW184970 se84g02.y1 Gm-cl023 Glycine max cDNA clone... 32 8.9  
 emb|Z46871|SOEXG1 S.occidentalis gene for exo-1,3-beta-glucanase... 32 8.9  
 15 emb|AI163250|AI163250 A038p15u Hybrid aspen plasmid library Popu... 32 8.9  
 emb|AL023592|SPCC550 S.pombe chromosome III cosmid c550. 32 8.9  
 emb|AW668371|AW668371 GA\_Ea0013L20 Gossypium arboreum 7-10 dpa ... 26 9.3  
 emb|AW255363|AW255363 ML376 peppermint glandular trichome Menth... 26 9.5  
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 20 emb|AW255126|AW255126 ML1418 peppermint glandular trichome Menth... 26 9.8

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 (1869 letters)

30 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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35 Score E  
 Sequences producing significant alignments: (bits) Value

emb|AW622865|AW622865 EST306935 tomato flower buds 3-8 mm, Corne... 246 3e-64  
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 60 emb|AB002141|AB002141 Pyrus pyrifolia mRNA for S5-RNase, complet... 35 1.3  
 dbj|D88282|D88282 Pyrus serotina mRNA for S5-RNase, complete cds. 35 1.3

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	emb AI780435 AI780435 EST261314 tomato susceptible, Cornell Lyco...	34	2.4
	emb AL355928 NCB1D4 <i>Neurospora crassa</i> DNA linkage group II BAC c...	34	2.4
	emb AF188714 AF188714 <i>Emericella nidulans</i> chromosome VIII cosmid...	34	2.4
	emb AF138284 AF138284 <i>Emericella nidulans</i> molybdopterin synthase...	34	2.4
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	emb AJ223010 SCP223010 <i>Schizosaccharomyces pombe</i> pmt2 gene.	34	3.3
	emb AL356456 LMFLUNK01 <i>Leishmania major</i> Friedlin cosmid clones L...	34	3.3
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25	gb M76671 TOMEXTENB <i>L.esculentum</i> extensin (class II) gene, compl...	33	4.6
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50	emb AW725268 AW725268 GA_Ea0015L23 <i>Gossypium arboreum</i> 7-10 dpa ...	32	8.6
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Database: plantfungal



661,018 sequences; 426,114,510 total letters

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15 Database: plantfungal  
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Sequences producing significant alignments: (bits) Value

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	emb AW706119 AW706119 sj52a11.y1 Gm-c1033 Glycine max cDNA clone...	146	1e-34
	emb AW311107 AW311107 sg33a02.y1 Gm-c1025 Glycine max cDNA clone...	124	2e-34
	emb AW200806 AW200806 se93g05.y1 Gm-c1027 Glycine max cDNA clone...	123	3e-34
	emb AW830450 AW830450 sm27b08.y1 Gm-c1028 Glycine max cDNA clone...	145	3e-34
15	emb AW458429 AW458429 sh09b05.y1 Gm-c1016 Glycine max cDNA clone...	127	4e-34
	emb AW559537 AW559537 EST314585 DSIR Medicago truncatula cDNA cl...	79	5e-34
	emb AW559584 AW559584 EST314632 DSIR Medicago truncatula cDNA cl...	79	5e-34
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	emb AW011055 AW011055 ST16B07 Pine TriplEx shoot tip library Pin...	142	2e-33
	emb AW687043 AW687043 NF005D02RT1F1016 Developing root Medicago ...	133	2e-33
	gb BE022312 BE022312 sm73c09.y1 Gm-c1028 Glycine max cDNA clone...	142	3e-33
	emb AW620826 AW620826 sj47a07.y1 Gm-c1033 Glycine max cDNA clone...	119	3e-33
	emb AW666225 AW666225 sk34a04.y1 Gm-c1028 Glycine max cDNA clone...	140	9e-33
25	emb AI494896 AI494896 sb06g10.y1 Gm-c1004 Glycine max cDNA clone...	140	9e-33
	emb AI443387 AI443387 sa31d11.x1 Gm-c1004 Glycine max cDNA clone...	139	1e-32
	emb AW203753 AW203753 sf37h02.y1 Gm-c1028 Glycine max cDNA clone...	139	2e-32
	emb AW559725 AW559725 EST314717 DSIR Medicago truncatula cDNA cl...	78	4e-32
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30	emb AW234737 AW234737 sf18f10.y1 Gm-c1028 Glycine max cDNA clone...	136	2e-31
	emb AW351059 AW351059 GM210010B10G3R Gm-r1021 Glycine max cDNA 3...	136	2e-31
	emb AW684772 AW684772 NF021H06NR1F1000 Nodulated root Medicago t...	120	5e-31
	emb AW775144 AW775144 EST334295 KV3 Medicago truncatula cDNA clo...	76	9e-31
35	emb AI495113 AI495113 sb03f02.y1 Gm-c1004 Glycine max cDNA clone...	133	1e-30
	emb AW472306 AW472306 si23e07.y1 Gm-c1029 Glycine max cDNA clone...	117	2e-30
	emb AW035139 AW035139 EST280401 tomato callus, TAMU Lycopersicon...	131	5e-30
	emb AI496590 AI496590 sb13g02.y1 Gm-c1004 Glycine max cDNA clone...	129	2e-29
	emb AW351151 AW351151 GM210011A10E12R Gm-r1021 Glycine max cDNA ...	81	2e-29
40	emb AW460064 AW460064 si08g11.y1 Gm-c1029 Glycine max cDNA clone...	105	4e-29
	emb AW432674 AW432674 sh83h05.y1 Gm-c1016 Glycine max cDNA clone...	126	1e-28
	emb AW507521 AW507521 si53a07.y1 Gm-r1030 Glycine max cDNA clone...	106	1e-28
	emb AI461088 AI461088 sa73g10.y1 Gm-c1004 Glycine max cDNA clone...	123	8e-28
	emb AI461045 AI461045 sa73c04.y1 Gm-c1004 Glycine max cDNA clone...	123	8e-28
45	emb AW010003 AW010003 ST01B12 Pine TriplEx shoot tip library Pin...	123	8e-28
	gb BE021390 BE021390 sm48e04.y1 Gm-c1028 Glycine max cDNA clone...	122	2e-27
	gb BE022539 BE022539 sm86c09.y1 Gm-c1015 Glycine max cDNA clone...	121	4e-27
	emb AW559258 AW559258 EST306094 DSIR Medicago truncatula cDNA cl...	118	3e-26
	emb AW760707 AW760707 sl36a09.y1 Gm-c1027 Glycine max cDNA clone...	95	8e-26
50	emb AI941013 AI941013 sb83c06.y1 Gm-c1010 Glycine max cDNA clone...	95	8e-26
	emb AW745074 AW745074 LG1_386_D11.b1_A002 Light Grown 1 (LG1) So...	91	3e-25
	emb AI900284 AI900284 sc03d11.y1 Gm-c1012 Glycine max cDNA clone...	111	4e-25
	emb AW666457 AW666457 sk36g12.y1 Gm-c1028 Glycine max cDNA clone...	114	7e-25
	emb AI522845 AI522845 sa74e03.y1 Gm-c1004 Glycine max cDNA clone...	114	7e-25
55	emb AW350289 AW350289 GM210008A10D4R Gm-r1021 Glycine max cDNA 3...	113	9e-25
	emb AW233771 AW233771 sf26e08.y1 Gm-c1028 Glycine max cDNA clone...	105	1e-24
	gb BE021431 BE021431 sm49a02.y1 Gm-c1028 Glycine max cDNA clone...	111	4e-24
	emb AW495792 AW495792 NXNV_065_D12_FF Nsf Xylem Normal wood Vert...	110	8e-24
60	emb AI441701 AI441701 sa60b06.y1 Gm-c1004 Glycine max cDNA clone...	110	8e-24
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 10 gb|BE021658|BE021658 sm60g09.y1 Gm-c1028 Glycine max cDNA clone ... 101 3e-21  
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 emb|AI920195|AI920195 1725 Pine Lambda Zap Xylem library Pinus t... 73 2e-20  
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 emb|AW684941|AW684941 NF023D03NR1F1000 Nodulated root Medicago t... 88 1e-19  
 15 emb|AI494665|AI494665 sb18f10.y1 Gm-c1004 Glycine max cDNA clone... 89 1e-19  
 emb|AW277935|AW277935 sf87g05.y1 Gm-c1019 Glycine max cDNA clone... 97 1e-19  
 gb|BE023344|BE023344 sm70f11.y1 Gm-c1028 Glycine max cDNA clone ... 78 2e-19  
 emb|AV422621|AV422621 AV422621 Lotus japonicus young plants (two... 60 2e-19  
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 (393 letters)  
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 30 661,018 sequences; 426,114,510 total letters  
 Searching.....done  
 Score E  
 35 Sequences producing significant alignments: (bits) Value  
 emb|AW218792|AW218792 EST301272 tomato root during/after fruit s... 104 2e-30  
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 emb|AI781536|AI781536 EST262415 tomato susceptible, Cornell Lyco... 104 2e-30  
 40 emb|AI894486|AI894486 EST263929 tomato callus, TAMU Lycopersicon... 100 3e-29  
 emb|AW255546|AW255546 ML580 peppermint glandular trichome Menta... 96 4e-25  
 emb|AW781055|AW781055 sl88d08.y1 Gm-c1037 Glycine max cDNA clone... 95 5e-25  
 emb|AW980335|AW980335 EST391488 GVN Medicago truncatula cDNA clo... 94 1e-24  
 emb|AW982334|AW982334 HVSMEg0002O20f Hordeum vulgare pre-anthesi... 86 1e-24  
 45 gb|H74448|H74448 150 Standard Brassica napus cDNA clone R29F, mR... 92 4e-24  
 emb|AI960943|AI960943 sc93a04.y1 Gm-c1019 Glycine max cDNA clone... 92 5e-24  
 emb|AU036790|AU036790 AU036790 Cryptomeria japonica seedling lea... 88 5e-24  
 emb|AW598247|AW598247 sj42f01.y1 Gm-c1008 Glycine max cDNA clone... 80 3e-23  
 emb|AW100651|AW100651 sd58b12.y1 Gm-c1008 Glycine max cDNA clone... 89 4e-23  
 50 emb|AW208200|AW208200 M110845e GVSIN Medicago truncatula cDNA clo... 88 5e-23  
 emb|AW559726|AW559726 EST314718 DSIR Medicago truncatula cDNA cl... 83 2e-22  
 emb|AW101120|AW101120 sd74c08.y1 Gm-c1008 Glycine max cDNA clone... 94 2e-22  
 emb|AW926990|AW926990 HVSMEg0009D05 Hordeum vulgare pre-anthesis... 103 8e-22  
 gb|BE124173|BE124173 EST394298 DSIL Medicago truncatula cDNA clo... 94 1e-21  
 55 emb|AT000903|AT000903 AT000903 Brassica rapa guard cell Brassica... 54 2e-20  
 emb|AW690635|AW690635 NF031H11ST1F1000 Developing stem Medicago ... 75 6e-20  
 emb|AW126039|AW126039 N100235e rootphos(-) Medicago truncatula c... 75 6e-20  
 emb|AW126127|AW126127 N100324e rootphos(-) Medicago truncatula c... 75 7e-20  
 emb|AI812959|AI812959 2A11 Pine Lambda Zap Xylem library Pinus t... 75 2e-19  
 60 emb|AI043565|AI043565 L30-578T3 Ice plant Lambda Uni-Zap XR expr... 75 3e-19  
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	gb BE059263 BE059263 sn28d04.y1 Gm-c1016 Glycine max cDNA clone ...	95	3e-19
	emb AW736823 AW736823 NXNV_083_D01_F Nsf Xylem Normal wood Verti...	73	3e-19
	emb AW461253 AW461253 NXNV060C05F Nsf Xylem Normal wood Vertical...	70	7e-18
	emb AW126244 AW126244 N100089e rootphos(-) Medicago truncatula c...	53	2e-17
5	emb AW683890 AW683890 NF003A10NR1F1000 Nodulated root Medicago t...	49	4e-17
	emb AW922806 AW922806 DG1_46_G06.g1_A002 Dark Grown 1 (DG1) Sorg...	84	4e-17
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	emb AW567768 AW567768 si54f04.y1 Gm-r1030 Glycine max cDNA clone...	64	7e-16
	emb AW568036 AW568036 si56f04.y1 Gm-r1030 Glycine max cDNA clone...	64	7e-16
10	emb AW461226 AW461226 NXNV048H05F Nsf Xylem Normal wood Vertical...	74	9e-15
	emb AW720025 AW720025 LjNEST15c3r Lotus japonicus nodule library...	78	2e-14
	emb AI812590 AI812590 13F9 Pine Lambda Zap Xylem library Pinus t...	54	1e-13
	emb AW350351 AW350351 GM210008A10G1R Gm-r1021 Glycine max cDNA 3...	73	1e-12
	emb AI779006 AI779006 EST259885 tomato susceptible, Cornell Lyco...	73	1e-12
15	emb AA557075 AA557075 917 Loblolly pine N Pinus taeda cDNA clone...	70	2e-12
	emb AI899615 AI899615 EST269058 tomato susceptible, Cornell Lyco...	72	2e-12
	emb AW394975 AW394975 sh37h12.y1 Gm-c1017 Glycine max cDNA clone...	69	1e-11
	emb AU036851 AU036851 AU036851 Cryptomeria japonica seedling lea...	69	1e-11
	emb AW394753 AW394753 sh34h05.y1 Gm-c1017 Glycine max cDNA clone...	68	2e-11
20	emb AI965467 AI965467 sc72c05.y1 Gm-c1018 Glycine max cDNA clone...	68	3e-11
	emb AI495151 AI495151 sa88f06.y1 Gm-c1004 Glycine max cDNA clone...	67	6e-11
	gb BE034744 BE034744 ML03G11 ML Mesembryanthemum crystallinum cD...	44	2e-10
	emb AI771301 AI771301 EST252317 tomato ovary, TAMU Lycopersicon ...	64	6e-10
	emb AW424128 AW424128 sh61c09.y1 Gm-c1015 Glycine max cDNA clone...	63	8e-10
25	emb AI736289 AI736289 sb26d05.y1 Gm-c1008 Glycine max cDNA clone...	59	1e-08
	emb AW888120 AW888120 NXNV_129_D10_F Nsf Xylem Normal wood Verti...	56	2e-08
	emb AW784020 AW784020 NXNV_103_A11_F Nsf Xylem Normal wood Verti...	54	8e-08
	emb AI938510 AI938510 sb46e12.y1 Gm-c1015 Glycine max cDNA clone...	55	2e-07
	emb AT000179 AT000179 AT000179 Apple young fruit cDNA library Ma...	41	0.004
30	emb AW234162 AW234162 sf22a01.y1 Gm-c1028 Glycine max cDNA clone...	40	0.006
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	gb BE034795 BE034795 ML04D08 ML Mesembryanthemum crystallinum cD...	40	0.008
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	gb L01433 SOYSCAM4X Soybean calmodulin (SCaM-4) mRNA, complete cds.	40	0.008
35	gb U20292 STU20292 Solanum tuberosum clone PCM3 calmodulin gene,...	40	0.008
	emb AW458431 AW458431 sh09b07.y1 Gm-c1016 Glycine max cDNA clone...	40	0.012
	emb AW704882 AW704882 sk40g04.y1 Gm-c1019 Glycine max cDNA clone...	39	0.016
	emb AW706736 AW706736 sk02d02.y1 Gm-c1023 Glycine max cDNA clone...	39	0.022
	gb M88307 BNACALM Brassica juncea calmodulin mRNA, complete cds.	38	0.030
40	gb U10150 BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,...	38	0.030
	emb AW266313 AW266313 L30-3052T3 Ice plant Lambda Uni-Zap XR exp...	38	0.041
	emb AW317381 AW317381 sg48f11.y1 Gm-c1025 Glycine max cDNA clone...	38	0.041
	emb AI973796 AI973796 sd10d10.y1 Gm-c1020 Glycine max cDNA clone...	37	0.078
	emb AW704342 AW704342 sk18b05.y1 Gm-c1028 Glycine max cDNA clone...	36	0.15
45	gb U13736 PSU13736 Pisum sativum Alaska calmodulin-like protein ...	35	0.20
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emb|AW145395|AW145395 gal9g01.y1 Moss EST library PPU Physcomitr... 33 1.4  
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5 gb|U25841|YSCP9677 Saccharomyces cerevisiae chromosome XVI cosmi... 32 2.6  
emb|AL354107|L2187X Leishmania major Friedlin cosmid L2187 t3Hyg... 31 3.5  
emb|Y10156|BNMYAP12 B.napus for myrosinase-associated protein, c... 31 3.5  
emb|AA901634|AA901634 NCM7H7T7 Mycelial Neurospora crassa cDNA c... 31 3.5  
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10 emb|AL109820|SPAC1952 S.pombe chromosome I cosmid c1952. 31 4.8  
emb|AV388698|AV388698 AV388698 Chlamydomonas reinhardtii C9 Chla... 31 4.8  
emb|AQ852174|AQ852174 LMAJFV1\_lm62c09.x1 Leishmania major FV1 ra... 31 4.8  
emb|AW772887|AW772887 925001C07.y1 C. reinhardtii CC-2290, norma... 31 4.8  
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emb|AW348772|AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3... 222 3e-  
35 57  
gb|BE057559|BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ... 210 1e-53  
emb|AW133238|AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone... 200 8e-51  
emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 190 9e-48  
emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 190 9e-48  
40 emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell-U... 189 2e-47  
emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47  
emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47  
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45 emb|AW832123|AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone... 178 3e-44  
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50 emb|AW153022|AW153022 se33h12.y1 Gm-c1015 Glycine max cDNA clone... 158 6e-38  
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55 gb|BE024006|BE024006 sm95c09.y1 Gm-c1015 Glycine max cDNA clone ... 122 2e-27  
gb|T14912|T14912 crs394 lambdaZAPST Ricinus communis cDNA clone ... 72 3e-27  
emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 119 2e-26  
emb|AW030966|AW030966 EST274273 tomato callus, TAMU Lycopersicon... 96 1e-25  
emb|AI938035|AI938035 sc40e07.x1 Gm-c1014 Glycine max cDNA clone... 116 3e-25  
60 emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 111 7e-24  
emb|AI938013|AI938013 sc40a07.x1 Gm-c1014 Glycine max cDNA clone... 110 1e-23

	emb AI776842 AI776842 EST257942 tomato resistant, Cornell Lycopersicon...	110	2e-23
	emb AA556663 AA556663 518 Loblolly pine CA Pinus taeda cDNA clon...	61	2e-20
	emb AI736542 AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone...	68	2e-17
	emb AI899328 AI899328 EST268771 tomato ovary, TAMU Lycopersicon ...	82	6e-15
5	gb BE021003 BE021003 sm54e07.y1 Gm-c1028 Glycine max cDNA clone ...	55	1e-12
	emb AW217201 AW217201 EST295915 tomato callus, TAMU Lycopersicon...	73	2e-12
	emb AI443600 AI443600 sa42b08.y1 Gm-c1004 Glycine max cDNA clone...	72	5e-12
	gb BE123900 BE123900 EST394025 DSIL Medicago truncatula cDNA clo...	58	7e-08
	gb BE022589 BE022589 sm86h09.y1 Gm-c1015 Glycine max cDNA clone ...	57	2e-07
10	gb BE022911 BE022911 sm89a12.y1 Gm-c1015 Glycine max cDNA clone ...	55	6e-07
	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone...	52	6e-06
	emb AW185963 AW185963 se61h02.y1 Gm-c1019 Glycine max cDNA clone...	52	6e-06
	emb AW153055 AW153055 se34d02.y1 Gm-c1015 Glycine max cDNA clone...	45	7e-04
	emb AI727849 AI727849 BNLGH9260 Six-day Cotton fiber Gossypium ...	39	0.056
15	emb AI965877 AI965877 sc79a11.y1 Gm-c1018 Glycine max cDNA clone...	30	0.082
	emb AF157837 AF157837 Trypanosoma cruzi putative 90 kDa surface ...	35	0.52
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai...	35	0.98
	emb AL112108 CNS019UC Botrytis cinerea strain T4 cDNA library un...	34	1.4
	emb AF101023 AF101023 Picea abies clone PAA12E3 family 2 repetit...	34	1.4
20	emb AA520766 AA520766 TgESTzz67g11.r1 TgME49 invivo Bradyzoite c...	34	1.4
	emb AA519752 AA519752 TgESTzz28f05.r1 TgME49 invivo Bradyzoite c...	34	1.4
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	emb AI069155 AI069155 mgae0005dA02f Magnaporthe grisea Appressor...	27	7.0

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5 emb|AF206700|AF206700 Neurospora crassa heterokaryon incompatibi... 31 9.1  
emb|AW621293|AW621293 EST312091 tomato root during/after fruit s... 31 9.1  
dbj|D15051|BLYIDS2NK Hordeum vulgare gene for ids2, complete cds. 31 9.1  
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10 emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 9.1

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15 (777 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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Score E  
Sequences producing significant alignments: (bits) Value

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emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 190 9e-48  
emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 189 2e-47

35 emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47  
emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47  
emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47  
emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycop... 133 2e-44  
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emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 177 9e-44  
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	emb AC004157 AC004157 Plasmodium falciparum chromosome 12 clone ...	31	5.2
	emb AE001376 AE001376 Plasmodium falciparum chromosome 2, sectio...	31	5.2
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60	emb AQ949411 AQ949411 Sheared DNA-38N10.TF Sheared DNA Trypanoso...	31	5.2



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 (375 letters)

Database: plantfungal  
 10 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E  
 15 Sequences producing significant alignments: (bits) Value

emb|AW685341|AW685341 NF026D08NR1F1000 Nodulated root Medicago t... 162 1e-39  
 gb|BE124622|BE124622 EST393657 GVN Medicago truncatula cDNA clon... 162 1e-39  
 emb|AI943438|AI943438 MF02E10 MF Mesembryanthemum crystallinum c... 158 2e-38  
 20 gb|BE033541|BE033541 MF02E10 MF Mesembryanthemum crystallinum cD... 158 2e-38  
 emb|AW667752|AW667752 GA\_Ea0010I06 Gossypium arboreum 7-10 dpa ... 155 1e-37  
 emb|AW747419|AW747419 WS1\_68\_E10.b1\_A002 Water-stressed 1 (WS1) ... 155 2e-37  
 emb|AW981480|AW981480 EST392633 DSIL Medicago truncatula cDNA cl... 154 4e-37  
 emb|AW441269|AW441269 EST310665 tomato fruit red ripe, TAMU Lyco... 153 5e-37  
 25 emb|AW223703|AW223703 EST300514 tomato fruit red ripe, TAMU Lyco... 153 5e-37  
 emb|AW034892|AW034892 EST279121 tomato callus, TAMU Lycopersicon... 153 5e-37  
 emb|AW224013|AW224013 EST300824 tomato fruit red ripe, TAMU Lyco... 153 5e-37  
 emb|AW907232|AW907232 EST343355 potato stolon, Cornell Universit... 153 7e-37  
 emb|AW747501|AW747501 WS1\_68\_E10.g1\_A002 Water-stressed 1 (WS1) ... 152 9e-37  
 30 emb|AW730496|AW730496 GA\_Ea0026O23 Gossypium arboreum 7-10 dpa ... 152 9e-37  
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 emb|AI960575|AI960575 sc86c01.y1 Gm-cl018 Glycine max cDNA clone... 151 2e-36  
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 emb|AI166395|AI166395 xylem.est.231 Poplar xylem Lambda ZAPII li... 150 5e-36  
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 emb|AW738874|AW738874 gb03e09.y1 Moss EST library PPN Physcomitr... 99 2e-20  
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 50 emb|AL049558|SPBC216 S.pombe chromosome II cosmid c216. 67 2e-19  
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 emb|AW617209|AW617209 EST323620 L. hirsutum trichome, Cornell Un... 90 5e-18  
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 60 emb|AW220746|AW220746 EST297215 tomato fruit mature green, TAMU ... 90 5e-18  
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 emb|AI026521|AI026521 TENU0733 T. cruzi epimastigote normalized ... 73 1e-16  
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 gb|T36700|T36700 EST101687 S. cerevisiae strain X2180-1A Sacchar... 79 1e-14  
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 emb|AW739119|AW739119 gb26a12.y1 Moss EST library PPN Physcomitr... 79 1e-14  
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 10 gb|N81594|N81594 TgESTzy60e01.r1 TgRH Tachyzoite cDNA Toxoplasma... 55 1e-12  
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 15 emb|AW351206|AW351206 GM210011A20E12R Gm-r1021 Glycine max cDNA ... 61 5e-09  
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 20 emb|AW931744|AW931744 EST357587 tomato fruit mature green, TAMU ... 46 9e-05  
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(844 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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15	emb AW561007 AW561007 EST316055 DSIR Medicago truncatula cDNA cl...	287	8e-77
	emb AI489189 AI489189 EST247528 tomato ovary, TAMU Lycopersicon ...	273	1e-72
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	emb AW625207 AW625207 EST319114 tomato radicle, 5 d post-imbibit...	258	5e-68
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25	emb AA495616 AA495616 c425 Zhou and Ragan 1993 Gracilaria gracil...	118	3e-52
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35	emb Z48639 SC9920 S.cerevisiae chromosome XIII cosmid 9920.	67	2e-34
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	emb Z28301 SCYKR076W S.cerevisiae chromosome XI reading frame OR...	77	5e-32
	emb AW931289 AW931289 EST357132 tomato fruit mature green, TAMU ...	123	1e-27
	emb X85807 SCCVIIRA S.cerevisiae chromosome VII 27kbp right arm ...	51	2e-23
40	emb Z72939 SCYGR154C S.cerevisiae chromosome VII reading frame O...	51	2e-23
	emb AA788015 AA788015 r4b01a1.r1 Aspergillus nidulans 24hr asexu...	90	1e-22
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	emb AW686971 AW686971 NF004E10RT1F1082 Developing root Medicago ...	104	1e-21
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45	emb AI327824 AI327824 j0c06a1.r1 Aspergillus nidulans 24hr asexu...	77	1e-17
	emb AI212279 AI212279 x1e09a1.r1 Aspergillus nidulans 24hr asexu...	90	2e-17
	emb AI165879 AI165879 B002P45U Hybrid aspen plasmid library Popu...	84	2e-15
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	emb AW704348 AW704348 sk18b11.y1 Gm-c1028 Glycine max cDNA clone...	77	2e-13
	emb AW221318 AW221318 EST297787 tomato fruit mature green, TAMU ...	68	9e-11
	emb AQ875035 AQ875035 V120D9 mTn-3xHA/lacZ Insertion Library, st...	67	2e-10
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	emb AA787149 AA787149 m8a03a1.fl Aspergillus nidulans 24hr asexu...	46	5e-04
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	emb X88851 SCESTGENE	S.cerevisiae DNA for hypothetical proteins a...	34	1.5
	emb AF043087 AF043087	Hordeum vulgare dehydrin 1 (dhn1) gene, co...	34	1.5
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	emb AF197947 AF197947	Glycine max receptor protein kinase-like p...	160	3e-83
55	emb AF197946 AF197946	Glycine max receptor protein kinase-like p...	154	8e-81
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	emb A67434 A67434	Sequence 7 from Patent WO9743429.	143	2e-72
	emb AW650851 AW650851	EST329305 tomato germinating seedlings, TA...	123	4e-72
60	emb AF053995 AF053995	Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ...	144	2e-71
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	emb A57130 A57130 Sequence 1 from Patent WO9531564.	150 4e-70
5	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	150 4e-70
	emb A57133 A57133 Sequence 4 from Patent WO9531564.	150 4e-70
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10	emb A67432 A67432 Sequence 5 from Patent WO9743429.	144 7e-60
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25	emb AW621923 AW621923 EST312721 tomato root during/after fruit s...	94 2e-43
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	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	85 2e-42
	emb AI484701 AI484701 EST242962 tomato ovary, TAMU Lycopersicon ...	89 2e-41
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	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon ...	85 4e-40
	emb AV427160 AV427160 AV427160 Lotus japonicus young plants (two...	117 4e-39
45	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	84 4e-39
	emb AA557073 AA557073 915 Loblolly pine N Pinus taeda cDNA clone...	96 4e-39
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	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	85 3e-38
50	emb AW727470 AW727470 GA_Ea0012H16 Gossypium arboreum 7-10 dpa ...	93 3e-38
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55	emb AW040672 AW040672 EST283536 tomato mixed elicitor, BTI Lycop...	102 4e-38
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5 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 91 6e-37  
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10 emb|AW185015|AW185015 se85e10.y1 Gm-c1023 Glycine max cDNA clone... 100 2e-36  
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15 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 85 8e-36  
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35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi)  
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40 Database: plantfungal  
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Sequences producing significant alignments: (bits) Value

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50 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 510 0.0  
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emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 504 0.0  
emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 501 0.0  
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55 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 489 0.0  
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emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 483 0.0  
gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 461 0.0  
60 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 458 0.0  
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5	emb Y12530 BOARLKGEN B.oleraceae gene encoding serine/threonine ...	652	0.0
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	emb AB024417 AB024417 Brassica oleracea SLG13 gene, partial cds.	498	e-178
15	dbj D85206 D85206 Brassica oleracea DNA for S blycoprotein, part...	406	e-177
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25	emb X55274 BCSLG8 B.campestris SLG-8 gene for S-locus glycoprotein.	482	e-175
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30	emb AB009681 AB009681 Raphanus sativus SLG(S5) gene for S glycop...	406	e-173
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35	dbj D85227 D85227 Brassica campestris DNA for S glycoprotein, pa...	293	e-172
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40	dbj D85216 D85216 Brassica campestris DNA for S glycoprotein, pa...	409	e-171
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	emb AB009684 AB009684 Raphanus sativus SLG(S7) gene for S glycop...	397	e-171
	emb X79432 BOSRK3 B.oleracea SRK3 gene.	396	e-171
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	emb Z30211 BOSRK29G B.oleracea (alboglaba) srk29 gene.	288	e-169
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55	emb Z21608 BNESLOGPA B.napus mRNA for endogenous S-locus glycopr...	477	e-168
	gb L10736 BNASLGGA Brassica napus S-locus related glycoprotein (...)	477	e-168
	dbj D85222 D85222 Brassica campestris DNA for S glycoprotein, pa...	243	e-166
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60	dbj D85212 D85212 Brassica oleracea DNA for S glycoprotein, part...	244	e-164
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 5 emb|Z19548|BNSLGPII *B. napus* mRNA for S-locus glycoprotein type II. 286 e-163  
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 emb|AJ245480|BNA245480 *Brassica napus* slg gene for S-locus glyco... 380 e-160  
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 20 emb|Y12321|BOY12321 *Brassica oleracea* SLG-Sc and SLA-Sc genes an... 285 e-149  
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 emb|X57673|BOSLR2RNA *B. oleracea* RNA for S-locus-related glycopr... 167 e-149  
 emb|AB009873|AB009873 *Cheiranthus cheiri* gene for SLR1, partial ... 163 e-147  
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 25 emb|X52089|BOSLRG *Brassica* gene for S locus related glycoprotein. 272 e-143

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 (2673 letters)

Database: plantfungal  
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| emb AF053998 AF053998 <i>Lycopersicon esculentum</i> Hcr2-5D (Hcr2-5D) ...    | 148    | 4e-74 |
| 45 emb A67434 A67434 Sequence 7 from Patent WO9743429.                        | 148    | 4e-74 |
| emb AF053993 AF053993 <i>Lycopersicon esculentum</i> disease resistance...    | 148    | 4e-74 |
| emb A67429 A67429 Sequence 2 from Patent WO9743429.                           | 148    | 4e-74 |
| emb A67428 A67428 Sequence 1 from Patent WO9743429.                           | 148    | 4e-74 |
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| 50 emb AF053997 AF053997 <i>Lycopersicon esculentum</i> Hcr2-5B (Hcr2-5B) ... | 146    | 1e-72 |
| emb A67432 A67432 Sequence 5 from Patent WO9743429.                           | 146    | 1e-72 |
| gb U42445 U42445 <i>Lycopersicon pimpinellifolium</i> leucine rich repe...    | 150    | 3e-71 |
| emb A57133 A57133 Sequence 4 from Patent WO9531564.                           | 150    | 3e-71 |
| gb U42444 U42444 <i>Lycopersicon pimpinellifolium</i> leucine rich repe...    | 150    | 8e-71 |
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| emb AB029327 AB029327 <i>Nicotiana tabacum</i> mRNA for elicitor-induci...    | 97     | 4e-65 |
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| emb AF119040 AF119040 <i>Lycopersicon esculentum</i> haplotype Northern...    | 143    | 3e-36 |
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| 60 emb AF119041 AF119041 <i>Lycopersicon esculentum</i> haplotype Southern... | 139    | 2e-33 |
| emb AJ002235 LHJ002235 <i>Lycopersicon hirsutum</i> Cf-4 resistance gen...    | 139    | 3e-33 |

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10 emb|X81370|TAAWJL236 *T.aestivum* (subclone pAWJL236) AWJL236 gene. 115 8e-27  
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15 emb|X81367|TAAWJL172 *T.aestivum* (subclone pAWJL172) AWJL172 gene. 99 7e-23  
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30 emb|AW032163|AW032163 EST275617 tomato callus, TAMU *Lycopersicon*... 64 1e-18  
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emb|AW650508|AW650508 EST328962 tomato germinating seedlings, TA... 91 1e-18  
emb|AI488023|AI488023 EST246345 tomato ovary, TAMU *Lycopersicon* ... 91 1e-18  
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35 emb|AW307311|AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone... 66 2e-18  
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emb|AI727073|AI727073 BNLGHi7256 Six-day Cotton fiber *Gossypium* ... 95 2e-18  
emb|AW306675|AW306675 se53h08.y1 Gm-c1017 Glycine max cDNA clone... 95 3e-18  
40 emb|X79130|TSLRRR *Triticum* sp. (pAWJL3) leucine rich repeat regi... 84 4e-18  
emb|AW031498|AW031498 EST274952 tomato callus, TAMU *Lycopersicon*... 94 5e-18  
emb|AW775087|AW775087 EST334238 KV3 *Medicago truncatula* cDNA clo... 94 6e-18  
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45 emb|AI895893|AI895893 EST265336 tomato callus, TAMU *Lycopersicon*... 61 9e-18  
emb|AW647847|AW647847 EST326301 tomato germinating seedlings, TA... 91 1e-17  
emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 92 2e-17  
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50 emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 91 4e-17  
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55 emb|AI896313|AI896313 EST265756 tomato callus, TAMU *Lycopersicon*... 60 1e-16  
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emb|AW980804|AW980804 EST391957 GVN *Medicago truncatula* cDNA clo... 69 2e-16  
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60 emb|AW127035|AW127035 ga20c02.y1 Moss EST library PPU *Physcomitr*... 88 4e-16  
emb|AI895669|AI895669 EST265112 tomato callus, TAMU *Lycopersicon*... 88 4e-16



emb|AW618685|AW618685 EST320671 *L. pennellii* trichome, Cornell U... 88 4e-16  
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 emb|AI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 87 5e-16  
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 5 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem *Medicago* ... 78 6e-16  
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 emb|AW761367|AW761367 sl66e07.y1 Gm-c1027 *Glycine max* cDNA clone... 86 1e-15  
 emb|AW649208|AW649208 EST327662 tomato germinating seedlings, TA... 86 1e-15  
 10 emb|AV428126|AV428126 AV428126 *Lotus japonicus* young plants (two... 85 2e-15  
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 emb|AI352869|AI352869 MB70-4A PZ204.BNlib *Brassica napus* cDNA cl... 85 2e-15  
 emb|AA661049|AA661049 00946 MtrHE *Medicago truncatula* cDNA 5' si... 85 2e-15  
 emb|AW455303|AW455303 EST311841 tomato root during/after fruit s... 85 3e-15  
 15 emb|AW869870|AW869870 NXNV\_122\_E02\_F Nsf Xylem Normal wood Verti... 85 3e-15  
 emb|AW398651|AW398651 EST309151 *L. pennellii* trichome, Cornell U... 84 4e-15  
 emb|AW398661|AW398661 EST309161 *L. pennellii* trichome, Cornell U... 84 4e-15  
 emb|AF049920|AF049920 *Petunia x hybrida* PGPS/D4 (PGPS/D4) mRNA, ... 84 4e-15  
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 20 emb|AW618879|AW618879 EST320865 *L. pennellii* trichome, Cornell U... 62 4e-15  
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Database: plantfungal  
 30 661,018 sequences; 426,114,510 total letters

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35	Sequences producing significant alignments:	(bits) Value
	emb X82273 BOACCS <i>B. oleracea</i> mRNA for ACC synthase.	986 0.0
	emb X72676 BJMACC <i>B. juncea</i> mRNA for 1-Aminocyclopropane-1-carbo...	875 0.0
	emb AF057563 AF057563 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-...	765 0.0
40	emb AJ005002 NTAJ5002 <i>Nicotiana tabacum</i> mRNA for 1-aminocyclopro...	761 0.0
	emb AB034992 AB034992 <i>Malus domestica</i> MdACS-5A mRNA for 1-aminoc...	754 0.0
	emb AB034993 AB034993 <i>Malus domestica</i> MdACS-5B mRNA for 1-aminoc...	755 0.0
	gb U72389 LEU72389 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1...	756 0.0
	gb U72390 LEU72390 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1...	753 0.0
45	emb AB033503 AB033503 <i>Populus euramericana</i> peacs-2 mRNA for 1-am...	741 0.0
	gb U68216 CPU68216 <i>Carica papaya</i> ACC synthase mRNA, complete cds.	461 0.0
	emb AF061605 AF061605 <i>Nicotiana glutinosa</i> ACC synthase mRNA, com...	742 0.0
	emb AB013100 AB013100 <i>Lycopersicon esculentum</i> LE-ACS6 mRNA for 1...	741 0.0
	emb AJ012551 CSI012551 <i>Citrus sinensis</i> mRNA for ACC synthase.	449 0.0
50	emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy...	739 0.0
	emb AB033502 AB033502 <i>Populus euphratica</i> peacs-1 mRNA for 1-amin...	620 0.0
	gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca...	455 0.0
	emb Z11613 VRACCSYNM <i>V. radiata</i> mRNA for ACC synthase.	456 0.0
	emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone...	455 0.0
55	emb X67100 GMCACCS1 <i>G. max</i> mRNA for ACC synthase.	454 0.0
	emb Z18952 DCAMCRBSY <i>D. caryophyllus</i> mRNA for 1-aminocyclopropane...	716 0.0
	emb AJ012696 CSI012696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC...	449 0.0
	emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac...	452 0.0
	emb Z18953 PHAMCRBSY <i>P. hybrida</i> mRNA for 1-aminocyclopropane 1-ca...	450 0.0
60	emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth...	451 0.0
	emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	711 0.0

	emb AF016459 AF016459 <i>Pisum sativum</i> 1-aminocyclopropane-1-carbox...	445	0.0
	emb AF109927 AF109927 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	707	0.0
	dbj D30805 CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy...	705	0.0
	emb AB021906 AB021906 <i>Musa acuminata</i> MA-ACS1 mRNA for ACC syntha...	703	0.0
5	emb AB006803 AB006803 <i>Cucumis sativus</i> CS-ACS1 mRNA for ACC synth...	703	0.0
	emb AF129508 AF129508 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	702	0.0
	emb X65982 NTXACCSYN <i>N.tabacum</i> mRNA for 1-aminocyclopropane-1-ca...	438	0.0
	emb AB031026 AB031026 <i>Prunus mume</i> PM-ACS1 mRNA for ACC synthase,...	434	0.0
	emb AB015625 AB015625 <i>Pyrus pyrifolia</i> pPPACS3 mRNA for 1-aminocy...	418	0.0
10	dbj D01032 CUCACCW <i>Cucurbita maxima</i> mRNA for 1-aminocyclopropane...	695	0.0
	dbj E03724 E03724 cDNA encoding detriment induced type 1-aminocy...	695	0.0
	gb M58323 CUCACCSYN <i>Cucurbita pepo</i> 1-aminocyclopropane-1-carboxy...	692	0.0
	emb Y11357 CP1A1CS <i>C.papaya</i> mRNA for 1-aminocyclopropane-1-carbo...	430	0.0
	emb X62536 LEACC <i>L.esculentum</i> mRNA for ACC synthase.	327	0.0
15	emb AF057562 AF057562 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-...	437	0.0
	emb X59145 LEACC2MR <i>Lycopersicon esculentum</i> LE-ASCC2 mRNA (ptACC...	326	0.0
	gb U79999 MAU79999 <i>Musa acuminata</i> ACC synthase (acs3) mRNA, comp...	687	0.0
	emb Y15739 MAACSYNTH <i>Musa acuminata</i> mRNA for 1-aminocyclopropane...	687	0.0
	gb M34289 TOMACS <i>Tomato</i> 1-aminocyclopropane-1-carboxylate syntha...	327	0.0
20	gb M63490 TOMACCS <i>Tomato</i> 1-aminocyclopropane-1-carboxylate synth...	682	0.0
	emb X59146 LEACC4MR <i>Lycopersicon esculentum</i> LE-ACC4 mRNA (ptACC4...	681	0.0
	gb U17229 PHU17229 <i>Pelargonium hortorum</i> clone pGAC-1 1-aminocycl...	438	0.0
	gb U17231 PHU17231 <i>Pelargonium hortorum</i> clone pGAC-2 1-aminocycl...	423	0.0
	emb AF038945 AF038945 <i>Rumex palustris</i> 1-aminocyclopropane-1-carb...	407	0.0
25	gb L20634 POTACCSYN <i>Solanum tuberosum</i> 1-aminocyclopropane-1-carb...	403	0.0
	emb AJ276295 CSI276295 <i>Citrus sinensis</i> partial mRNA for ACC synt...	446	0.0
	emb AF239987 AF239987 <i>Prunus persica</i> ACC synthase ACS1 mRNA, par...	662	0.0
	emb AF178076 AF178076 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	395	0.0
	emb X82265 CAACC1 <i>C.annuum</i> mRNA for 1-aminocyclopropane-1-carboxyl...	639	0.0
30	gb U70842 STU70842 <i>Solanum tuberosum</i> 1-aminocyclopropane-1-carbo...	637	0.0
	emb AF144746 AF144746 <i>Solanum melongena</i> 1-aminocyclopropane-1-ca...	636	0.0
	emb AJ012577 CPA012577 <i>Carica papaya</i> mRNA for 1-aminocyclopropan...	387	e-180
	gb U73815 MDU73815 <i>Malus domestica</i> ACC synthase (MdACS-2) mRNA, ...	623	e-178
	dbj D37937 D37937 <i>Cucumis melo</i> mRNA for 1-aminocyclopropane-1-ca...	380	e-177
35	emb Z11562 VRACCSYN <i>V.radiata</i> mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814 <i>Antirrhinum majus</i> ACC synthase 1 (ACS1) mR...	605	e-172
	emb AF178077 AF178077 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	316	e-172
	emb AF239989 AF239989 <i>Prunus persica</i> ACC synthase ACS25 mRNA, pa...	597	e-170
40	gb U22523 MIU22523 <i>Mangifera indica</i> 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS <i>D.caryophyllus</i> mRNA for 1-aminocyclopropane-1-...	396	e-168
	gb L31347 MAUACCSYN <i>Malus domestica</i> 1-aminocyclopropane-1-carbox...	378	e-168
	emb AB015624 AB015624 <i>Pyrus pyrifolia</i> mRNA for 1-aminocyclopropan...	377	e-168
	emb AF049137 AF049137 <i>Dianthus caryophyllus</i> 1-aminocyclopropane-...	338	e-167
45	emb AF170705 AF170705 <i>Mangifera indica</i> 1-aminocyclopropane-1-car...	290	e-167
	gb U03294 MSU03294 <i>Malus sylvestris</i> 1-aminocyclopropane-1-carbox...	372	e-166
	emb Z77854 PSPACS1 <i>Phalaenopsis</i> species mRNA for 1-aminocyclopro...	513	e-166
	emb AJ277160 CPA277160 <i>Carica papaya</i> partial paccs1A gene for 1-...	266	e-165
	gb U73816 MDU73816 <i>Malus domestica</i> ACC synthase (MdACS-3) mRNA, ...	505	e-164
50	emb AB007449 AB007449 <i>Actinidia deliciosa</i> mRNA for 1-aminocyclop...	355	e-164
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	dbj D01033 CUCACCA <i>Cucurbita maxima</i> mRNA for 1-aminocyclopropane...	366	e-164
	emb X87112 PCPCACS1G <i>P.communis</i> mRNA for 1-aminocyclopropane-1-c...	363	e-163
	gb U17972 LEU17972 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1...	362	e-163
55	emb AB015495 AB015495 <i>Passiflora edulis</i> PE-ACS2 mRNA for ACC syn...	368	e-162
	emb AB006805 AB006805 <i>Cucumis sativus</i> CS-ACS3 mRNA for ACC synth...	360	e-160
	emb AB000679 AB000679 <i>Vigna radiata</i> mRNA for 1-aminocyclopropane...	365	e-158
	gb U34987 VRU34987 <i>Vigna radiata</i> 1-aminocyclopropane-1-carboxyli...	325	e-157
	gb M66619 DINCARACC <i>D.caryophyllus</i> 1-aminocyclopropane-1-carboxy...	496	e-156
60	gb U34986 VRU34986 <i>Vigna radiata</i> 1-aminocyclopropane-1-carboxyli...	362	e-156
	gb U64031 DCU64031 <i>Dendrobium crumenatum</i> ACC synthase gene, comp...	259	e-154

5 emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 355 e-154  
 emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 237 e-152  
 emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 232 e-152  
 emb|AF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 236 e-150  
 gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 234 e-150  
 gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149  
 gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149  
 emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 232 e-146  
 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). 376 e-145  
 10 gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-144  
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 emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141  
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 emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138  
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 http://www3.ncbi.nlm.nih.gov/htbin-  
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 (1950 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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30	gb U79958 PSU79958 Pisum sativum BP-80 vacuolar sorting receptor... 630 0.0		
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35	emb AW309187 AW309187 sg05d06.y1 Gm-c1019 Glycine max cDNA clone... 326 e-108		
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	emb AW932529 AW932529 EST358372 tomato fruit mature green, TAMU ... 303 1e-83		
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45	emb AW747297 AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ... 286 4e-76		
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	emb AW397829 AW397829 sg68h03.y1 Gm-c1007 Glycine max cDNA clone... 225 1e-57		
55	emb AW289687 AW289687 NXNV004E04F-Nsf Xylem Normal-wood Vertical... 182 7e-55		
	emb AW690002 AW690002 NF026G04ST1F1000 Developing stem Medicago ... 143 4e-54		
	emb AA660289 AA660289 00158 MtrHE Medicago truncatula cDNA 5', m... 138 2e-53		
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	emb AV428420 AV428420 AV428420 Lotus japonicus young plants (two... 134 1e-51		
60	emb AW623959 AW623959 EST321904 tomato flower buds 3-8 mm, Corne... 74 1e-49		
	emb AW568619 AW568619 si60a11.y1 Gm-r1030 Glycine max cDNA clone... 165 2e-47		



- emb|AI967865|AI967865 Ljimpest14-100-f3 Ljirnp Lambda HybriZap ... 180 5e-47  
emb|AW309191|AW309191 sg05d10.y1 Gm-c1019 Glycine max cDNA clone... 105 2e-46  
emb|AW398931|AW398931 EST309431 L. pennellii trichome, Cornell U... 132 2e-45  
5 emb|AW737369|AW737369 EST338892 tomato flower buds, anthesis, Co... 182 6e-45  
emb|AW096632|AW096632 EST289812 tomato mixed elicitor, BTI Lycop... 81 7e-45  
emb|AF209910|AF209910 Prunus dulcis vacuolar sorting receptor pr... 76 8e-44  
emb|AW056624|AW056624 ST53G07 Pine TriplEx shoot tip library Pin... 178 1e-43  
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10 emb|AW290400|AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical... 170 4e-41  
gb|BE125908|BE125908 DG1\_59\_E01.b1\_A002 Dark Grown 1 (DG1) Sorgh... 164 2e-39  
emb|AI161766|AI161766 A006P54U Hybrid aspen plasmid library Popu... 76 3e-39  
emb|AI162330|AI162330 A016P01U Hybrid aspen plasmid library Popu... 130 2e-37  
gb|BE049814|BE049814 NXNV\_144\_F04\_F Nsf Xylem Normal wood Vertic... 156 4e-37  
emb|AW508719|AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone... 155 8e-37  
15 gb|L38113|L38113 BNAF0628E Mustard flower buds Brassica rapa cDN... 153 4e-36  
emb|AW616461|AW616461 EST322872 L. hirsutum trichome, Cornell Un... 102 4e-33  
emb|AA660955|AA660955 00852 MtRHE Medicago truncatula cDNA 5' si... 72 4e-31  
emb|AW774190|AW774190 EST333273 KV3 Medicago truncatula cDNA clo... 134 2e-30  
emb|AW201441|AW201441 sf03b09.y1 Gm-c1027 Glycine max cDNA clone... 73 5e-30  
20 emb|AW906386|AW906386 EST342508 potato stolon, Cornell Universit... 78 2e-27  
emb|AW126100|AW126100 N100297e rootphos(-) Medicago truncatula c... 73 9e-27  
emb|AW620693|AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone... 77 1e-26  
emb|AW317388|AW317388 sg48g10.y1 Gm-c1025 Glycine max cDNA clone... 72 2e-26  
emb|AW706755|AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone... 117 3e-25  
25 emb|AW125944|AW125944 N100139e rootphos(-) Medicago truncatula c... 71 1e-23  
emb|AW932524|AW932524 EST358367 tomato fruit mature green, TAMU ... 69 1e-22  
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30 emb|AW119909|AW119909 sd54d08.y1 Gm-c1016 Glycine max cDNA clone... 88 2e-16  
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35 emb|AW760128|AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone... 66 8e-14  
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emb|AW256398|AW256398 EST304465 KV2 Medicago truncatula cDNA clo... 72 7e-13  
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40 emb|AW747372|AW747372 WS1\_67\_G06.g1\_A002 Water-stressed 1 (WS1) ... 64 4e-09  
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45 gb|B67199|B67199 CpG0015B CpIOWAgDNA1 Cryptosporidium parvum gen... 38 0.31  
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emb|AW626172|AW626172 EST320079 tomato radicle, 5 d post-imbibit... 37 0.42  
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50 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 35 1.5  
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60 emb|AZ216543|AZ216543 Sheared DNA-116G5.TR Sheared DNA Trypanoso... 35 2.8  
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 5 emb|AA749476|AA749476 L30-23M13T3 Ice plant Lambda Uni-Zap XR ex... 31 3.3  
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 emb|AI822187|AI822187 L0-664T3 Ice plant Lambda Uni-Zap XR expre... 31 3.3  
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 30 emb|AW267789|AW267789 EST305917 *DSIR Medicago truncatula* cDNA cl... 169 4e-81  
 emb|AW329160|AW329160 N200369e rootphos(-) *Medicago truncatula* c... 224 2e-80  
 emb|AW696127|AW696127 NF102F09ST1F1078 Developing stem *Medicago* ... 298 4e-80  
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 35 emb|AW399617|AW399617 EST310117 *L. pennellii* trichome, Cornell U... 281 5e-75  
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 emb|AW756208|AW756208 sl17d10.y1 *Gm-c1036 Glycine max* cDNA clone... 264 5e-70  
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 40 emb|AJ223291|SRAJ3291 *Sesbania rostrata* mRNA for putative chalco... 115 2e-64  
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 45 gb|U13925|MSU13925 *Medicago sativa* Apollo clone CHR7 chalcone re... 117 6e-61  
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 50 gb|U13924|MSU13924 *Medicago sativa* Apollo clone CHR12 chalcone r... 114 8e-60  
 emb|X55730|GMREDUC *Soybean* mRNA for reductase involved in deoxyc... 111 1e-59  
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 60 emb|AB002106|AB002106 *Candida tropicalis* DNA for D-xylose reduct... 124 2e-57  
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- dbj|D83718|GYCPKR *Glycyrrhiza echinata* mRNA for polyketide reduc... 111 6e-57  
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 dbj|D86559|D86559 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56  
 dbj|D86558|D86558 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56  
 5 emb|AF074484|AF074484 *Candida tenuis* xylose reductase (xylr) gen... 127 2e-54  
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 emb|AW730093|AW730093 GA\_\_Ea0027M16 *Gossypium arboreum* 7-10 dpa ... 128 1e-51  
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 10 gb|U83687|AGU83687 *Apium graveolens* NADPH-dependent mannose 6-ph... 80 2e-51  
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 emb|AF219625|AF219625 *Aspergillus niger* D-xylose reductase (xylA... 86 6e-49  
 15 emb|AF108435|AF108435 *Papaver somniferum* NADPH-dependent codeino... 85 1e-48  
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 20 emb|AL021815|SPBC8E4 *S.pombe* chromosome I cosmid c8E4. 84 3e-47  
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 25 emb|AL110661|CNS018Q6 *Botrytis cinerea* strain T4 cDNA library un... 108 2e-45  
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 30 emb|X13228|SCGCY Yeast GCY gene (homologous to vertebrate eye le... 57 2e-44  
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 55 emb|AW728632|AW728632 GA\_\_Ea0017G17 *Gossypium arboreum* 7-10 dpa ... 80 3e-36  
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Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

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40	emb AW924990 AW924990 WS1_74_A05.b1_A002 Water-stressed 1 (WS1) ...	134	1e-30
	emb AW888070 AW888070 NXNV_126_H09_F Nsf Xylem Normal wood Verti...	134	1e-30
	emb AW694653 AW694653 NF078G03ST1F1023 Developing stem Medicago ...	108	2e-30
	emb AV425340 AV425340 AV425340 Lotus japonicus young plants (two...	132	5e-30
	emb AW030490 AW030490 EST273745 tomato callus, TAMU Lycopersicon...	132	7e-30
45	emb AW738715 AW738715 EST340142 tomato flower buds, anthesis, Co...	132	7e-30
	emb AW040512 AW040512 EST283472 tomato mixed elicitor, BTI Lycop...	131	1e-29
	emb AW780617 AW780617 sl73c03.y1 Gm-c1027 Glycine max cDNA clone...	131	1e-29
	emb AW287232 AW287232 LG1_268_C02.b1_A002 Light Grown 1 (LG1) So...	130	2e-29
	emb AV410940 AV410940 AV410940 Lotus japonicus young plants (two...	130	2e-29
50	emb AW286886 AW286886 LG1_222_F11.b1_A002 Light Grown 1 (LG1) So...	129	3e-29
	emb AW399232 AW399232 EST309732 L. pennellii trichome, Cornell U...	129	5e-29
	emb AW287673 AW287673 LG1_271_A05.b1_A002 Light Grown 1 (LG1) So...	129	5e-29
	emb AV412063 AV412063 AV412063 Lotus japonicus young plants (two...	128	7e-29
	emb AV421682 AV421682 AV421682 Lotus japonicus young plants (two...	128	7e-29
55	emb AW759175 AW759175 sl38a01.y1 Gm-c1027 Glycine max cDNA clone...	128	7e-29
	emb AW672543 AW672543 LG1_360_B12.b1_A002 Light Grown 1 (LG1) So...	128	7e-29
	emb AW596590 AW596590 sj14c04.y1 Gm-c1032 Glycine max cDNA clone...	128	9e-29
	emb AW694511 AW694511 NF077A11ST1F1084 Developing stem Medicago ...	128	9e-29
60	emb AV415908 AV415908 AV415908 Lotus japonicus young plants (two...	127	2e-28

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(834 letters)

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Database: plantfungal  
661,018 sequences; 426,114,510 total letters

Searching.....done

10

Score E

Sequences producing significant alignments: (bits) Value

15	gb U21848 BNU21848 Brassica napus chitinase class IV (LSC222) mR...	225	e-134
	emb X61488 BNCHITIN B.napus mRNA for chitinase.	156	7e-88
	gb U97521 VVU97521 Vitis vinifera class IV endochitinase (VvChi4...	173	3e-77
	gb U97522 VVU97522 Vitis vinifera class IV endochitinase (VvChi4...	174	2e-76
	emb X57187 PVCHITIN P.vulgaris mRNA for chitinase.	149	2e-74
	emb AF112966 AF112966 Triticum aestivum chitinase IV precursor (...)	157	5e-70
20	dbj D45181 D45181 Chenopodium amaranticolor mRNA for chitinase, ...	100	5e-67
	gb U52845 DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP...	114	7e-67
	gb U52846 DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP...	111	9e-66
	gb BE034166 BE034166 MG05H02 MG Mesembryanthemum crystallinum cD...	129	1e-65
	gb U52847 DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP...	110	8e-65
25	gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3...	111	2e-64
	gb BE034975 BE034975 ML07H10 ML Mesembryanthemum crystallinum cD...	125	2e-64
	gb BE034428 BE034428 MH04G02 MH Mesembryanthemum crystallinum cD...	123	2e-63
	gb BE034976 BE034976 ML07H11 ML Mesembryanthemum crystallinum cD...	120	6e-63
	dbj D45183 D45183 Chenopodium amaranticolor mRNA for chitinase, ...	96	1e-62
30	dbj D45184 D45184 Chenopodium amaranticolor mRNA for chitinase, ...	100	3e-62
	dbj D45182 D45182 Chenopodium amaranticolor mRNA for chitinase, ...	100	4e-60
	emb X75945 BVCH4RNA B.vulgaris Ch4 mRNA for chitinase.	92	6e-60
	emb A23392 A23392 B.vulgaris mRNA for chitinase 4 (B15).	92	6e-60
	emb X88803 VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p...	118	3e-59
35	emb AI897733 AI897733 EST267176 tomato ovary, TAMU Lycopersicon ...	110	1e-58
	gb BE034406 BE034406 MH04D10 MH Mesembryanthemum crystallinum cD...	105	2e-58
	gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds.	158	3e-58
	gb BE034497 BE034497 MH05H03 MH Mesembryanthemum crystallinum cD...	89	8e-58
	gb L42467 PIACHI Picea glauca chitinase (chi) mRNA, complete cds.	93	2e-57
40	emb AF090336 AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA...	166	2e-57
	emb AI897843 AI897843 EST267286 tomato ovary, TAMU Lycopersicon ...	103	1e-56
	emb AF112963 AF112963 Triticum aestivum chitinase II precursor (...)	149	9e-56
	gb BE035287 BE035287 MM04H04 MM Mesembryanthemum crystallinum cD...	162	4e-54
	emb AW680953 AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S...	178	3e-52
45	gb BE033502 BE033502 ME03F10-ME Mesembryanthemum crystallinum cD...	87	4e-50
	gb M94105 ALCCHITIN Allium sativum chitinase mRNA, 3' end.	100	6e-49
	emb AI898279 AI898279 EST267722 tomato ovary, TAMU Lycopersicon ...	83	1e-48
	gb U83592 MSU83592 Medicago sativa class I chitinase mRNA, compl...	109	1e-48
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50	emb AW030814 AW030814 EST274069 tomato callus, TAMU Lycopersicon...	83	3e-48
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55	emb AI485982 AI485982 EST244303 tomato ovary, TAMU Lycopersicon ...	83	1e-47
	emb AF061805 AF061805 Elaeagnus umbellata acidic chitinase mRNA,...	99	1e-47
	emb AW648023 AW648023 EST326477 tomato germinating seedlings, TA...	83	3e-47
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60	emb X15494 STCHITIN Potato endochitinase gene (EC 3.2.1.14).	95	6e-47
	emb X07130 STCHIT Solanum tuberosum mRNA for endochitinase (EC 3...	95	6e-47



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 emb|X88800|VURNACHII *V.unguiculata* mRNA for chitinase clase 1 (p... 105 1e-45  
 5 emb|AJ012821|CAR012821 *Cicer arietinum* mRNA for class I chitinase. 108 6e-45  
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 emb|Y10373|MTCHITIN1 *M.truncatula* mRNA for chitinase. 109 8e-45  
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 gb|M94106|ALCCHINTIA *Allium sativum* chitinase mRNA, 3' end. 102 3e-44  
 10 emb|AW746018|AW746018 WS1\_38\_H11.g1\_A002 Water-stressed 1 (WS1) ... 170 3e-44  
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 emb|AW746695|AW746695 WS1\_54\_E02.g1\_A002 Water-stressed 1 (WS1) ... 178 4e-44  
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 95 5e-44  
 gb|M15173|TOBECH Tobacco (*N.tabacum*) endochitinase mRNA, partial... 95 5e-44  
 15 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 105 1e-43  
 emb|Z54234|VVCHIT1MR *V.vinifera* mRNA for chitinase. 98 1e-43  
 gb|S44869|S44869 basic chitinase [*Nicotiana tabacum*=tobacco, cv ... 95 2e-43  
 emb|X16939|NTECHITR *Nicotiana tabacum* mRNA for endochitinase (EC... 95 2e-43  
 emb|X76041|TACHIG *T.aestivum* (Chinese spring) chi gene for endoc... 93 4e-43  
 20 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 97 6e-43  
 emb|Z46948|SNCHJET15 *S.nigra* mRNA for chitinase, pathogenesis-re... 104 2e-42  
 gb|U02605|STU02605 *Solanum tuberosum* chitinase (chtB1) mRNA, par... 95 3e-42  
 gb|U02606|STU02606 *Solanum tuberosum* chitinase (chtB2) mRNA, par... 95 4e-42  
 emb|Z46950|SNCHJET19 *S.nigra* mRNA chitinase class II, pathogenes... 104 6e-42  
 25 gb|U78888|GHU78888 *Gossypium hirsutum* class I endochitinase mRNA... 102 1e-41  
 gb|BE034450|BE034450 MH05B01 MH *Mesembryanthemum crystallinum* cD... 81 3e-41  
 emb|Z15140|LECHI9 *L.esculentum* mRNA for chitinase. 95 3e-41  
 gb|U02607|STU02607 *Solanum tuberosum* chitinase (chtB3) mRNA, par... 95 6e-41  
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 95 6e-41  
 30 emb|AF034566|AF034566 *Gossypium hirsutum* class I chitinase mRNA,... 100 6e-41  
 gb|BE033398|BE033398 ME01A01 ME *Mesembryanthemum crystallinum* cD... 165 7e-41  
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 35 emb|AF000965|AF000965 *Poa pratensis* chitinase (Chi3) pseudogene ... 91 4e-40  
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 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (pHS2) mRNA, compl... 106 6e-39  
 emb|AW924229|AW924229 WS1\_51\_H04.b1\_A002 Water-stressed 1 (WS1) ... 161 7e-39  
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 emb|AW267781|AW267781 EST305909 DSIR *Medicago truncatula* cDNA cl... 109 7e-39  
 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root *Medicago* t... 78 3e-38  
 gb|U02287|HVVU02287 *Hordeum vulgare* cultivar NK1558 chitinase gen... 96 4e-38  
 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU *Lycopersicon* ... 101 1e-37  
 50 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 106 1e-37  
 emb|AW746429|AW746429 WS1\_53\_G09.b1\_A002 Water-stressed 1 (WS1) ... 97 4e-37  
 emb|X74919|PVGEC9 *P.vulgaris* gene for endochitinase. 149 6e-37

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60 Database: plantfungal  
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	emb AB001379 AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto...	323	e-137
	emb AJ238439 CAR238439 Cicer arietinum mRNA for a cytochrome P45...	328	e-136
	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	322	e-136
10	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450, ...	291	e-134
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	324	e-134
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 ...	237	3e-82
15	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro...	290	3e-79
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	280	3e-74
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	emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone...	264	1e-69
20	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	258	1e-67
	emb AW733691 AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone...	253	3e-66
	emb AW171738 AW171738 N100632e rootphos(-) Medicago truncatula c...	251	1e-65
	emb AJ249801 CAR249801 Cicer arietinum partial mRNA for cytochro...	242	5e-63
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25	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	224	1e-57
	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium...	180	4e-57
	emb AI495626 AI495626 sb11c08.y1 Gm-c1004 Glycine max cDNA clone...	222	6e-57
	emb AW100311 AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone...	206	5e-56
	emb AW257188 AW257188 EST305325 KV2 Medicago truncatula cDNA clo...	177	6e-56
30	emb AI774414 AI774414 EST255514 tomato resistant, Cornell Lycopers...	144	5e-54
	emb AW171672 AW171672 N100566e rootphos(-) Medicago truncatula c...	212	7e-54
	emb AW932147 AW932147 EST357990 tomato fruit mature green, TAMU ...	211	1e-53
	emb AI731481 AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ...	168	3e-51
	emb AI731081 AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ...	200	2e-50
35	emb AI728374 AI728374 BNLGHi10609 Six-day Cotton fiber Gossypium...	163	9e-50
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	emb AF156976 AF156976 Gerbera hybrida flavone synthase II (CYP93...	100	8e-46
	dbj E13663 E13663 cDNA encoding cytochrome P450 which is induced...	104	1e-45
40	dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)...	104	1e-45
	emb Y10492 GMC450CP5 G.max mRNA for putative cytochrome P450, cl...	106	6e-44
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45	emb AI973839 AI973839 sd11c06.y1 Gm-c1020 Glycine max cDNA clone...	104	2e-43
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	emb AW734404 AW734404 sk19f09.y1 Gm-c1028 Glycine max cDNA clone...	157	2e-43
	gb U29333 PSU29333 Pisum sativum novel wound-inducible cytochrom...	160	5e-43
	emb AF124372 AF124372 Nicotiana tabacum NT7 mRNA, partial cds.	134	6e-43
50	gb U72654 EGU72654 Eustoma grandiflorum flavonoid 3'5'-hydroxyla...	149	2e-42
	dbj D86351 D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,...	102	2e-42
	emb AW688601 AW688601 NF009D12ST1F1000 Developing stem Medicago ...	173	4e-42
	emb AW616170 AW616170 EST307209 L. hirsutum trichome, Cornell Un...	148	5e-42
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55	emb AJ011862 CRO011862 Catharanthus roseus mRNA for flavonoid 3'...	155	6e-42
	emb Z22545 PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA.	148	8e-42
	dbj D14588 PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h...	148	8e-42
	emb AW616482 AW616482 EST322893 L. hirsutum trichome, Cornell Un...	148	1e-41
	emb AW617814 AW617814 EST324213 L. hirsutum trichome, Cornell Un...	148	1e-41
60	emb AW309826 AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone...	166	1e-41
	emb AB024931 AB024931 Lotus japonicus mRNA for cytochrome P450, ...	100	2e-41

- emb|AW299084|AW299084 EST305758 KV2 *Medicago truncatula* cDNA clo... 171 2e-41  
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 emb|Z22544|PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. 146 3e-41  
 emb|AW616075|AW616075 EST296834 *L. hirsutum* trichome, Cornell Un... 148 3e-41  
 5 emb|AF195800|AF195800 *Medicago sativa* isoflavone synthase 1 (ifs... 99 4e-41  
 emb|AW255096|AW255096 ML139 peppermint glandular trichome *Mentha*... 157 5e-41  
 emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycopersicon... 111 5e-41  
 emb|AF135484|AF135484 *Glycine max* cytochrome P450 monooxygenase ... 98 6e-41  
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 10 emb|AF195810|AF195810 *Trifolium pratense* isoflavone synthase 1 (... 98 6e-41  
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 emb|AF255014|AF255014 *Citrus sinensis* cinnamate 4-hydroxylase CY... 145 7e-41  
 emb|AW651341|AW651341 EST329795 tomato germinating seedlings, TA... 148 7e-41  
 emb|AF195798|AF195798 *Glycine max* isoflavone synthase 1 (ifs1) m... 98 8e-41  
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 20 emb|AI782402|AI782402 EST263281 tomato susceptible, Cornell Lycopersicon... 144 2e-40  
 emb|AF195799|AF195799 *Glycine max* isoflavone synthase 2 (ifs2) m... 96 2e-40  
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 25 emb|AF195817|AF195817 *Beta vulgaris* isoflavone synthase 2 (ifs2)... 97 2e-40  
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 30 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 147 4e-40  
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 emb|Z17369|HTTC4MMR H.tuberosus mRNA for trans-cinnamate 4-monoo... 143 5e-40  
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 35 emb|AW616066|AW616066 EST296823 *L. hirsutum* trichome, Cornell Un... 145 5e-40  
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 40 gb|L07634|PHVC4HYDRO *Phaseolus aureus* cinnamate 4-hydroxylase mR... 141 9e-40  
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 45 emb|AF195816|AF195816 *Beta vulgaris* isoflavone synthase 1 (ifs1)... 97 1e-39

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 (2805 letters)

55 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E  
 Sequences producing significant alignments: (bits) Value



- emb|AF109392|AF109392 Brassica napus ligand gated channel-like p... 142 3e-57  
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5 emb|AI759920|AI759920 sb66c06.y1 Gm-c1017 Glycine max cDNA clone... 84 4e-15  
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10 emb|AW928584|AW928584 EST337372 tomato flower buds 8 mm to pre-a... 66 1e-09  
emb|AW622410|AW622410 EST313197 tomato root during/after fruit s... 40 3e-06  
emb|AW160184|AW160184 EST290041 L. pennellii trichome, Cornell U... 40 4e-06  
emb|AW933376|AW933376 EST359219 tomato fruit mature green, TAMU ... 52 2e-05  
emb|AI441698|AI441698 sa60b02.y1 Gm-c1004 Glycine max cDNA clone... 49 2e-04  
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emb|AW284671|AW284671 LG1\_214\_A11.g1\_A002.Light Grown 1 (LG1) So... 47 8e-04  
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25 emb|AW443041|AW443041 EST307971 tomato mixed elicitor, BTI Lycop... 31 0.42  
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emb|AW931511|AW931511 EST357354 tomato fruit mature green, TAMU ... 31 0.42  
emb|AW218030|AW218030 EST296745 tomato flower buds, anthesis, Co... 31 0.42  
30 emb|AW224605|AW224605 EST303048 tomato root, plants pre-anthesis... 31 0.42  
emb|AW441557|AW441557 EST310953 tomato fruit red ripe, TAMU Lyco... 31 0.42  
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35 emb|AW455351|AW455351 EST311889 tomato root during/after fruit s... 31 0.42  
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45 emb|AW222971|AW222971 EST299782 tomato fruit red ripe, TAMU Lyco... 31 0.59  
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emb|AI774678|AI774678 EST255778 tomato resistant, Cornell Lycope... 37 0.85  
emb|AW982678|AW982678 HVSMEg0003O16f Hordeum vulgare pre-anthesi... 35 1.0  
50 emb|AW933175|AW933175 EST359018 tomato fruit mature green, TAMU ... 36 1.6  
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emb|AI484282|AI484282 EST248834 tomato susceptible, Cornell Lyco... 31 2.0  
emb|AW925473|AW925473 HVSMEg0001O11 Hordeum vulgare pre-anthesis... 35 2.2  
emb|Z69727|SPAC4G9 S.pombe chromosome I cosmid c4G9. 35 2.2  
55 emb|AB008750|AB008750 Schizosaccharomyces pombe gene for Alp11, ... 35 2.2  
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60 gb|L36897|YSCMTCG13 Saccharomyces cerevisiae mitochondrion oxi3 ... 35 3.0  
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emb|Z46869|KLEXG1 K.lactis gene for exo-1,3-beta-glucanase/1,3-b... 35 3.0  
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emb|AW257203|AW257203 EST305340 KV2 Medicago truncatula cDNA clo... 35 4.2  
5 emb|AC005504|AC005504 Plasmodium falciparum chromosome 12, \*\*\* S... 35 4.2  
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emb|AI965479|AI965479 sc72e01.y1 Gm-c1018 Glycine max cDNA clone... 35 4.2  
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10 emb|AC004710|AC004710 Plasmodium falciparum chromosome 12, \*\*\* S... 35 4.2  
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15 emb|AV406712|AV406712 AV406712 Lotus japonicus young plants (two... 34 5.7  
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20 gb|U08622|SPU08622 Schizosaccharomyces pombe cAMP-dependent prot... 34 5.7  
emb|AV411500|AV411500 AV411500 Lotus japonicus young plants (two... 34 5.7  
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25 emb|AW719775|AW719775 LjNEST9G5r Lotus japonicus nodule library ... 34 5.7  
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30 gb|B07277|B07277 G267T3 MVAT4 sheared genomic library Trypanosom... 34 7.8  
emb|AW982385|AW982385 HVSMEg0003C03f Hordeum vulgare pre-anthesi... 34 7.8  
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emb|X15601|CMCHPSBA C.moewusii chloroplast psbA gene. 34 7.8  
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http://www3.ncbi.nlm.nih.gov/htbin-  
40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af071527|/ncgi  
http://www.ncgr.org/cgi-bin/ff?af071527  
(1926 letters)  
  
Database: plantfungal  
45 661,018 sequences; 426,114,510 total letters  
  
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-55 emb|AI729861|AI729861 BNLGH5428 Six-day Cotton fiber Gossypium ... 52 2e-05  
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60 emb|AI896054|AI896054 EST265497 tomato callus, TAMU Lycopersicon... 47 4e-04  
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15	emb AW256577 AW256577 EST304714 KV2 Medicago truncatula cDNA clo...	30	0.064
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	emb X02390 ANTRPC1 Aspergillus nidulans trpC gene.	35	2.0
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	emb Z49595 SCYJR095W S.cerevisiae chromosome X reading frame ORF...	35	2.0
	gb L47610 PLAEMB4R Picea glauca EMB4 mRNA.	35	2.0
	emb Z49594 SCYJR094C S.cerevisiae chromosome X reading frame ORF...	35	2.0
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45	emb AQ639089 AQ639089 927P1-1D11.TP 927P1 Trypanosoma brucei gen...	33	7.2
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50	emb AQ656501 AQ656501 Sheared DNA-12B14.TF Sheared DNA Trypanoso...	33	7.2
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60	emb X87941 SCDNAGENS S.cerevisiae CRM1, YML9, PET54, SMI1, PHO81...	28	7.5
	emb AZ124240 AZ124240 T223104b Medicago truncatula BAC library M...	31	7.9



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 5 emb|AW924917|AW924917 WS1\_73\_B03.b1\_A002 Water-stressed 1 (WS1) ... 33 9.9  
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 emb|AW991081|AW991081 SsS0293 Suaeda salsa ZAP cDNA library Suae... 33 9.9  
 10 emb|AW399343|AW399343 EST309843 L. pennellii trichome, Cornell U... 33 9.9  
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 35 gb|L42466|PIAEFE Picea glauca ethylene-forming enzyme (EFE) mRNA... 156 4e-75  
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 emb|AW574101|AW574101 EST316692 GVN Medicago truncatula cDNA clo... 198 2e-67  
 emb|AW268031|AW268031 EST306309 DSIR Medicago truncatula cDNA cl... 126 6e-65  
 40 emb|AW775553|AW775553 EST334618 DSIL Medicago truncatula cDNA cl... 210 3e-63  
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 45 emb|AF082862|AF082862 Pisum sativum unknown mRNA, partial cds. 220 2e-56  
 emb|Z22543|PHFLASYNA P.hybrida flavonol synthase mRNA. 99 1e-55  
 emb|X83229|NTRNA1A1C N.tabacum mRNA for 1-aminocyclopropane-1-ca... 176 1e-54  
 emb|AF184273|AF184273 Daucus carota leucoanthocyanidin dioxygena... 110 9e-54  
 emb|AW030000|AW030000 EST273255 tomato callus, TAMU Lycopersicon... 186 1e-53  
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 60 emb|AF028602|AF028602 Ipomoea purpurea anthocyanidin synthase (A... 108 1e-50  
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- emb|AB023786|AB023786 Ipomoea batatas ans I mRNA for anthocyanid... 111 4e-50  
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 10 gb|U68215|CPU68215 Carica papaya ACC oxidase mRNA, complete cds. 152 5e-49  
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 25 emb|AB023790|AB023790 Ipomoea batatas f3h III mRNA for flavanone... 96 2e-48  
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 35 gb|U23066|PAU23066 Persea americana flavanone 3-hydroxylase mRNA... 100 6e-48  
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 40 emb|AW685110|AW685110 NF025C04NR1F1000 Nodulated root Medicago t... 158 1e-47  
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 45 emb|Y10034|PP1AMCSYN R.palustris mRNA for 1-aminocyclopropane-1-... 159 2e-47  
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15 (1731 letters)

Database: plantfungal  
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emb|AF213936|AF213936 Prunus dulcis amino acid/peptide transport... 132 2e-87  
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30 emb|X92852|LENIT2 L.esculentum exon 1 of NIT2 gene. 140 1e-80  
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35 emb|AW278758|AW278758 sf97b05.y1 Gm-c1019 Glycine max cDNA clone... 127 2e-47  
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40 emb|AW219289|AW219289 EST301771 tomato root during/after fruit s... 144 3e-34  
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(828 letters)

Database: plantfungal  
661,018 sequences; 426,114,510 total letters  
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	emb A82380 A82380 Sequence 5 from Patent WO9856811.	175	4e-43
45	emb AJ010829 TSP010829 Triticum sp. mRNA for GRAB1 protein.	175	4e-43
	emb A82384 A82384 Sequence 9 from Patent WO9856811.	175	4e-43
	emb AW737167 AW737167 EST338594 tomato flower buds, anthesis, Co...	148	4e-43
	emb AW560823 AW560823 EST315871 DSIR Medicago truncatula cDNA cl...	146	6e-43
	emb AI486492 AI486492 EST244813 tomato ovary, TAMU Lycopersicon ...	144	9e-43
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55	emb AW164307 AW164307 se70g05.y1 Gm-c1023 Glycine max cDNA clone...	143	5e-41
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	emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon...	146	1e-40
	emb AW306698 AW306698 sf47c01.y1 Gm-c1009 Glycine max cDNA clone...	151	1e-40
60	emb AI729055 AI729055 BNLGHi12472 Six-day Cotton fiber Gossypium...	135	1e-40

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 (1290 letters)

5

Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

10

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15

Score E  
 Sequences producing significant alignments: (bits) Value

gb|BE052217|BE052217 GA\_\_Ea0033E06f Gossypium arboreum 7-10 dpa ... 358 4e-98  
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 emb|AW472288|AW472288 si23c10.y1 Gm-c1029 Glycine max cDNA clone... 297 2e-79  
 emb|AW720283|AW720283 LjNEST20a9r Lotus japonicus nodule library... 295 4e-79  
 emb|AW234168|AW234168 sf22a07.y1 Gm-c1028 Glycine max cDNA clone... 288 7e-77  
 gb|BE021080|BE021080 sm55b08.y1 Gm-c1028 Glycine max cDNA clone ... 282 3e-75  
 20 emb|AW509358|AW509358 si22a10.y1 Gm-c1029 Glycine max cDNA clone... 272 3e-72  
 emb|AW622811|AW622811 EST306797 tomato flower buds 3-8 mm, Corne... 252 4e-66  
 emb|AV390505|AV390505 AV390505 Chlamydomonas reinhardtii C9 Chla... 147 4e-58  
 emb|AW234504|AW234504 sf15a07.y1 Gm-c1028 Glycine max cDNA clone... 225 7e-58  
 emb|AI773174|AI773174 EST254274 tomato resistant, Cornell Lycopersicon ... 218 9e-56  
 25 emb|AI774300|AI774300 EST255316 tomato resistant, Cornell Lycopersicon ... 210 1e-53  
 gb|BE024350|BE024350 894002D06.y1 C. reinhardtii CC-1690, normal... 192 5e-48  
 gb|BE056488|BE056488 894009G03.y1 C. reinhardtii CC-1690, normal... 189 3e-47  
 emb|AW691828|AW691828 NF044F04ST1F1000 Developing stem Medicago ... 179 2e-44  
 emb|AW719571|AW719571 LjNEST6g3r Lotus japonicus nodule library,... 175 6e-43  
 30 emb|AW981392|AW981392 EST392545 DSIL Medicago truncatula cDNA cl... 162 4e-39  
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 40 emb|AV389740|AV389740 AV389740 Chlamydomonas reinhardtii C9 Chla... 113 3e-24  
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 10 emb|AV391798|AV391798 AV391798 *Chlamydomonas reinhardtii* C9 Chla... 37 0.37  
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 20 emb|AJ277161|CPA277161 *Carica papaya* partial paccs1B gene for 1-... 35 0.60  
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 25 emb|AW703931|AW703931 sk25h05.y1 *Gm-c1028* Glycine max cDNA clone... 36 0.69  
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 50 emb|AW216510|AW216510 EST295224 tomato callus, TAMU Lycopersicon... 34 3.4  
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 emb|Z11613|VRACCSYNM *V.radiata* mRNA for ACC synthase. 34 3.4

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 (990 letters)

60 Database: plantfungal  
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45	emb AW226128 AW226128 ST77F07 Pine TriplEx shoot tip library Pin...	136	2e-31
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	emb AW678403 AW678403 WS1_15_D11.g1_A002 Water-stressed 1 (WS1) ...	70	5e-22
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	emb AW707360 AW707360 832006H03.y1 C. reinhardtii CC-125 nutrien...	71	5e-17



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<http://www.ncgr.org/cgi-bin/ff?al022373>  
 (1518 letters)

55 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

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60 Score E  
 Sequences producing significant alignments: (bits) Value

- gb|BE052481|BE052481 GA\_Ea0034B15f Gossypium arboreum 7-10 dpa ... 248 8e-65  
 emb|AW933316|AW933316 EST359159 tomato fruit mature green, TAMU ... 127 2e-28  
 emb|AI897506|AI897506 EST266949 tomato ovary, TAMU Lycopersicon ... 120 3e-26  
 5 emb|AI055630|AI055630 coau0004J11 Cotton Boll Abscission Zone cD... 113 4e-24  
 emb|AW032891|AW032891 EST276450 tomato callus, TAMU Lycopersicon... 103 4e-21  
 emb|AV427652|AV427652 AV427652 Lotus japonicus young plants (two... 88 2e-16  
 emb|AW307385|AW307385 sf56c11.y1 Gm-c1009 Glycine max cDNA clone... 72 1e-11  
 emb|AW726477|AW726477 GA\_Ea0021M14 Gossypium arboreum 7-10 dpa ... 60 5e-10  
 10 emb|AW747181|AW747181 WS1\_66\_B09.b1\_A002 Water-stressed 1 (WS1) ... 59 2e-09  
 emb|AW091888|AW091888 EST285068 tomato mixed elicitor, BTI Lycop... 53 5e-08  
 emb|AW306935|AW306935 sf50f05.y1 Gm-c1009 Glycine max cDNA clone... 58 1e-07  
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 emb|AW306722|AW306722 sf47e06.y1 Gm-c1009 Glycine max cDNA clone... 58 1e-07  
 15 emb|AW221657|AW221657 EST298468 tomato fruit red ripe, TAMU Lyco... 58 2e-07  
 emb|AW574131|AW574131 EST316722 GVN Medicago truncatula cDNA clo... 52 1e-05  
 emb|AW222358|AW222358 EST299169 tomato fruit red ripe, TAMU Lyco... 43 0.005  
 emb|AW738043|AW738043 EST339470 tomato flower buds, anthesis, Co... 43 0.005  
 emb|AW774865|AW774865 EST334016 KV3 Medicago truncatula cDNA clo... 43 0.007  
 20 emb|AW832220|AW832220 sm21a01.y1 Gm-c1027 Glycine max cDNA clone... 38 0.011  
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 emb|AQ324712|AQ324712 mgxb0019H15r CUGI Rice Blast BAC Library P... 37 0.12  
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 25 emb|AV428867|AV428867 AV428867 Lotus japonicus young plants (two... 36 0.60  
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 emb|AW757802|AW757802 874003G04.x1 C. reinhardtii CC-1690, Lambd... 36 0.83  
 emb|AW720369|AW720369 LjNEST21g3r Lotus japonicus nodule library... 36 0.83  
 emb|Z75009|SCYOR101W S.cerevisiae chromosome XV reading frame OR... 35 1.6  
 30 gb|U32307|SCU32307 Saccharomyces cerevisiae oligosaccharyltransf... 35 1.6  
 emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 35 1.6  
 emb|Z75010|SCYOR102W S.cerevisiae chromosome XV reading frame OR... 35 1.6  
 emb|AW573717|AW573717 EST316308 GVN Medicago truncatula cDNA clo... 35 2.1  
 emb|AL049769|SPBC9B6 S.pombe chromosome II cosmid c9B6. 34 2.9  
 35 emb|AW395612|AW395612 sg73b12.y1 Gm-c1007 Glycine max cDNA clone... 34 4.0  
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 40 emb|AL354513|LMFL6783 Leishmania major Friedlin cosmid L6783, PR... 33 5.6  
 emb|AQ940380|AQ940380 Sheared DNA-33M12.TF Sheared DNA Trypanoso... 33 5.6  
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 45 emb|A86068|A86068 Sequence 727 from Patent EP0866129. 33 5.6  
 emb|AW690594|AW690594 NF031E09ST1F1000 Developing stem Medicago ... 33 5.6  
 emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, \*\*\* S... 33 5.6  
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 50 gb|BE055549|BE055549 GA\_Ea0034M01f Gossypium arboreum 7-10 dpa ... 33 5.6  
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 emb|AW719319|AW719319 LjNEST2f7r Lotus japonicus nodule library,... 33 5.6  
 emb|AW696984|AW696984 NF111A10ST1F1072 Developing stem Medicago ... 33 7.6  
 gb|L07391|NEUNIT6X Neurospora crassa nitrite reductase (nit-6) g... 33 7.6  
 55 emb|AQ645907|AQ645907 RPCI93-DpnII-28N21.TV RPCI93-DpnII Trypano... 33 7.6

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 [arabidopsis thaliana] /blast\_score 1.00e-110 /ec\_number /family  
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 http://www3.ncbi.nlm.nih.gov/htbin-

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 http://www.ncgr.org/cgi-bin/ff?ac005956  
 (711 letters)

5 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters

Searching.....done

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	emb AW032769 AW032769 EST276328 tomato callus, TAMU Lycopersicon...	108	6e-32
15	emb AI731540 AI731540 BNLGHi10032 Six-day Cotton fiber Gossypium...	82	2e-21
	emb AW775221 AW775221 EST331943 GVN Medicago truncatula cDNA clo...	72	2e-19
	gb BE124796 BE124796 EST393831 GVN Medicago truncatula cDNA clon...	72	2e-19
	emb AW399006 AW399006 EST309506 L. pennellii trichome, Cornell U...	77	1e-17
	emb AW442210 AW442210 EST311606 tomato fruit red ripe, TAMU Lyco...	75	2e-17
20	emb AW703663 AW703663 sk11g09.y1 Gm-c1023 Glycine max cDNA clone...	69	2e-16
	emb AI727683 AI727683 BNLGHi8604 Six-day Cotton fiber Gossypium ...	79	3e-14
	emb AI729941 AI729941 BNLGHi5757 Six-day Cotton fiber Gossypium ...	79	3e-14
	emb AW329822 AW329822 N201096e rootphos(-) Medicago truncatula c...	72	5e-14
	emb AI727293 AI727293 BNLGHi7657 Six-day Cotton fiber Gossypium ...	78	5e-14
25	emb AF150724 AF150724 AF150724 Gossypium hirsutum 24 days postan...	78	5e-14
	emb AW219270 AW219270 EST301752 tomato root during/after fruit s...	74	7e-14
	emb AI730749 AI730749 BNLGHi7802 Six-day Cotton fiber Gossypium ...	78	1e-13
	emb AW219137 AW219137 EST301619 tomato root during/after fruit s...	75	1e-13
	gb BE033932 BE033932 MG02C06 MG Mesembryanthemum crystallinum cD...	77	1e-13
30	emb AW508608 AW508608 si34c01.y1 Gm-r1030 Glycine max cDNA clone...	64	2e-13
	emb AW220356 AW220356 EST302839 tomato root during/after fruit s...	77	2e-13
	emb AW267973 AW267973 EST306195 DSIR Medicago truncatula cDNA cl...	75	2e-13
	emb AV413409 AV413409 AV413409 Lotus japonicus young plants (two...	76	3e-13
	emb AW931758 AW931758 EST357601 tomato fruit mature green, TAMU ...	75	5e-13
35	emb AW728679 AW728679 GA_Ea0017M02 Gossypium arboreum 7-10 dpa ...	75	5e-13
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	emb AI443646 AI443646 sa42f12.y1 Gm-c1004 Glycine max cDNA clone...	75	5e-13
	emb AW682867 AW682867 NF001B05LF1F1044 Developing leaf Medicago ...	75	6e-13
	gb BE059421 BE059421 sn30h03.y1 Gm-c1016 Glycine max cDNA clone ...	75	6e-13
40	emb AW348175 AW348175 GM210001A21E9R Gm-r1021 Glycine max cDNA 3...	75	6e-13
	emb AW279542 AW279542 sf90h11.y1 Gm-c1019 Glycine max cDNA clone...	75	6e-13
	emb AW277724 AW277724 sf85g08.y1 Gm-c1019 Glycine max cDNA clone...	74	9e-13
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45	emb AW622165 AW622165 EST312963 tomato root during/after fruit s...	73	2e-12
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	emb AW185181 AW185181 se88a05.y1 Gm-c1023 Glycine max cDNA clone...	73	2e-12
	emb AW223330 AW223330 EST300141 tomato fruit red ripe, TAMU Lyco...	73	2e-12
	emb AW597455 AW597455 sj85c04.y1 Gm-c1034 Glycine max cDNA clone...	69	2e-12
50	emb AZ044879 AZ044879 Gm_UMb001_030_J12R UMN Soybean BAC Library...	73	3e-12
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60	emb AW267780 AW267780 EST305908 DSIR Medicago truncatula cDNA cl...	71	8e-12
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- gb|BE052202|BE052202 GA\_Ea0034A22f *Gossypium arboreum* 7-10 dpa ... 71 1e-11  
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 5 gb|BE054849|BE054849 GA\_Ea0033N22f *Gossypium arboreum* 7-10 dpa ... 71 1e-11  
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 emb|AW727187|AW727187 GA\_Ea0023M11 *Gossypium arboreum* 7-10 dpa ... 71 1e-11  
 10 emb|AI484163|AI484163 EST248970 tomato resistant, Cornell Lycope... 69 1e-11  
 emb|AW981615|AW981615 PC14F10 Pine TriplEx pollen cone library P... 70 2e-11  
 emb|AI727213|AI727213 BNLGHi7517 Six-day Cotton fiber *Gossypium* ... 70 2e-11  
 emb|AW218481|AW218481 EST303664 tomato radicle, 5 d post-imbibit... 70 2e-11  
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 15 emb|AI731895|AI731895 BNLGHi1234 Six-day Cotton fiber *Gossypium*... 70 2e-11  
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 20 gb|BE055048|BE055048 GA\_Ea0001G22f *Gossypium arboreum* 7-10 dpa ... 70 2e-11  
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 emb|AW441213|AW441213 EST310609 tomato fruit red ripe, TAMU Lyco... 70 2e-11  
 25 emb|AW219914|AW219914 EST302397 tomato root during/after fruit s... 70 2e-11  
 emb|AW108574|AW108574 gate0001G22f *Gossypium arboreum* 7-10 dpa f... 70 2e-11  
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 30 emb|Y14573|HVCH4H *Hordeum vulgare* DNA for chromosome 4H. 69 3e-11  
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 35 emb|AW685535|AW685535 NF028H02NR1F1000 Nodulated root *Medicago t...* 69 4e-11  
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 40 emb|AI485408|AI485408 EST243729 tomato ovary, TAMU Lycopersicon ... 68 7e-11  
 emb|AI483478|AI483478 EST249299 tomato ovary, TAMU Lycopersicon ... 68 7e-11  
 emb|AW031045|AW031045 EST274352 tomato callus, TAMU Lycopersicon... 68 7e-11  
 emb|AI483537|AI483537 EST249386 tomato ovary, TAMU Lycopersicon ... 68 7e-11  
 gb|BE034706|BE034706 ML03C10 ML *Mesembryanthemum crystallinum* cD... 68 1e-10  
 45 emb|AW980667|AW980667 EST391820 *GVN Medicago truncatula* cDNA clo... 67 1e-10  
 emb|AW349023|AW349023 GM210003B22B3R Gm-r1021 *Glycine max* cDNA 3... 67 1e-10  
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 emb|AW984973|AW984973 NXNV\_118\_A01\_F Nsf Xylem Normal wood Verti... 66 3e-10  
 emb|AW737702|AW737702 EST339129 tomato flower buds, anthesis, Co... 66 3e-10  
 50 emb|AW666412|AW666412 sk36c04.y1 Gm-c1028 *Glycine max* cDNA clone... 66 3e-10  
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60 (168 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

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	emb AI727531 AI727531 BNLGHi8333 Six-day Cotton fiber Gossypium ...	107	3e-24
	emb AW266829 AW266829 L48-172T3 Ice plant Lambda Uni-Zap XR expr...	102	1e-22
	emb AW756795 AW756795 sl27c08.y1 Gm-cl027 Glycine max cDNA clone...	102	2e-22
	emb AI901283 AI901283 sc31d08.y1 Gm-cl014 Glycine max cDNA clone...	98	3e-21
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	emb AW597214 AW597214 si71g06.y1 Gm-cl031 Glycine max cDNA clone...	94	5e-20
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	emb AW687777 AW687777 NF013D03RT1F1028 Developing root Medicago ...	86	1e-17
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40	emb AW040672 AW040672 EST283536 tomato mixed elicitor, BTI Lycop...	81	3e-16
	emb AW039328 AW039328 EST281585 tomato mixed elicitor, BTI Lycop...	81	3e-16
	emb AW220489 AW220489 EST297042 tomato fruit mature green, TAMU ...	81	4e-16
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	emb AW220491 AW220491 EST297044 tomato fruit mature green, TAMU ...	81	4e-16
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	emb AI896462 AI896462 EST265893 tomato callus, TAMU Lycopersicon...	81	5e-16
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	emb AJ271954 TCA271954 Theobroma cacao microsatellite DNA, clone...	65	6e-16
	emb AW685205 AW685205 NF026F12NR1F1000 Nodulated root Medicago t...	79	1e-15
50	emb AW568064 AW568064 si68a06.y1 Gm-r1030 Glycine max cDNA clone...	53	2e-15
	emb AF131222 AF131222 Lophopyrum elongatum protein serine/threon...	78	2e-15
	gb BE060160 BE060160 HVSMeg0011B12f Hordeum vulgare pre-anthesis...	78	3e-15
	emb AW929662 AW929662 EST338450 tomato flower buds 8 mm to pre-a...	78	3e-15
	emb AW684940 AW684940 NF023C12NR1F1000 Nodulated root Medicago t...	77	4e-15
55	emb AW284352 AW284352 LG1_275_D12.g1_A002 Light Grown 1 (LG1) So...	77	4e-15
	emb AI896953 AI896953 EST266396 tomato callus, TAMU Lycopersicon...	57	5e-15
	emb AI727374 AI727374 BNLGHi7892 Six-day Cotton fiber Gossypium ...	77	6e-15
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	emb AW278089 AW278089 sf39e12.y1 Gm-cl009 Glycine max cDNA clone...	50	6e-15
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emb|A67797|A67797 Sequence 2 from Patent WO9743427. 73 8e-14  
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20 emb|AW621294|AW621294 EST312092 tomato root during/after fruit s... 73 8e-14  
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25 gb|T14833|T14833 crs280 lambdaZAPST Ricinus communis cDNA clone ... 47 1e-13  
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(1602 letters)

55 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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60 Score E  
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5 emb|AW688778|AW688778 NF011E05ST1F1000 Developing stem Medicago ... 244 1e-65  
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 20 http://www.ncgr.org/cgi-bin/ff?x98676  
 (643 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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gb|L46574|L46574 BNAF1975 Mustard flower buds *Brassica rapa* cDNA... 84 2e-29  
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 emb|AI483886|AI483886 EST249757 tomato ovary, TAMU *Lycopersicon* ... 64 2e-21  
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 45 emb|AI488341|AI488341 EST246663 tomato ovary, TAMU *Lycopersicon* ... 55 8e-20  
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5 emb|AW030314|AW030314 EST273569 tomato callus, TAMU Lycopersicon... 53 4e-07  
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(643 letters)

15 Database: plantfungal  
661,018 sequences; 426,114,510 total letters

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20 Score E  
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emb|AW033868|AW033868 EST277439 tomato callus, TAMU Lycopersicon... 62 1e-18  
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emb|AI485123|AI485123 EST243427 tomato ovary, TAMU Lycopersicon ... 60 2e-18  
45 emb|AI771824|AI771824 EST252924 tomato ovary, TAMU Lycopersicon ... 59 5e-18  
emb|AW685937|AW685937 NF031H10NR1F1000 Nodulated root Medicago t... 59 9e-18  
emb|AW216442|AW216442 EST295072 tomato callus, TAMU Lycopersicon... 57 1e-17  
emb|AW684455|AW684455 NF017B06NR1F1000 Nodulated root Medicago t... 62 5e-17  
emb|AW687462|AW687462 NF009H03RT1F1031 Developing root Medicago ... 57 8e-17  
50 emb|AV422177|AV422177 AV422177 Lotus japonicus young plants (two... 56 8e-17  
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dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 56 3e-16  
emb|AW680050|AW680050 WS1\_3\_G12.g1\_A002 Water-stressed 1 (WS1) S... 57 1e-15  
55 emb|AW033574|AW033574 EST277145 tomato callus, TAMU Lycopersicon... 53 2e-15  
emb|AI487993|AI487993 EST246315 tomato ovary, TAMU Lycopersicon ... 53 2e-15  
emb|AW034640|AW034640 EST278324 tomato callus, TAMU Lycopersicon... 53 2e-15  
emb|AI896031|AI896031 EST265474 tomato callus, TAMU Lycopersicon... 53 3e-15  
emb|AW030858|AW030858 EST274148 tomato callus, TAMU Lycopersicon... 53 3e-15  
60 emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 53 3e-15  
emb|AI771191|AI771191 EST252387 tomato ovary, TAMU Lycopersicon ... 53 3e-15

- emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 53 3e-15  
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emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 51 1e-14  
5 emb|AW030876|AW030876 EST274166 tomato callus, TAMU Lycopersicon... 53 4e-14  
emb|AI488445|AI488445 EST246784 tomato ovary, TAMU Lycopersicon ... 55 2e-13  
emb|AB035133|AB035133 Petunia x hybrida gene for C2H2 zinc-finge... 53 2e-13  
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dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds. 47 3e-13  
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20 emb|AW924443|AW924443 WS1\_69\_C08.g1\_A002 Water-stressed 1 (WS1) ... 57 3e-12  
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dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 50 1e-11  
emb|AW219517|AW219517 EST301915 tomato root during/after fruit s... 52 1e-11  
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35 emb|AW729218|AW729218 GA\_Ea0024G18 Gossypium arboreum 7-10 dpa ... 48 2e-11  
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60 emb|AI960244|AI960244 sc80g07.y1 Gm-cl018 Glycine max cDNA clone... 54 9e-07  
emb|AB000452|AB000452 Petunia hybrida mRNA for PETHy;ZPT2-6, com... 54 9e-07

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(639 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

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emb|Y11607|MSMP2C M.sativa mRNA for protein phosphatase 2C. 164 7e-70

emb|AJ242803|SST242803 Sporobolus stapfianus partial mRNA for pu... 154 4e-61

emb|AI055336|AI055336 coau0003L08 Cotton Boll Abscission Zone cD... 163 7e-56

emb|AI488711|AI488711 EST247050 tomato ovary, TAMU Lycopersicon ... 158 5e-46

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emb|AI489841|AI489841 EST248180 tomato ovary, TAMU Lycopersicon ... 173 1e-42

emb|AW832587|AW832587 sm14b05.y1 Gm-c1027 Glycine max cDNA clone... 119 5e-40

emb|AW676724|AW676724 DG1\_13\_B08.g1\_A002 Dark Grown 1 (DG1) Sorg... 152 2e-36

emb|AW423616|AW423616 sh69d07.y1 Gm-c1015 Glycine max cDNA clone... 110 3e-36

emb|AW278110|AW278110 sf39h03.y1 Gm-c1009 Glycine max cDNA clone... 119 2e-35

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emb|AW698103|AW698103 NXNV\_066\_C09\_F Nsf Xylem Normal wood Verti... 120 2e-33

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emb|AV428740|AV428740 AV428740 Lotus japonicus young plants (two... 59 2e-19

emb|AF092431|AF092431 Lotus japonicus nodule-enhanced protein ph... 64 1e-18

emb|AF092432|AF092432 Lotus japonicus protein phosphatase type 2... 73 8e-18

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emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 80 4e-16

emb|AW458317|AW458317 sh86c05.y1 Gm-c1016 Glycine max cDNA clone... 77 7e-16

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emb|AW647646|AW647646 EST307124 tomato germinating seedlings, TA... 84 1e-15

emb|AW621460|AW621460 EST312258 tomato root during/after fruit s... 84 1e-15

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emb|AW776573|AW776573 EST335638 DSIL Medicago truncatula cDNA cl... 78 2e-15

emb|AW164504|AW164504 se73e07.y1 Gm-c1023 Glycine max cDNA clone... 76 5e-15

gb|H07534|H07534 cbn054 BNL2 Brassica napus cDNA 5'/3', mRNA seq... 82 5e-15

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emb|AA080599|AA080599 EST054 Sugarcane leaf roll Saccharum sp. c... 74 3e-14

emb|AW328993|AW328993 N200187e rootphos(-) Medicago truncatula c... 78 8e-14

emb|AW926387|AW926387 HVSMEg0007B08 Hordeum vulgare pre-anthesis... 78 8e-14

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emb|AW560026|AW560026 EST315074 DSIR Medicago truncatula cDNA cl... 77 1e-13

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emb|AW930922|AW930922 EST356765 tomato fruit mature green, TAMU ... 69 1e-13

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emb|AW126261|AW126261 N100368e rootphos(-) Medicago truncatula c... 71 3e-13

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gb|BE055043|BE055043 GA\_Ea0031H07f Gossypium arboreum 7-10 dpa ... 71 1e-11



- emb|AI895824|AI895824 EST265267 tomato callus, TAMU Lycopersicon... 66 1e-11  
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5 emb|AW309195|AW309195 sg05e02.y1 Gm-c1019 Glycine max cDNA clone... 62 2e-11  
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emb|AW736469|AW736469 EST332483 KV3 Medicago truncatula cDNA clo... 69 3e-11  
emb|AI052979|AI052979 Mpc9 Ice plant seedlings, RT-PCR, pCRII M... 63 3e-11  
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10 emb|AW224147|AW224147 EST300958 tomato fruit red ripe, TAMU Lyco... 69 3e-11  
emb|AW623772|AW623772 EST321717 tomato flower buds 3-8 mm, Corne... 68 5e-11  
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emb|AW039555|AW039555 EST281836 tomato mixed elicitor, BTI Lycop... 66 3e-10  
emb|AW094483|AW094483 EST287663 tomato mixed elicitor, BTI Lycop... 66 3e-10  
25 emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 48 6e-10  
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35 emb|AW739238|AW739238 gb39a01.y1 Moss EST library PPN Physcomitr... 59 3e-08  
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emb|Z48008|SC8119 S.cerevisiae chromosome IV cosmid 8119. 53 2e-06  
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Database: plantfungal

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	emb AB022319 AB022319 <i>Pisum sativum</i> mRNA for apyrase, complete cds.	64	1e-30
15	emb AB027616 AB027616 <i>Pisum sativum</i> mRNA for apyrase, partial cd...	64	2e-29
	emb AW925295 AW925295 HVSMEg0001H23 <i>Hordeum vulgare</i> pre-anthesis...	69	2e-29
	emb AF156782 AF156782 <i>Medicago sativa</i> nod factor binding lectin-...	66	8e-29
	emb AW983120 AW983120 HVSMEg0008D22f <i>Hordeum vulgare</i> pre-anthesi...	70	2e-28
	emb AI771115 AI771115 EST252215 tomato ovary, TAMU Lycopersicon ...	71	4e-28
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	emb AF139807 AF139807 <i>Dolichos biflorus</i> nod factor binding lecti...	65	6e-22
25	emb AW928903 AW928903 EST337691 tomato flower buds 8 mm to pre-a...	71	7e-22
	emb AB032754 AB032754 <i>Solanum melongena</i> EEF45 mRNA, partial cds.	65	2e-21
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30	emb AL121741 SPAC824 <i>S.pombe</i> chromosome I cosmid c824:	53	2e-17
	emb AL121783 SPCC11E10 <i>S.pombe</i> chromosome III cosmid c11E10.	52	1e-16
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	emb AW233919 AW233919 sf32a09.y1 Gm-c1028 Glycine max cDNA clone...	72	6e-16
35	emb AI729322 AI729322 BNLGH13103 Six-day Cotton fiber <i>Gossypium</i> ...	56	4e-15
	gb U18779 SCE8199 <i>Saccharomyces cerevisiae</i> chromosome V cosmid 8...	47	9e-15
	gb L19560 YSCGUANDIP <i>Saccharomyces cerevisiae</i> guanosine diphosph...	47	1e-14
	emb AI855475 AI855475 sc16e11.y1 Gm-c1013 Glycine max cDNA clone...	56	6e-13
	emb AI488582 AI488582 EST246921 tomato ovary, TAMU Lycopersicon ...	60	8e-13
40	emb AJ388942 AJ388942 AJ388942 <i>Medicago truncatula</i> R108 <i>Medicago</i> ...	63	1e-12
	emb AW620334 AW620334 sj03g08.y1 Gm-c1032 Glycine max cDNA clone...	61	2e-12
	emb AF156781 AF156781 <i>Dolichos biflorus</i> apyrase mRNA, complete cds.	62	7e-12
	emb AA660474 AA660474 00360 MTRHE <i>Medicago truncatula</i> cDNA 5' si...	65	7e-12
	emb AI441990 AI441990 sa82g03.y1 Gm-c1004 Glycine max cDNA clone...	60	2e-11
45	emb AW696828 AW696828 NF109D12ST1F1101 Developing stem <i>Medicago</i> ...	57	2e-11
	gb BE059022 BE059022 sn24b03.y1 Gm-c1016 Glycine max cDNA clone ...	53	4e-11
	emb AW306606 AW306606 se53a03.y1 Gm-c1017 Glycine max cDNA clone...	56	8e-11
	emb AI490444 AI490444 EST248770 tomato ovary, TAMU Lycopersicon ...	61	2e-10
	emb AW564791 AW564791 LG1_301_H10.b1_A002 Light Grown 1 (LG1) So...	51	2e-10
50	emb AI771846 AI771846 EST252946 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI897295 AI897295 EST266654 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI485852 AI485852 EST244173 tomato ovary, TAMU Lycopersicon...	61	3e-10
	emb AI899079 AI899079 EST268522 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AW922880 AW922880 DG1_47_F10.b1_A002 Dark Grown 1 (DG1) Sorg...	48	4e-10
55	emb AI490499 AI490499 EST249033 tomato ovary, TAMU Lycopersicon ...	61	5e-10
	emb AI488302 AI488302 EST246624 tomato ovary, TAMU Lycopersicon ...	60	1e-09
	emb AV418181 AV418181 AV418181 <i>Lotus japonicus</i> young plants (two...	57	2e-09
	emb AW924275 AW924275 WS1_52_E03.b1_A002 Water-stressed 1 (WS1) ...	64	3e-09
	emb AW257004 AW257004 EST305141 KV2 <i>Medicago truncatula</i> cDNA clo...	48	8e-09
60	emb AI771696 AI771696 EST252796 tomato ovary, TAMU Lycopersicon ...	61	3e-08
	emb AW623313 AW623313 EST321258 tomato flower buds 3-8 mm, Corne...	58	2e-07

- emb|AA231755|AA231755 CDO38.R cDNA from oat Avena sativa cDNA cl... 56 7e-07  
 emb|AW736308|AW736308 EST332392 KV3 Medicago truncatula cDNA clo... 54 4e-06  
 emb|AW563435|AW563435 LG1\_214\_E12.b1\_A002 Light Grown 1 (LG1) So... 38 4e-05  
 emb|AB010444|AB010444 Neospora caninum mRNA for NTPase, complete... 41 1e-04  
 5 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 44 0.004  
 emb|AF203695|AF203695 Saccharomyces cerevisiae golgi nucleoside ... 43 0.005  
 gb|U18778|SCE9537 Saccharomyces cerevisiae chromosome V cosmids ... 43 0.005  
 emb|AZ124337|AZ124337 T223080b Medicago truncatula BAC library M... 41 0.026  
 emb|AW225681|AW225681 ST70C07 Pine TriplEx shoot tip library Pin... 41 0.026  
 10 emb|AW774350|AW774350 EST333501 KV3 Medicago truncatula cDNA clo... 41 0.026  
 emb|AI974272|AI974272 T110271e KV0 Medicago truncatula cDNA clon... 40 0.035  
 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 39 0.13  
 emb|AI728079|AI728079 BNLGH19928 Six-day Cotton fiber Gossypium ... 29 0.23  
 emb|X61608|BNLHCB3A B.napus gene for LHCII Type III chlorophyll ... 37 0.33  
 15 emb|AW671082|AW671082 LG1\_284\_C02.b1\_A002 Light Grown 1 (LG1) So... 37 0.33  
 emb|AZ124338|AZ124338 T223081b Medicago truncatula BAC library M... 36 0.85  
 emb|AF188744|AF188744 Brassica napus high-affinity ammonium tran... 35 1.2  
 dbj|D37795|D37795 Ipomoea nil Tpn1 gene. 35 1.2  
 dbj|E08493|E08493 gDNA encoding transposable element, Tpn1 which ... 35 1.2  
 20 emb|AL356192|NCB24B19 Neurospora crassa DNA linkage group II BAC... 30 1.3  
 emb|AF106939|AF106939 Phanerochaete chrysosporium 1,4-benzoquino... 29 1.4  
 emb|AL163492|LMFL787 Leishmania major Friedlin chromosome 19 cos... 35 1.5  
 emb|AW234282|AW234282 sf23d03.y1 Gm-c1028 Glycine max cDNA clone... 35 1.6  
 emb|AL116534|CNS01D9A Botrytis cinerea strain T4 cDNA library un... 35 1.6  
 25 emb|AW428880|AW428880 Ljirnp25-999-b7 Ljirnp Lambda HybriZap ... 35 1.6  
 gb|N60092|N60092 TgESTzy11d09.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2  
 emb|AW056764|AW056764 ST55E11 Pine TriplEx shoot tip library Pin... 35 2.2  
 gb|N81562|N81562 TgESTzy59h03.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2  
 emb|AW286610|AW286610 LG1\_335\_A07.g1\_A002 Light Grown 1 (LG1) So... 35 2.2  
 30 emb|AQ656308|AQ656308 Sheared DNA-27M14.TR Sheared DNA Trypanoso... 35 2.2  
 emb|AL162692|SPBP4H10 S.pombe chromosome II P1 clone p4H10. 34 3.0  
 emb|AQ652731|AQ652731 Sheared DNA-18C6.TR Sheared DNA Trypanosom... 34 3.0  
 emb|AF016222|AF016222 Schizosaccharomyces pombe Rsv1p (rsv1) gen... 34 3.0  
 emb|AW350237|AW350237 GM210008A10B2R Gm-r1021 Glycine max cDNA 3... 34 4.1  
 35 emb|AQ943814|AQ943814 Sheared DNA-34A9.TF Sheared DNA Trypanosom... 34 4.1  
 emb|AW666160|AW666160 sk32h08.y1 Gm-c1028 Glycine max cDNA clone... 34 4.1  
 emb|AL109736|SPCC18B5 S.pombe chromosome III cosmid c18B5. 27 4.6  
 emb|AW441608|AW441608 EST311004 tomato fruit red ripe, TAMU Lyco... 33 5.7  
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 5.7  
 40 emb|AW398001|AW398001 sg71a06.y1 Gm-c1007 Glycine max cDNA clone... 33 5.7  
 emb|AW933585|AW933585 EST359428 tomato fruit mature green, TAMU ... 33 5.7  
 emb|AI069343|AI069343 mgae0006cG03f Magnaporthe grisea Appressor... 33 5.7  
 emb|X62697|NCACU3 N.crassa acu-3 gene for isocitrate lyase. 26 5.7  
 emb|AI488866|AI488866 EST247205 tomato ovary, TAMU Lycopersicon ... 31 6.2  
 45 emb|Z79690|ANPFKA A.niger pfkA gene. 26 7.3  
 emb|X13508|HVGHRDSP Barley gene for storage protein gamma-hordein. 28 7.8  
 gb|M36378|BLYG1HORDA Barley gamma-1 hordein storage protein gene... 28 7.8  
 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 33 7.8  
 emb|AI900865|AI900865 sb95d08.y1 Gm-c1012 Glycine max cDNA clone... 33 7.8  
 50 emb|AZ124341|AZ124341 T223084b Medicago truncatula BAC library M... 33 7.8

Query= AL035679.144\_at 17653\_at /id\_source genbank /description  
 emb|cab38823.1| (al035679) putative protein [arabidopsis thaliana]  
 /blast\_score 0 /ec\_number /family /chip nova /gb\_link  
 55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)  
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)  
<http://www.ncgr.org/cgi-bin/ff?al035679>  
 (1455 letters)

- 60 Database: plantfungal  
 661,018 sequences; 426,114,510 total letters



Searching.....done

		Score	E	
5	Sequences producing significant alignments:	(bits)	Value	
	emb AW091895 AW091895 EST285075 tomato mixed elicitor, BTI Lycop...	306	3e-82	
	emb AW040183 AW040183 EST282682 tomato mixed elicitor, BTI Lycop...	306	3e-82	
	emb AW776130 AW776130 EST335195 DSIL Medicago truncatula cDNA cl...	204	2e-51	
10	emb AI897609 AI897609 EST267052 tomato ovary, TAMU Lycopersicon ...	182	4e-45	
	emb AI055000 AI055000 coau0002L23 Cotton Boll Abscission Zone cD...	90	1e-42	
	emb AI055639 AI055639 coau0004K19 Cotton Boll Abscission Zone cD...	107	2e-22	
	emb AW693198 AW693198 NF061D12ST1F1000 Developing stem Medicago ...	66	6e-10	
	emb AW684256 AW684256 NF014F09NR1F1000 Nodulated root Medicago t...	43	0.007	
15	emb AW667681 AW667681 GA_Ea0010D15 Gossypium arboreum 7-10 dpa ...	43	0.007	
	emb AW736130 AW736130 EST332126 KV3 Medicago truncatula cDNA clo...	39	0.12	
	emb AW683515 AW683515 NF015C12LF1F1097 Developing leaf Medicago ...	36	0.21	
	emb AI781902 AI781902 EST262781 tomato susceptible, Cornell Lyco...	36	0.57	
	gb U12141 SCU12141 Saccharomyces cerevisiae chromosome XIV left ...	35	0.73	
20	emb AW277626 AW277626 sf84e07.y1 Gm-cl019 Glycine max cDNA clone...	36	0.79	
	emb Z71330 SCYNL054W S.cerevisiae chromosome XIV reading frame O...	35	0.80	
	emb AW692595 AW692595 NF057C11ST1F1000 Developing stem Medicago ...	35	1.1	
	emb X54145 ANPECT A.niger gene for pectinesterase.	35	1.5	
	emb A35008 A35008 A.niger PE gene.	35	1.5	
25	emb A34997 A34997 A.niger pectinesterase coding sequence.	35	1.5	
	emb AQ162316 AQ162316 mgxb0012I08r CUGI Rice Blast BAC Library P...	34	2.8	
	emb AF132029 AF132029 Hortonia floribunda chloroplast atpB-rbcL ...	34	2.8	
	emb AW567917 AW567917 si67c02.y1 Gm-r1030 Glycine max cDNA clone...	34	2.8	
	emb AQ951657 AQ951657 Sheared DNA-48F5.TR Sheared DNA Trypanosom...	34	2.8	
30	gb U81520 CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl...	34	3.9	
	emb AZ047925 AZ047925 LMAJFV1_lm68e11.x1 Leishmania major FV1 ra...	34	3.9	
	emb AI730144 AI730144 BNLGHi6313 Six-day Cotton fiber Gossypium ...	34	3.9	
	emb AQ942723 AQ942723 Sheared DNA-42J12.TR Sheared DNA Trypanoso...	34	3.9	
	gb U05812 HMU05812 Herpetomonas muscarum ATCC 30261 kinetoplast ...	34	3.9	
35	emb AW681095 AW681095 WS1_8_B09.g1_A002 Water-stressed 1 (WS1) S...	34	3.9	
	emb AL049180 PFMAL13P1 Plasmodium falciparum chromosome 13 strai...	27	4.9	
	emb AW832107 AW832107 sm30e05.y1 Gm-cl028 Glycine max cDNA clone...	33	5.3	
	gb N82224 N82224 TgESTzy37d01.r1 TgRH Tachyzoite cDNA Toxoplasma...	33	5.3	
	emb A94222 A94222 Sequence 5 from Patent EP0952222.	33	5.3	
40	emb AA741851 AA741851 LmLv39p3/584B Leishmania major promastigot...	33	5.3	
	emb AW728096 AW728096 GA_Ea0029O02 Gossypium arboreum 7-10 dpa ...	33	7.3	
	emb AW278032 AW278032 sf89g07.y1 Gm-cl019 Glycine max cDNA clone...	33	7.3	
	gb N82117 N82117 TgESTzy36b06.r1 TgRH Tachyzoite cDNA Toxoplasma...	33	7.3	
	emb AL355930 NCB2O8 Neurospora crassa DNA linkage group II BAC c...	32	10.0	
45	emb AW688738 AW688738 NF011A11ST1F1000 Developing stem Medicago ...	32	10.0	
	emb AI781529 AI781529 EST262408 tomato susceptible, Cornell Lyco...	32	10.0	
	emb AI397765 AI397765 NCC5A11T7 Conidial Neurospora crassa cDNA ...	32	10.0	
	emb AF127239 AF127239 Nicotiana tabacum cultivar Burley 21 argin...	32	10.0	
	emb AW180260 AW180260 MgA0351fMgA Library Mycosphaerella gramin...	32	10.0	
50	emb AF127240 AF127240 Nicotiana tabacum cultivar Xanthi arginine...	32	10.0	
	gb BE055666 BE055666 GA_Ea0009H20f Gossypium arboreum 7-10 dpa ...	32	10.0	
	gb BE036548 BE036548 MP01C02 MP Mesembryanthemum crystallinum cD...	32	10.0	
	emb AW038750 AW038750 EST280611 tomato mixed elicitor, BTI Lycop...	32	10.0	
	emb AL133484 LMFL236 Leishmania major Friedlin chromosome 19 cos...	32	10.0	
55	gb BE123936 BE123936 EST394061 DSIL Medicago truncatula cDNA clo...	32	10.0	

#### Example 4

##### Immediate Early Transcriptional Responses Controlled by a Salicylic Acid Dependent Local Resistance Pathway

Salicylic Acid (SA) is an important mediator of local and systemic defense responses. In *Arabidopsis*, accumulation of SA is essential for local resistance against many pathogens including *Peronospora parasitica* (*Peronospora*) isolates. Furthermore, numerous defense-related genes can be activated by SA treatment. In addition to local resistance, SA-accumulation is required for systemic acquired resistance (SAR). In the SAR pathway, SA has been shown to act upstream of *NPR1*, which is also essential for SAR. Short application of the SA analog BTH (e.g., 4 hours) to plant tissue appears to simulate local defense responses to *Peronospora parasitica*, whereas sustained SA treatment (e.g., 48 hours) elicits SAR-related plant responses (Maleck et al., 2000).

A previous cDNA microarray study identified a cluster of roughly 30 co-regulated genes that appear to be specifically involved in resistance of the *Arabidopsis* ecotype WS against the *Peronospora* isolate Noco2 (Maleck et al., 2000). These genes are strongly activated in response to infection with Noco2 (incompatible interaction) and 4 hours after BTH treatment. However, these genes were not markedly activated during a compatible interaction with the *Peronospora* isolate Emwal or an incompatible interaction with *Pseudomonas syringae* (DC3000 avrRpt2) bacteria. BTH treatment for 48 hours (that simulates SAR) even strongly repressed these genes. Thus, a rapid and transient SA peak may control Noco2 triggered defense genes.

Resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Emoy2 appears to be regulated by a similar pathway that also is dependent on accumulation of SA. Emoy2 resistance in Col-0 is controlled by the resistance gene *RPP4*. To further explore early SA-dependent gene regulatory events and to relate these to *Peronospora*-induced resistance responses, immediate-early target genes of SA were identified using Affymetrix chip experiments with the protein biosynthesis inhibitor cycloheximide (CHX). Genes of this category likely are linked to transcriptional regulators acting closely downstream of SA. Results from these "SA-chip" experiments were combined with those from a set of chip experiments examining expression

profiles triggered in the *Arabidopsis* ecotype Col-0 by the *Peronospora* isolate Emoy2 to identify clusters of co-regulated *RPP4* controlled SA-dependent immediate early genes.

### Results

5 To identify genes controlled by the *RPP4* pathway, interactions between the *Peronospora* isolate Emoy2 and Col-0 wild type plants, the defense mutants *ndr1*, *npr1* and *pad4* as well as transgenic NahG plants were examined by chip experiments. The interactions between Emoy2 and Col-0, *ndr1* or *npr1* are incompatible (plant is disease resistant), whereas the interactions involving *pad4* and NahG are compatible (plant is susceptible, i.e., disease develops). For each interaction three different time points were analyzed: 0, 12 and 48 hours post infection with 50,000 Emoy2 spores/ml. Genes that were at one or more time points more strongly expressed in Col-0, *ndr1* and *npr1* as compared to *pad4* and NahG were considered as controlled by the *RPP4* pathway. Genes represented by 271 probe sets showed at least one 2-fold expression difference in comparison between Col-0 and *pad4* or NahG and were selected for further analysis.

To identify immediate early target genes of SA, Col-0 wt seedlings were pretreated with CHX or mock treated 15 minutes before spraying with 2 mM SA or water and harvested 2 hours later (Table 28).

Table 28

<u>Plants</u>	<u>Treatment</u>
Col-0	untreated (mock)
25 Col-0	+ SA
Col-0	+ SA + CHX
Col-0	+ CHX

271 probe sets were found to be upregulated in a *RPP4* pathway-specific manner (SEQ ID NOs: 400-684). Emoy2-induced upregulation of these genes is compromised in *pad4* and *NahG* plants. These *RPP4* controlled genes were further analyzed concerning their responses to SA, CHX and SA + CHX. The 271 probe sets were subcategorized by K-means clustering over the SA/CHX data set. Nine K-means clusters comprised three subgraphs. For each of these subgraphs, the first data point represented the untreated control value, the second data point represented the response to combined SA/CHX treatment, the third



data point represented CHX treatment alone and the fourth data point represented SA treatment alone. K-means clustering defined two categories of RPP4 controlled CHX/SA-responsive genes: immediate early genes (SA-responsive, not CHX affected) and super-induced genes (additive effects of SA and CHX).

Two K-means clusters represent *RPP4*-controlled SA-induced immediate early genes (Table 29; SEQ ID NOs: 150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615 and 526). *RPP4*-controlled upregulation of these genes is SA dependent and SA induction is not compromised by CHX, which blocks or reduces protein biosynthesis. Thus, all essential regulators that mediate SA-responsiveness of these genes must be already preformed and, hence, are likely to act closely downstream of SA. This set of 15 genes includes seven potential regulator genes that may be involved in the control of secondary response genes (which require protein biosynthesis) or other late responses.

Table 29

12354_g_at	gb AAC23641.1  (AC004684) putative receptor-like protein kinase
14978_at	gb AAB64024.1  (AC002333) putative glucosyltransferase
15479_at	emb CAB39671.1  (AL049483) putative protein
15616_s_at	emb CAA08794.1  (AJ009696) wall-associated kinase 1
16061_s_at	gb AAB97145.1  (AF000977) MEK1
16109_s_at	gb AAC05342.1  (AC002521) putative protein kinase
16140_s_at	emb CAB42872.1  (AJ012423) wall-associated kinase 2
16603_s_at	gb AAB58497.1  (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase
17499_s_at	gb AAD19610.1  (AF107726) cyclic nucleotide gated channel
17930_s_at	emb CAA07352.1  (AJ006960) peroxidase
18966_at	gb AAC95196.1  (AC004561) putative glutathione S-transferase
20429_s_at	emb CAB10219.1  (Z97336) hypothetical protein - weak similarity to NF-kappa-B
20685_at	emb CAB41928.1  (AL049751) short-chain alcohol dehydrogenase like protein
13702_s_at	emb CAA19683.1  (AL024486) putative protein
14704_s_at	gb AAD15461.1  (AC006067) unknown protein

To further subcategorize these genes and to more precisely define a cluster of strictly co-regulated genes, the set of 15 genes was analyzed by K-means clustering over the *RPP4* data set (Emoy2 infections). This allows to use *RPP4* triggered expression timing as an additional criterion for subclustering. Normalized absolute expression levels at 0, 12 and 48 hpi in Emoy2 infected

Col-0 (w.t.), *ndr1*, *npr1*, *pad4* and *NahG* plants are displayed. Genes that share a pronounced almost linear and sustained expression increase were chosen for further analysis. These 5 genes (Table 30, which show a pronounced Emoy2-induced SA-dependent but *npr1*-independent linear expression increase and which encode potential regulators) are upregulated by the *RPP4* pathway, respond to Emoy2 recognition with a steep, sustained, almost linear expression increase. This pronounced "upregulation" is SA dependent and independent of *de novo* protein biosynthesis. Transcription factors that mediate this response must be present when SA is perceived and may act closely downstream of SA.

The mechanism that switches these genes on may involve posttranslational modifications of such preformed transcription factors.

Table 30

12354_g_at	gb AAC23641.1  (AC004684) putative receptor-like protein kinase
15616_s_at	emb CAA08794.1  (AJ009696) wall-associated kinase 1
16140_s_at	emb CAB42872.1  (AJ012423) wall-associated kinase 2
17499_s_at	gb AAD19610.1  (AF107726) cyclic nucleotide gated channel
20429_s_at	emb CAB10219.1  (Z97336) hypothetical protein - weak similarity to NF-kappa-B

To identify the potential binding sites of such key transcription factors, the promoters of these five genes were searched for conserved compact sequence motifs (Table 31; SEQ ID NOs: 757-764; SEQ ID NO:765 is a consensus sequence). Using the program "AlignACE", a strikingly conserved motif was found that is present in all five promoters. This motif resembles the described consensus binding site of WRKY transcription factors, W box. However, the W box core motif, TGAC, is followed by an "A". The permutation TGACA has never been associated with WRKY binding. In addition to this, four more positions are highly conserved. This motif may be the specific binding site of an unconventional WRKY transcription factor or a factor of a novel so far unknown type. Yeast one hybrid screens can reveal the identity of this factor.

Table 31

W box-like Motif		
MAP Score: 4.4		
ACAGTGACA 0 391 1	(12345)	SEQ ID NO:757
ACAGTGACA 1 236 1	(16140)	SEQ ID NO:758

ACAGTGACA 1 317 1 (16140) SEQ ID NO:759  
 ACAGTGACA 2 281 1 (15616) SEQ ID NO:760  
 ACAGTAACA 3 84 1 (17498) SEQ ID NO:761  
 AAAGTAACA 3 1557 0 (17498) SEQ ID NO:762  
 5 AAAGTGACA 4 1840 0 (20429) SEQ ID NO:763  
 AAAGTGACA 4 2131 0 (20429) SEQ ID NO:764

\*\*\*\*\*

ACAGTGACA SEQ ID NO:765

A

10 Expt. Frequency: 0.02/1kb  
 Obs. in SOMc7: 0.06/1kb  
 Obs. in this cluster: 0.50/1kb

15 One K-means cluster of the 271 RPP4 controlled probe sets represents  
*RPP4*-controlled SA/CHX super-induced genes (Table 32; SEQ ID NOs: 214,  
 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551).  
*RPP4*-controlled upregulation of these genes is SA-dependent; these genes are  
 weakly inducible upon both SA and CHX treatment alone. The response to  
 20 combined treatment with SA and CHX is stronger than the response to either  
 single treatment. Induction of genes in response to CHX alone has been  
 described before and has been attributed to hypothetical proteins that are rapidly  
 turned over and either repress transcription of the respective gene or control  
 degradation of the respective mRNA. Block of synthesis of such hypothetical  
 25 proteins may lead to increased mRNA levels by either increased transcription or  
 reduced mRNA degradation. Like the set of immediate early SA responsive  
 genes shown before, genes of this set also appear not to require *de novo* protein  
 biosynthesis for their response to SA. In contrast to the previous gene set,  
 however, the observed CHX-induced up-regulation may point to a de-repression  
 30 mechanism.

Table 32

	12505_s_at	gb AAC63643.1  (AC005309) putative CONSTANS-like B-box zinc finger protein
35	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function
	14116_at	gb AAC26243.1  (AF077407) contains similarity to sugar transporters
	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein
40	14223_at	emb CAA19683.1  (AL024486) putative protein



14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to
	gb X97864 cytochrome P450
14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to
	gb AF038007 FIC1, member of the PF 00122 E1-E2 ATPase
5	family.
14614_at	gb AAC16958.1  (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1  (L42212) serine acetyltransferase
16054_s_at	emb CAA74639.1  (Y14251) glutathione S-transferase
16105_s_at	gb AAC31756.1  (U68017) heat shock transcription factor 4
10 16968_at	emb CAA17559.1  (AL021961) glucosyltransferase -like protein
18235_at	gb AAB61480.1  (AC000348) T7N9.4
18567_at	gb AAC34217.1  (AC004411) putative alcohol dehydrogenase
18591_at	emb CAA52772.1  (X74756) ATAF2
19845_g_at	emb CAB37510.1  (AL035540) monooxygenase 2 (MO2)
15 20017_at	gb AAC16079.1  (AC004521) unknown protein

To further subcategorize these genes based on *RPP4* triggered expression timing, the set of 17 SA/CHX super induced genes was K-means clustered over the *RPP4* (Emoy2) data set (Table 33; SEQ ID NOs: 214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). A group of five

20 genes was identified that consistently respond quickly ("fast", within 12 hpi) and that have elevated expression ground states in the *npr1* mutant. The fast response is SA dependent (is abolished or attenuated in *pad4* and *NahG*). The elevated expression ground states in *npr1* together with the observed CHX inducibility may point to an *NPR1*-dependent repression mechanism. Since

25 *NPR1* has been shown previously to act closely at the level of transcriptional regulation, a *NPR1* dependent repressor may shut expression of these genes down. Upon CHX treatment this hypothetical repressor is not synthesized anymore and expression of these genes is elevated. This repressor may also participate in *RPP4* triggered activation of these genes and allow Emoy2-

30 induced de-repression.

Table 33

18591_at	emb CAA52772.1  (X74756) ATAF2
14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to
35	gb X97864 cytochrome P450
14614_at	gb AAC16958.1  (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1  (L42212) serine acetyltransferase
16105_s_at	gb AAC31756.1  (U68017) heat shock transcription factor 4

To identify binding sites of activating or repressing factors responsible for the co-regulation of this small cluster, the promoters of these genes were searched for conserved compact motifs with "AlignACE" (Table 34; SEQ ID NOs: 766-772, SEQ ID NO:773 is a consensus sequence). One strictly  
 5 conserved octameric motif was found, which, however, is absent in one of the promoters. Yeast one hybrid screens can identify factors binding to this motif.

Table 34

Motif 15		
10	MAP Score: 1.23758	
	AATCGAAT 0 40 0	(18591) SEQ ID NO:766
	AATCGAAT 0 1741 1	(18591) SEQ ID NO:767
	AATCGAAT 1 386 1	(PAD3, 14248) SEQ ID NO:768
	AATCGAAT 2 334 1	(14614) SEQ ID NO:769
15	AATCGAAT 2 660 1	(14614) SEQ ID NO:770
	AATCGAAT 2 2105 1	(14614) SEQ ID NO:771
	AATCGAAT 3 1570 1	(15646) SEQ ID NO:772
	*****	
	AATCGAAT	SEQ ID NO:773
20	expt.: 0.08/kb	
	obs.: 0.70/kb	
	SOMc7: 0.06/kb	
	Random20: 0.00/kb	
25	SOMc3: 0.10/kb	
	SOMc1: 0.10/kb	

As described hereinbelow, sets of genes specifically controlled by the *RPP7* and *RPP8* pathways were defined. Similarly a set of *RPP4* pathway  
 30 controlled genes was defined (see Figure 4). Figure 4 shows a "Venn diagram" including only the transcription factor genes of these *RPP4*, *RPP7* and *RPP8* controlled genes. Three transcription factor genes were found to be specifically upregulated by each of the three *Peronospora* defense pathways: AtERF1, HSF4, ATAF2. Furthermore, ERF transcription factors appear to play an  
 35 important role in controlling defense responses directed against *Peronospora* in general. Table 35 gives four potential target genes of ERF transcription factors. These genes contain ERF binding motifs in their promoters.

Table 35

40 Genes with potential ERF binding sites (GCCGCC or GCCGAC):

thioredoxin (13189) RPP7/RPP8 and (weakly) RPP4 controlled  
 C2H2 zinc finger (15665) RPP7/RPP4 and (weakly) RPP8 controlled  
 SigA binding protein (14148) RPP7/RPP4 controlled  
 HSP70 (13284) RPP7/RPP8 controlled

5

These genes are specifically controlled by at least two different *Peronospora* defense pathways and show an almost linear increase of transcript levels during incompatible Hiks1 interactions (K-means clusters 3+5).

6 potential ERF binding sites in K-means cluster 3+5: 0.5 motifs /

10 1kbExpected: 0.1 motif / 1kb; Enrichment in K-means cluster 3+5: 5-fold

SEQ ID NO:789

MPTSATAVAPSTGSGVQKKDQDWRAILSPEQFRVLREKGTENRGKGEYT  
 KLFDDGIYSCAGCATPLYKSTTKFDSGCGWPSFFDAIPGAIKQTDMFGSN  
 15 AADGSIVTSGLDYILISINEKLKAYT

SEQ ID NO:790

1 tgcattcttt tgaggggttt aattttctgc atagctttgt ctaatctctt agagctcaat  
 61 aagagaagat ggatgtcca cggccagctt tcaaagtgtt tgatgacgat ggccggctta  
 20 121 aacgttcagg gacggtttg accgcgagtg cgcatacat aaccgccgtg attggatctg  
 181 gtgttctatc gcttgcgtgg gctataggtc aactcgggtg gatcgcaggt cctacagtga  
 241 tgttgttgtt ctctttgtc acttactact ctccacgct tcttagcgac tgctacagaa  
 301 ccggagatcc tgtctctggg aagagaaact atacttacet ggacgctgtc cgatcaatcc  
 361 taggtggctt taggttcaag atttgtgggc tgattcagta ttgaatctg ttggtatca  
 25 421 cggtcgggta cacaatcgca gcattctataa gtatgatggc gatcaagagg tccaactgtt  
 481 tccacgagag cggagggaaa aaccgcgtgc acatgtcgag caatccatac atgatcatgt  
 541 ttggtgtgac cgagatcttg ctctctcaga tcaaagattt tgaccagatt tgggtggctct  
 601 ccattgtcgc tgctatcatg tctttcacat actctgcaat cggtttagct ctcggaatca  
 661 ttcaagtcgc ggcaaatgga gttgtcaagg gaagtctcac cggaattagc atcggcgcag  
 30 721 tgactcagac ccaaaaaata tggagaacct ttcaagcact tggagacatt gcctttgctt  
 781 attcatactc tgttgttctt attgaaattc aggacactgt aagatctcca ccagcagaat  
 841 caaaaacgat gaagatcgcc acaagaatca gcacgctgt tacaacgaca ttttacctgc  
 901 tatgtggttg tatgggctat gcggccttcg gagataaagc accgggaaac ctcttaaccg  
 961 gttttgggtt ctacaatccg ttttggctcc ttgacgtggc taacgctgcc atagtattcc  
 35 1021 acctgtagg agcttatcaa gtctttgctc agcccatctt cgcctttatt gagaacaac  
 1081 tggccgctag gttcccgac agtgacttgg tgaccaagga atacgaaatc cgaatccctg  
 1141 gttttaggtc accgtacaaa gtcaacgttt tcagagcagt ttaccgaagc gggtttgttg  
 1201 tttgaccac tgtgatatcc atgcttatgc cgttttcaa cgacgtcgta gggattttag  
 1261 gtgcgttagg gttttggcct ttgacgggtt actttccggt ggagatgtat ataagacaga  
 40 1321 ggaaggttga gagatggagt atgaagtggg ttgtctgca gatgttgagc tgtggttgtt  
 1381 tgatgatcac gttggtcgcc ggagttggct ccatcgccgg agtaatgcta gaccttaagg  
 1441 ttacaagcc gttcaagact acttactaaa caaacatga tgatagatga agaagaagaa  
 1501 ggtggtggag aaaaaaaca aaagatataa attttaatga tgattttcat tggggaaatg  
 1561 tgaataatgt aaaagtctt cgtttcgtat aattttatc ttgcgtaatt tatatacat

45

SEQ ID NO:791



MVKNLKVDP LAKVTASTTSMVILSSLFITDDSYVLVSAKENKNQSEAE  
 PSYYETLETYQGLPCPYGGYYGYYPGLDGSVGEAKDNGYYGYGTEVQ  
 YPVMQGENGSVIYLMPGFQSYDASQTYMPINPVGVSSQALHSPMYAAQ  
 GYYQNQFGYADVSSPTYLWDPVGDYVYGVASYTPPLKQNISSSSHNNH  
 5 NNYYSKSKNSFTGHGMGDRPKTPRKASQNSYAPPPLLNOEKGR IAYPM  
 DPVKKKSGALNRDETEKAKARTKENGTS MNDLANGQDHITNGECESCS  
 LDAEGNERSNGVGSVIRRDQYNLPSFQTKYEEAIF FVIKSYSEDDIHKSIK  
 YNVWSSTLNGNKKLDSAYQESQKKAADKSGKCPVFLFFSVNASGQFCG  
 VAEMIGRVDYEKSMEFWQQDKWTGYFPVKWHI IKDVPNPQLRHIILEN  
 10 NENKPV TNSRDTQEVRLPQGNEVLNIFKNYA AKTSILDDDFDYENREKV  
 MVQKKLRFPPVLKKKEEDLVADFKT MEMSNTVEEGNTELTGTVS

## SEQ ID NO:792

1 cgatcacgga tctggcttgg ttcatacaaa accgccgttg ccgcggcacg ggcctacgat  
 15 61 accgctgtgt ttacttacg tggctcttcg gcgagactca attccctga agaggtctt  
 121 aaggatggaa accggcgtga aggccttagga ggagatatgt ctccgacgtt gatacgggaag  
 181 aaggcggctg aggtgggagc tagagtcgac gcagagttgc ggtagagaa taggatggt  
 241 gagaacttag acatgaataa gttgccggag gcatatggat tgtaattat agtttggtag  
 301 ttatagggt ggagattgcc cggagacaga gtcaaacaga ggttctctga ctcatatgag  
 20 361 gcataatata gtaatatag taattttgt ttgagcata gtaattatgt cataacc

## SEQ ID NO:793

1 gggcaatgat taticgttcg ccggaaccag aagtcaaaat ttggtagat agggatccca  
 61 taaaaacttc tticgaggaa tgggctaaac ccggtcattt ctcaagaaca atagctaagg  
 25 121 gacctgatac taccacttgg atctggaacc tacatgctga tgctcacgat ttgatagtc  
 181 ataccagtga ttggaggaa atctctcgaa aagtatttag tggccatttc ggccaactct  
 241 ctatcatctt tctttggctg agtggcatgt attccatgg tgctcgttt tccaattatg  
 301 aagcatggct gagtgatcct actcacattg gacctagtgc tcaggtggtt tggccaatag  
 361 tgggccaaga aatcctgaat ggagtagtgg gcggaggctt ccgaggaata caaataacct  
 30 421 caggctttt tcagatttgg cgagcatccg gaataactag tgaattaca ctttattgta  
 481 ccgcaattgg cgcattggc ttcgcagcct taatgcttt tgctggttgg ttccattatc  
 541 acaaagcagc tccaaaattg gcttgggtcc aagatgtaga atctatgtg aatcaccatt  
 601 tagcagggt actaggactt gggtccttt cttgggcagg acatcaagta catgtatctt  
 661 atccgattaa ccaatttcta aacgctggag tagatcctaa agaaataccg ctctctcatg  
 35 721 aatttatctt gaatcgggat ctttggctc aactttatcc aagtttgct gaaggagcaa  
 781 ctccctttt taccttaaat tggcctaaat actcgggaatt tcttacttt cgtggcggat  
 841 tagatccagt gactgggggt ctatggttaa ccgatatagc acatcatcat ttacgtatcg  
 901 caattcttt tctaatacgc ggtcatatgt ataggaccaa ctgggggtatt ggtcatggta  
 961 taaaagatat ttagaggct cataaaggct cattacagg ccaaggccat aaaggcctat  
 40 1021 atgaaattct aacaacatca ttgccc

## SEQ ID NO:794

MEGSSSSSSSLISKSDAELEEM LDRMLTRLALCDDSKLESLVSNLLPLTISS  
 LSSQSPVVRNKAMCVDFIFQVLEILSHVNKR VKHQHEIGLPLLALWKLY  
 45 TDPAAPMVRNFAIVYVEMAFERAPAKVIGECHASKISDDVSAKYRSLIT  
 SQDKDLFLDFCLHMLLYQPSSQGGGSSPGLSVFQVNR IIGKQALKGDTLT  
 RRKLPSNTFLTKNYHFLKINQFLKQLGILNVIGNMDLPGESVYPLYIAAS  
 VDRVGM DLLVKIHSSQEPVAKRGEELLKKIASGTNLD DPKLINRLFLFN  
 GTTG TENVAPEHNVAPGNISLKMKLMSGFCRSIAAANSFPATLQCIFGC  
 50 MYDILFLLNLTFREKTEMAVRLFDALKLETQSLRSTIQEAIVSLAAAYKD

SPENILRDLEVLLLANSLAEQNEARFCALRWATSLYNHHCPSLYICMLS  
 AADPKLDIREIALEGLFLKEEGRSIVSNHDHKYPKFIEMLEYILKQQPKLL  
 DSSEMRSQKLLFPSQVYLVMIKFLVKCFELEMESNTQAVGTEFLDSAQ  
 KMCSLLEHSLAFEGSAELHACASKALVSVGSYLPPEMVELYFSRKIVWLR  
 5 SLLSHTDLSTRESVSRLLGMAASCALSDAESCSLLSELISSISQPQKLRFEAQ  
 HGGLCAVGFVSAHCLHRIPTVSKAVTQNAV KYLVEVVNLETAPLASVA  
 MEALGHIGICGALPFLVNDSSPGTQVLEILQERLSKLLSGDDIKSVQKIAL  
 SLGHICSNETSSSHLKIALDLLFSLRSKAEELFAAGEALSFLWGGVPVT  
 ADMILKTNYTSLSTDSNFLMKEVKSLSVDVKTDEEDSRTTTTRETITGKLF  
 10 DTTYSSRKEERCAGTVWMLSLTMYCGQQPSIQLMLPKIQEAFSHLLGD  
 QNELTQELASQGMSIYELGDASMKKSLVDALVNTLTGTSKRKRAIKLV  
 EESEVFQEGTIGESPSGGKISTYKELCNLANEMGQPDLIYKFMDLANHQA  
 SLNSKRGAAFGFSKIAKQAGDALRPHRLRLIPRLIRYQYDPDKNVQDAM  
 AHIWKALIQDPKKA VDEHLNHIFDDL VQCGSRLWRSREASCLALADIQ  
 15 GRKFDQVKEHLKKLWIAAFRAMDDIKETVRNAGDKLCRAVTSLTIRICD  
 VTLTELADAKQAMDIVLPFLSEGIMSKVNSVRKASIGVVMKLAKFYSK  
 HEINQFELLASFGELNVLLGNIDPLSDFVLFVTVCRLLHAANIGIETEKLE  
 NLRISISKGSPMWETLDCINIVDIESLEQLIPRLTQLVRGGVGLNTRVGV  
 ASFISLLVQKVGSEIKPFTGMLLRLLFPVAKEEKSSAAKRAFSSACGIVLK  
 20 YSSPSQAQSLIEETAALHSGDRSSQIACASLFKSFSSTAADIMSSHQSAIVP  
 AIFISRFEDKQISSLFEEVWEDITSGERVTLQLFLQEIVNHICESITSSSRFK  
 LSFSLGKDALLDALGALSVACHEAITKEDPTTPTTILSLICSACKKKLKKY  
 RESAFSCLEKVIAFGDPKFFHAVFPMLYEMCNTASIKTNTQVQAASDAV  
 KTESENGEDGHVPLEKIMECVKSCIQVATIDDILSAKADLIHVLIISLSPGF  
 25 LWTVKMSGISCVGKLC SRFPSLWTD SMDDLSPSDATK FVHEL FHS LVPK  
 LLECIHTVKIAQFHVAASQCLLELIELYSTISSLHPVEVDFKAEVVSLLLELE  
 KSEEAKSLLRKS RDALANLPSLN

SEQ ID NO:795

30 MDKETEILSRLAANHLHLAQFEPLKATLLALRVNPDALTLQTIVSNA  
 GRFDNVLWSRSCPSPLLSFLSTIELLRFENPTSPWGFDSETLSLRADFL  
 MVQVLIDRVTERIKEDEESEDENSGLGNCLRVLQGVLELGVERLKFFVVD  
 TSSSEGSNKIEEDAVVSLRSIVLDYSDVFDALCCNIQRQLAGCESYGTCL  
 VEEVQGEEQRKEMNEATCIGSPELDNINVFALIQRNVQLAQLDAMKTKL  
 35 DEGDERGAADRIRYLHLDYGVKENYHAVLKALLSRVMEKKDEYGDS  
 WHMVRQNLLFMYKEALSSNCGDLVQMIQGIQDDMLLPHSQLHLSLDNE  
 QIPLPLECFRRYLVDLKTERNIEDKSSPMSRAINSCLRDMYHYARISGSHV  
 LECVMCAALSSVKKEKLQEANDVLTLPRLRPLVASMGWDLLPGKTAT  
 RRKLMRLLWTSDSQALRLEESSLYGNQTDELELASFAACVNSGKSWTP  
 40 KASFLMHGNVSSAHDDAEVDPFVENLVLERLSAQSPRLVLFDVVPGIKF  
 QDAISLISMQPIASTAEAWKRIEDIELMHMRYALEAIVLALGAMEEAMK  
 DETDASHRVVFYHLKDLTNHLEAIKNVPRKIMMVNIVISLLHIDDIRLSST  
 QSASSACFSEKSNTPGLDPGDLGTEGEKEIVISFTKQLLDVLRNLP SHPIE  
 QECQLDGNYSTDGRQALEWRVSMAKRFIEDCEWRLSVMQHLLPLSERQ  
 45 WGLKEVLSILRAAPEKLLNLCMQRAKYDIGEEAVNRFALSAEDKATLEL  
 AEWVDNAFKGTLVEDVMSRTAEGAAAVQDLDFHSLGSQLSPLAMVLLF  
 AQSQVMLSEIYPGGAPKVGFTYWDQVHEVAIISVLRRLKRLQEFLEQDD  
 PQILQASFSGDTIISCTESHRRQGQKDRALAMLMHQMIEDAHRGKRQFLSG  
 KLHNLARALADEKPEVDVLKGDGSDMAVEKDGVGLGLKYTKQSPGS  
 50 ANRAVDGNPVSHETEDKGKKSFGPLSNKTSTYLSQFILYTAAGDIVDGT

DTTHDFNFFSLVYEWPKDLLTRLVFDRSSTDAAAKVAEVMSADVFHEVI  
 SACVPPVYPPRSGHWACIPVIPTTPCSHSEGKVLSPSIEAKPNCYVRSSA  
 TPGVPLYPLQLDVIRHLVKISPVRAVLACVFGGSILYNGSDSISSSLNDEF  
 PSSPDADRLFYEFSLDQSERYP T LNRWIQM QTNLHRVSEFVVTPKQKPD  
 5 DTRIKPDERTGIKRLLEHDSDESDETEETFSKNNIQPALTDGSARDGGSFE  
 NGVCRTDPTVFLSFDWENEVPYEKAVNRLIDEGKLMDALALSDRFLRN  
 GASDWLLQLLIKSREENPSTSGRSQGYGGQSNWSWQYCLRLKDKQLAAT  
 LALKCCIGDKLCRSTATYFRQMIAIIAGKRLSFFLLFEIMFGSWYARCVTL  
 KNLNGKQVEAECKEDPEGLALRLAGKGAVSAALEVAESAGLSIDLRREL  
 10 QGRQLVKLLTTDPLNGGGPAEASRFLSSLQDSADALPVVMGAMQLLPD  
 LRSKQLLILKEFPALRDNNVIMAYAAKAISVTIIPPPREPRITVSASRLRQK  
 SRAGPAVKASFTSSLSNFQREARRAFSWAPRNAENRTTSKDVYRKRKNS  
 GLGASERAWEAMTGIQEDQGSSYSADGQDRLPVSIAEEWMLTGDKT  
 KDEGVRASHKYESTPDILFKALLSLCSDELVSARSAMDLCISQMKNVLS  
 15 SKQLSEGASVETIGRAYHATEAFVQGLSYAKSLLRKLLGTTESTNNNGE  
 RSRDVDDISSDAGSSSVGSQSTDEPSDVLSTLTIWLGRAELLQSLLGSGIS  
 TSLDDIADQLSSECLRDRLISDERYSMAVYMCKKCKIDVFPVWKA WGL  
 ALLRMERYAQARVKFKQAFQLKGEDIPDVIQEIINTIEGGPPVDVSVIRS  
 MYDHLAKSAPTILDDSLSADSYLNVLHMPSTFPRRSERSRRSLESEKNSSV  
 20 PGSDFEDGPRSNLDTRYSECTNYLQEHARQNLLGFMFRHGHFKDACM  
 LFFPQSGLPPLQTSSVGA VSTSSSPQRTDPLATEYGTIESLCEFCVGYGAI  
 SSLEEVITERLESAKNQDQAINQYIAGALTRICAFFEINRHFNYLYKFLVL  
 KKDYVTSGYCCIQLFMNSTTQEDAVRHLEHAKKYWSLTILGVQAHFEE  
 ALTARHRGSDSKKLVTKGVRGKSAAEKLSEETLVKLSSRVKMQIDVVK  
 25 SFSDSEGAPWKHSLFGNPNDSETSRRRCEIVETLVEKNFDLAYSVIYEFK  
 LSAVDIYAGVATSLADRKKGSQLTELFKNIKGTIQDDDWDQVLNIADTG  
 KARSVWLIFCEMLQVLGAAINIYANKHKERPDRMLTSSHRKVLACV  
 VCGRLKSAFQIASKSGSVADVQYVAHQALHANSHTVLD MCKQWLAKY  
 M  
 30

### References

- Aarts et al., Proc Natl Acad Sci 95:10306 (1998).  
 Allison et al., (1986).  
 Altschul et al., J. Mol. Biol. 215:403 (1990).  
 35 Altschul et al., Nucleic Acids Res. 25:3389 (1997).  
 An et al., EMBO J. 4:277 (1985).  
 Aoyama T. et al., N-H Plant Journal, 11:605 (1997).  
 Bailey and Elkan In: Proceedings of the second international Conference on  
 Intelligent Systems for Molecular Biology (Altman, R., ed), pp 28-36, AAAI  
 40 press (1994).  
 Ballas et al., Nucleic Acids Res. 17:7891 (1989).  
 Bansal et al., Proc. Natl. Acad. Sci. USA, 89:3654 (1992).  
 Batzer et al., Nucleic Acid Res., 19:5081 (1991).



- Beals et al., Plant Cell, 9:1527 (1997).
- Belanger et al., Genetics, 129:863 (1991).
- Bevan et al., Nature, 304:184 (1983).
- Blochinger & Diggelmann, Mol Cell Biol, 4:2929.
- 5 Bourouis et al., EMBO J., 2:1099 (1983).
- Boyes et al., Proc Natl Acad Sci USA, 95:15849 (1998).
- Byrne et al. Plant Cell Tissue and Organ Culture, 8:3 (1987).
- Campbell and Gowri, Plant Physiol., 92:1 (1990).
- Cao et al., Plant Cell, 6:1583 (1994).
- 10 Cao et al., Cell, 88:57 (1997).
- Century et al., Science, 278:1963 (1997).
- Chandler et al., Plant Cell, 1:1175 (1989).
- Christou et al., Biotechnology, 9:957 (1991).
- Christou et al., Plant Physiol., 87:671 (1988).
- 15 Cordero et al., Plant J., 6:141 (1994).
- Corpet et al., Nucleic Acids Res. 16:10881 (1988).
- Crameri et al., Nature Biotech., 15:436 (1997).
- Crameri et al., Nature, 391:288 (1998).
- Creelman et al., Annu Rev Plant Physiol Plant Mol Biol 48:355 (1997).
- 20 Crossway et al., BioTechniques, 4:320 (1986).
- Czako et al., Mol. Gen. Genet. 23 5 (1), 33-40 (1992).
- Datta et al., Bio/Technology, 8, 736 (1990).
- Dayhoff et al., Atlas of Protein Sequence and Structure, Natl. Biomed. Res. Found., Washington, C.D. (1978).
- 25 De Blaere et al., Meth. Enzymol. 143:277 (1987).
- de Framond, FEBS, 290:103 (1991).
- Delaney et al., Proc. Natl. Acad. Sci. USA 92:6602 (1995).
- Della-Cioppa et al., Plant Physiology, 84:965 (1987).
- Dennis et al., Nucleic Acids Res., 12:3983 (1984).
- 30 Dong et al., Curr Opin Plant Biol 1:316 (1998).
- Dzelkalns et al., Plant Cell, 5:855 (1993).
- Eisen et al., Proc. Natl. Acad. Sci. USA, 95:14863 (1996)
- Eisen et al., Trends in Plant Sci. 95:14863 (2000).
- Ellis and Jones, Curr Opin Plant Bio 1:288 (1998).

- Elroy-Stein et al., PNAS USA, 86:6126 (1989).
- English, et al., Plant Cell 8:179 (1996).
- Eulgem et al., Trends in Plant Sci. 5:199 (2000).
- Falk et al., Proc Natl Acad Sci USA 96:3292 (1999).
- 5 Feys et al., Plant Cell 6:751 (1994).
- Franken et al., EMBO J., 10:2605 (1991).
- Fromm et al., Bio/Technology 8:833 (1990).
- Gallie et al., Molecular Biology of RNA, 237 (1989).
- Gallie et al., Nucl. Acids Res., 15:8693 (1987).
- 10 Gan et al., Science (1995), 270 (5244), 1986-8).
- Gatz Current Opinion in Biotechnology, 7:168 (1996).
- Gatz, C., Annu. Rev. Plant Physiol. Plant Mol. Biol., 48:89 (1997).
- Gelfand, eds., PCR Strategies (Academic Press, New York (1995)).
- Glazebrook et al., Genetics 143:973 (1996).
- 15 Glazebrook et al., Proc. Natl. Acad. Sci. USA 91:8955 (1994).
- Gordon-Kamm et al., Plant Cell, 2, 603 (1990).
- Graham et al., Biochem. Biophys. Res. Comm., 101:1164 (1981).
- Graham et al., J. Biol. Chem., 260:6555 (1985).
- Graham et al., J. Biol. Chem., 260:6561 (1985).
- 20 Guerineau et al., Mol. Gen. Genet. 262:141 (1991).
- Hammond-Kosack and Jones, Ann. Rev. Plant Physiol. Plant Mol. Biol., 48:575 (1997).
- Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA, 89:10915 (1989).
- Hiei et al., Plant J. 6:271 (1994).
- 25 Higgins et al., Gene 73:237 (1988).
- Higgins et al., CABIOS 5:151 (1989).
- Hinchee et al., Biotechnology, 6:915 (1988).
- Hoekema, In: The Binary Plant Vector System. Offset-drukkerij Kanters B.V.
- 30 Huang et al., CABIOS 8:155 (1992).
- Hudspeth & Grula, Plant Molec. Biol., 12:579 (1989).
- Huffman et al., J. Cell. Biochem., 17B: Abstract.
- Hunt et al., Mol. Plant-Microbe Int. 9:261 (1997).
- Ingelbrecht et al., Plant Cell, 1:671 (1989).

- Innis et al., eds., PCR Protocols: A Guide to Methods and Applications  
(Academic Press, New York (1995).
- Innis and Gelfand, eds., PCR Methods Manual (Academic Press, New York)  
(1999).
- 5 Jobling et al., Nature, 325:622 (1987).  
John et al., Proc. Natl. Acad. Sci. USA 89(13):5769 (1992).  
Jones et al., Adv Bot Res 24:89 (1997).  
Joshi et al., Nucleic Acid Res. 15:9627 (1987).  
Joshi, NAR, 15:6643 (1987).
- 10 Karlin and Altschul, Proc. Natl. Acad. Sci. USA 87:2264 (1990).  
Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873 (1993).  
Keller et al., Genes Dev., 3:1639 (1989).  
Kirsh et al., Plant J. 26:217 (2001).  
Klein et al., Bio/Technology, 6:559 (1988).
- 15 Klein et al., Nature (London) 327:70 (1987).  
Klein et al., Plant Physiol., 91:440 (1988).  
Klein et al., Proc. Natl. Acad. Sci. USA, 85:4305 (1988).  
Kohler et al., Plant Mol. Biol., 29:1293 (1995).  
Knauf, et al., Genetic Analysis of Host Range Expression by *Agrobacterium*
- 20 In: Molecular Genetics of the Bacteria-Plant Interaction, Puhler, A. ed.,  
Springer-Verlag, New York, 245 (1983).  
Koziel et al., Biotechnology, 11:194 (1993).  
Kridl et al., Seed Science Research, 1:209 (1991).  
Kriz et al., Mol. Gen. Genet., 207:90 (1987).
- 25 Kunkel, Proc. Natl. Acad. Sci. USA, 82:488 (1985).  
Kunkel et al., Methods in Enzymol., 154:367 (1987).  
Langridge et al., Cell, 34:1015 (1983).  
Lindstrom et al., Dev. Genet., 11:160 (1990).  
Lommel et al., Virology, 81:382 (1991).
- 30 Lorz et al. Mol. Gen. Genet. 199:178 (1985).  
Macejak et al., Nature, 353:90 (1991).  
Maleck et al., Nature Genetics, 26:403 (2000).  
Mansson et al., Gen. Genet., 200:356 (1985).  
Martin and Paz-Ares, Trends in Genetics 13:67 (1997).



- Martinez et al., J. Mol. Biol., 208:551 (1989).
- McBride et al., Proc. Natl. Acad. Sci. USA, 91:7301 (1994).
- McCabe et al., Bio/Technology, 6:923 (1988).
- McDowell et al., Plant J. 22:523 (2000).
- 5 McDowell et al., Plant Cell 10:1861 (1998).
- McNellis et al., Plant J. 1998, 14:247-257.
- Meinkoth and Wahl, Anal. Biochem., 138:267 (1984).
- Messing & Vierra, Gene, 19:259 (1982).
- Mogen et al., Plant Cell 2:1261 (1990).
- 10 Moore et al., J. Mol. Biol., 272:336 (1997).
- Munroe et al., Gene 91:151 (1990).
- Murray et al., Nucleic Acids Res., 17:477 (1989).
- Myers and Miller, CABIOS 4:11 (1988).
- Needleman and Wunsch, J. Mol. Biol. 48:443 (1970).
- 15 Odell et al., Nature, 313:810 (1985).
- Odell et al., Nature, 313:810 (1985).
- Ohtsuka et al., J. Biol. Chem., 260:2605 (1985).
- Okamuro et al., Biochemistry of Plants, 15:1 (1989).
- Paszkowski et al., EMBO J., 3:2717 (1984).
- 20 Pacciotti et al. Bio/Technology 3:241 (1985).
- Park et al., J. Plant Biol. 38(4):365 (1985).
- Pearson et al., Meth. Mol. Biol. 24:307 (1994).
- Pearson and Lipman, Proc. Natl. Acad. Sci. 85:2444 (1988).
- Penninck et al., Plant Cell 8:2309 (1996).
- 25 Perlak et al., Proc. Natl. Acad. Sci. USA, 88:3324 (1991).
- Pieterse et al., Plant Cell, 10:1571 (1996).
- Pieterse et al., Plant Cell, 8:1225 (1998).
- Potrykus Mol. Gen. Genet. 199:183 (1985).
- Proudfoot, Cell 64:671 (1991).
- 30 Quigley et al., J. Mol. Evol., 29:412 (1989).
- Ralston et al., Genetics, 119:185 (1988).
- Reina et al., Nucleic Acids Res., 18:6425 (1990).
- Reina et al., Nucleic Acids Res., 18:7449 (1990).
- Riggs et al., Proc. Natl. Acad. Sci. USA, 83:5602 (1986).

- Rochester et al., (1986).
- Ronald, Curr Opin Plant Biol 1:294 (1998).
- Rossolini et al., Mol. Cell. Probes, 8:91 (1994).
- Roth et al., Nature Biotechnology, 16:939 (1998).
- 5 Ruiz et al., Plant Cell 10:937 (1998).
- Ryals et al., Plant Cell 8:1809 (1996).
- Ryals et al., Plant Cell 9:425 (1997)
- Sambrook et al., Molecular Cloning: A Laboratory Manual (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York) (1989).
- 10 Sanfacon et al., Genes Dev. 5:141 (1991).
- Sanford et al., Particulate Science and Technology, 5:27 (1987).
- Schernthaner et al., EMBO J., 7:1249 (1988).
- Schindler et al., Plant Cell 4:1309 (1992).
- Schwob et al., Plant J., 4:423 (1993).
- 15 Shah et al., Mol. Plant-Microbe Interact. 10:69 (1997).
- Shimamoto et al., Nature, 338:274 (1989).
- Shirasu et al., Plant Cell 9:261 (1997).
- Shulaev et al., Plant Cell 7:1691 (1995).
- Simpson, Plant Mol. Biol., 19:699 (1985).
- 20 Skuzeski et al., Plant Molec. Biol., 15:65 (1990).
- Slater et al., Plant Mol. Biol., 5:137 (1985).
- Smith et al., Adv. Appl. Math. 2:482 (1981).
- Smith et al., Planta 168:94 (1986).
- Spencer et al., Theor Appl Genet, 79:625 (1990).
- 25 Staswick et al., Proc. Natl. Acad. Sci. USA 89:6837 (1992).
- Staub et al., EMBO J., 12:601 (1993).
- Staub et al., Plant Cell, 4:39 (1992).
- Stemmer, Nature, 370:389 (1994).
- Stemmer, Proc. Natl. Acad. Sci. USA, 91:10747 (1994).
- 30 Sukhapinda et al. Plant Mol. Biol. 8:209 (1987).
- Sullivan et al., Mol. Gen. Genet., 215:431 (1989).
- Svab et al., Proc. Natl. Acad. Sci. USA, 87:8526 (1990).
- Svab et al., Proc. Natl. Acad. Sci. USA, 90:913 (1993).

- Tijssen, Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes, part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York (1993).
- 5 Turner et al., Molecular Biotechnology, 3:225 (1995).  
VanTunen et al., EMBO J., 7:1257 (1988).  
Vasil et al., Biotechnology, 11:1553 (1993).  
Vernooij et al., Plant Cell 6:959 (1994).  
Vodkin, Prog. Clin. Biol. Res., 138:87 (1983).
- 10 Vogel et al., EMBO J., 11:157 (1992).  
Walker and Gastra, eds., Techniques in Molecular Biology, MacMillan Publishing Company, New York (1983).  
Wandelt et al., Nucleic Acids Res., 17:2354 (1989).  
Waterman, M.S. Introduction to Computational Biology: Maps, sequences  
15 and genomes. Chapman & Hall. London (1995).  
Weeks et al., Plant Physiol., 102:1077 (1993).  
Weissinger et al., Annual Rev. Genet., 22:421 (1988).  
Wenzler et al., Plant Mol. Biol., 13:347 (1989).  
Weymann et al., Plant Cell 7:2013 (1995).
- 20 White et al., Nucl Acids Res, 18:1062 (1990).  
Willitset al., Mol Plant-Microbe Interact 11:795 (1998).  
Xie et al., Science 280:1091 (1998).  
Yamamoto et al., Nucleic Acids Res., 18:7449 (1990).  
Yang & Klessig, PNAS 93:14972 (2000).
- 25 Yu et al., Proc Natl Acad Sci USA 95:7819 (1998).  
Zhang et al., Proc. Natl. Acad. Sci. USA, 94:4504 (1997).  
Zhou et al., Plant Cell 10:1021 (1998).  
Zhou et al., Plant Cell 8:2235 (1996).
- 30 All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the



details described herein may be varied considerably without departing from the basic principles of the invention.

**WHAT IS CLAIMED IS:**

1. An isolated polynucleotide comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 or the complement of the open reading frame, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
2. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which is substantially similar to an *Arabidopsis* nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
3. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
4. The isolated polynucleotide of claim 1, 2, or 3 which is DNA.
5. The isolated polynucleotide of claim 1, 2, or 3 which is RNA.
6. The isolated polynucleotide of claim 1 wherein the nucleotide sequence encodes a polypeptide having at least 90% amino acid sequence identity to the *Arabidopsis* polypeptide encoded by the open reading frame.
7. The isolated polynucleotide of claim 1 wherein the nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

8. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a dicot.
9. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a monocot.
10. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a cereal plant.
11. An isolated polypeptide encoded by the polynucleotide of claim 1, 2, or 3.
12. An expression cassette comprising the polynucleotide of claim 1, 2, or 3 operably linked to suitable regulatory sequences.
13. The expression cassette of claim 12 wherein the polynucleotide is linked to a promoter for expression in a plant.
14. A recombinant vector comprising the polynucleotide of claim 1, 2, or 3.
15. A host cell comprising the expression cassette of claim 12.
16. A host cell comprising the polynucleotide of claim 1, 2, or 3.
17. The host cell of claim 15 or 16 which is selected from the group consisting of yeast, bacteria and plant.
18. A transformed plant, the genome of which is augmented with the polynucleotide of claim 1, 2, or 3 or a polynucleotide which comprises one of SEQ ID NOs: 1-684 and 789-795 which is expressed in an amount which confers resistance or tolerance to the plant to pathogen infection.



19. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene corresponding to the polynucleotide of claim 1, 2, or 3 or a gene corresponding to one of SEQ ID NOs: 1-684 and 789-795.
20. The plant of claim 19 which is altered by T-DNA insertion, transposon insertion, or targeted DNA insertion.
21. The plant of claim 19 in which expression is inhibited by transcription or post-transcriptional mechanisms.
22. The plant of claim 18 or 19 which is a monocot.
23. The plant of claim 18 or 19 which is a dicot.
24. The plant of claim 18 or 19 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
25. A method of expressing a polynucleotide in a cell, comprising:  
introducing the polynucleotide of claim 1, 2, or 3 into a cell so as to express the open reading frame.
26. The method of claim 25 wherein the cell is a plant cell.
27. The method of claim 25 wherein the cell is a monocot cell.
28. The method of claim 25 wherein the cell is a dicot cell.
29. A composition comprising the polynucleotide of claim 1, 2, or 3 or comprising the polypeptide of claim 11.

30. A method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by oomycete infection of the cell, comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate with a probe comprising plant nucleic acid corresponding to RNA isolated from plant cells infected with an oomycete, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
  - b) comparing complex formation in a) to complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising plant nucleic acid corresponding to RNA from uninfected plant cells or from mutant plant cells which have a response to pathogen infection that is different than the plant cells in a), so as to identify which samples corresponding to genes having an open reading frame, the expression of which is altered in response to oomycete infection, wherein the genes comprise orthologs of *Arabidopsis* genes comprising one of SEQ ID NOs: 1-684 and 789-795.
31. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is induced in response to infection.
32. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is decreased in response to infection.
33. The method of claim 30 wherein the probe comprises nucleic acid from a dicot.
34. The method of claim 30 wherein the probe comprises nucleic acid from a monocot.

35. An isolated polynucleotide comprising an open reading frame of a gene identified by the method of claim 30.
36. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
  - a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by a nucleic acid sequence comprising an open reading frame comprising one of SEQ ID NOs: 1-684 and 789-795 so as to yield transformed plant cells; and
  - b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to the pathogen relative to a corresponding plant which does not comprise the expression cassette.
37. The method of claim 36 wherein the polynucleotide hybridizes under moderate hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
38. The method of claim 36 wherein the polynucleotide hybridizes under stringent hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
39. A transformed plant prepared by the method of claim 36.
40. A seed of the plant of claim 39.
41. A progeny plant of the plant of claim 39.
42. A method for identifying a plant cell infected with a pathogen, comprising:



- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence substantially similar to one or more of SEQ ID NOs:1-184, 301-494 or 500-803, or a portion thereof so as to yield an amplified product; and
  - b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the product is indicative of pathogen infection.
43. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising at least one of SEQ ID NOs: 685-788.
44. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which nucleotide sequence hybridizes under high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788 or which nucleotide sequence hybridizes under very high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788.
45. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, wherein the plant nucleotide sequence comprises SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 764 or SEQ ID NO: 773.
46. The isolated polynucleotide of claim 43, 44, 45 or 46 wherein the nucleotide sequence which directs transcription is 25 to 2000 nucleotides in length.

47. A recombinant vector comprising the polynucleotide of claim 43, 44, 45 or 46.
48. The vector of claim 47 which is a plasmid.
49. An expression cassette comprising the polynucleotide of claim 43, 44, 45 or 46 operatively linked to an open reading frame.
50. The expression cassette of claim 49 operably linked to other suitable regulatory sequences.
51. A host cell comprising the expression cassette of claim 49.
52. A transformed plant, the genome of which is augmented with the expression cassette of claim 49.
53. A plant cell containing the expression cassette of claim 49.
54. A transformed plant comprising transformed plant cells, the transformed plant cells containing the expression cassette of claim 49.
55. The transformed plant of claim 54 wherein the plant is a dicot.
56. The cell of claim 53 which is a dicot cell.
57. The transformed plant of claim 54 wherein the plant is a monocot.
58. The cell of claim 53 which is a monocot cell.
59. The transformed plant of claim 54 which is a cereal plant.
60. A method of augmenting a plant genome, comprising:
  - a) contacting plant cells with the expression cassette of claim 49 so as to yield transformed plant cells; and

- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.

- 61. A transformed plant prepared by the method of claim 60.
- 62. A seed of the plant of claim 61.
- 63. A progeny plant of the plant of claim 61.
- 64. A method of using a plant promoter, comprising: introducing the expression cassette of claim 49 to a plant cell and detecting the expression of the product of the open reading frame.
- 65. A recombinant vector comprising the expression cassette of claim 49.
- 66. A plant cell comprising the vector of claim 65.
- 67. A transformed plant, the cells of which comprise the vector of claim 65.
- 68. The plant of claim 52, 54, 61 or 67 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
- 69. The expression cassette of claim 49 wherein the open reading frame is in an antisense orientation.
- 70. The expression cassette of claim 49 wherein the open reading frame is in a sense orientation.
- 71. A transformed plant, the genome of which is augmented with a polynucleotide which is substantially similar to any one of SEQ ID NOs:



1-684 and 789-795 and which is expressed in an amount which inhibits or prevents pathogen infection.

72. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene comprising a polynucleotide substantially similar to any one of SEQ ID NOs: 1-684 and 789-795.
73. The plant of claim 71 or 72 wherein the polynucleotide is substantially similar to SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 792, SEQ ID NO: 57, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 102, SEQ ID NO: 111, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 682, SEQ ID NO: 129, SEQ ID NO: 137, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 157, SEQ ID NO: 161, SEQ ID NO: 165, SEQ ID NO: 170, SEQ ID NO: 174, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 184, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 197, SEQ ID NO: 208 or SEQ ID NO: 211.
74. The method of claim 36 wherein the polynucleotide is substantially similar to SEQ ID NO: 308, SEQ ID NO: 300, SEQ ID NO: 272, SEQ ID NO: 362, SEQ ID NO: 265, SEQ ID NO: 241, SEQ ID NO: 261, SEQ ID NO: 380, SEQ ID NO: 228, SEQ ID NO: 658, SEQ ID NO: 243, SEQ ID NO: 254, SEQ ID NO: 216, SEQ ID NO: 225, or one of SEQ ID NOs: 400-684.
75. The expression cassette of claim 12 wherein the polynucleotide is in antisense orientation.
76. The expression cassette of claim 12 wherein the polynucleotide is in sense orientation.

77. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading comprising sequences selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 so as to form a complex; and
  - b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.
78. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe comprising at least a portion of a polynucleotide that is substantially similar to any one of SEQ ID NOs: 1-684 and 789-795 under conditions effective to form a specific complex between the probe and the nucleic acid; and
  - b) detecting and determining the presence or amount of complex formation wherein the presence or amount of complex formation is indicative of pathogen infection.
79. A computer-readable medium having stored thereon a data structure comprising:
- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs: 1-791 or the complement thereof; and
  - b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

80. The computer readable medium of claim 79 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
81. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:
- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-791 or the complement thereof; and
  - b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.
82. The computer readable medium of claim 81 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
83. The method of claim 42, 60, 77 or 78 wherein the cells are dicot cells.
84. The method of claim 42, 60, 77 or 78 wherein the cells are monocot cells.
85. The method of claim 42, 60, 77 or 78 wherein the cells are maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat cells.



# RPP-DEPENDENT DEFENSE PATHWAYS

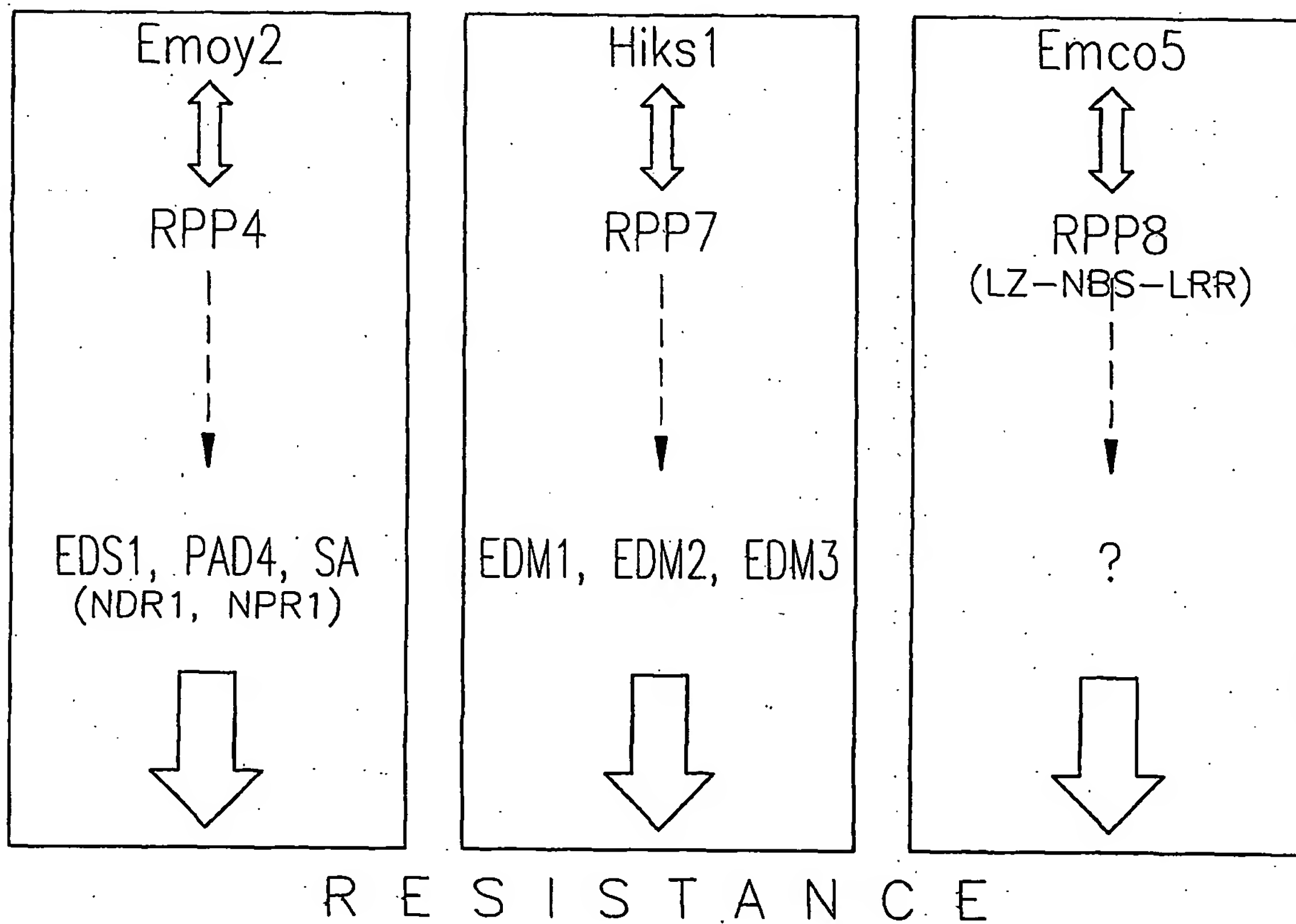


FIG. 1

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## motifs:

Motif 1/ MAP Score: 6.87857

CAACAATGAC

TT TT

Motif 2 MAP Score: 2.22382

GATGGGNCNAA

TT A

C

## Known stress-responsive cis-elements:

ttgacc, ttgact, ggtcaa and agtcaa W box

ttgaca and tgtcaa

W box-like

tgacg and cgtca

TGA-bZIP binding site

acgt

bZIP binding site core

cacgtg

G Box

gccgcc and ggcggc

GCC box

| Subcluster A  
17014 ribonuclease RNS1SEQ ID NO:  
774

tagaattgaaaaagggtaatgtgaaaagggtattctcaacaattattcaagataaaaat  
tgtataggtgttaaataataatgtgtgaaaagagaagacgatgtgaagtattaaaagaaa  
aaaaaaatggatgttgtatatataagtaaccattgtagatagtttaagcaagaaaaattga  
tgttgcattggaaattaaaaaatttcaataaaaattagaaaagcaactctaaatcattac  
ttattttattattttcaagaagttataaagtattaaacaattcgTTGACAaataagttt  
gatcgacattgtgtgacaaattttaaacacatcattaataacaacgaggacaaatacag  
ttcagatatcgtctactattaaaacacttcttctataggagcaaagaaaaattgtcggc  
aacgaactggggaccaataatattccgagtttgagttcaaactgagtaattttattttg  
agaaaatttgccaagttaacttataattctggtttACGTgtagtaattttattaagttgt  
tataggaaaatgagaaaataactaagacacatccaagaaagtttcacacgaaatttactt  
acaaaaagattgtttatttaataacttccgtatatagatatataaatatttaacacatta  
attataaagttcaagataattgattatctatctttttttgtcatctgaaattattatcg  
ctcaaacgaagtaattctgaggaaagttgtttacaaactagttattttcattattgtcta  
cttatataatagaattaaaaaaaattattgcttaatgcaatttagtttttagataaaatc

FIG. 2A

SUBSTITUTE SHEET (RULE 26)

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attaaacttaatagattatataagttagatatcaataattgggcttgcttaaaaacata  
aatataaaaatattattgggccgttACGTgcatacaaaaacgaaccttctaacaacaagt  
gtgaACGTtacgacttcaaaaattaaaaaaaaaacacacaactatgtccacACGTaatct  
catatgattcagattccaaggagaacaaaattaaaaacaaatctcgtaaacatacatat  
acttcacataaaaacaaaagggtacagtatataaccataaatctccgagattcttttgatgt  
atctgtccattttcattattacacaaaactaggaaactgatatctctctattcacattcct  
ctgattctattttctctttatatatatatccaccattaaccatctcaatcttataaccctc  
aaaatcacaaatcttctcttacaaaaaactttgaaagatg

14609 putative cytochrome P450

SEQ ID NO:

775

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taaaatataatgactagctaaaatgtgaggtatattgagaagtgagttcttaaaactact  
tggaacttgctacttagaatttgagacattataagtacaattgatgttaatctaaaagt  
gtagaacattgttaattttcttgaacagctgttagccaacaatgacggacgatacgatca  
ttgatcgaagaggcgattttgtttcacatcgatcagtggtatctcttggcgaagtacatg  
accaaccaccagatgatcagaagcattcaacacctctctatttatcccaatttgtaagt  
acatatatgtatgatagtatgtatgtatgtatatattatgagtacatatacattagaaa  
atactattaactttcaagtcgttatagtaattggacaatattattcgttaattatcaaaag  
cgctttttcatttttctatctgaacctaatgcctagcgagttgaaaacatagctacctaa  
taggctactactacacaatcttgaagcacaataatacaacgaaACGTcccttgggtat  
gagattatttagaagtttcataagattctagtccttattcaattgtgcccacatcaagcac  
aaagtacggaagcgataggaaggACGTCAcagtcctgttttgataatctaatgatcgta  
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acaaTGTCAAatattttaacaaattattttaaaaccttttaaatatgtgcatagtttttt  
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gcttttgtaaataaattatatataattcaaaaatcctcatcgtcgaaaacaatttttaaat  
aaaacaaccaagatattttccacaaattaaattaatttttagttttgaattcagatata  
taacaaacaatgatataaagaatatttcattaaataaaaagatattcttaactgaat  
ttatttattaatttggaatatacttattaccgaaataaaggattgtttattttcttacaac  
tcgtcttattagtggtgcatagcataacaagggtgaaagagaaaacatg

16649 putative S-adenosyl-L-methionine:trans-caffeoyl-  
Coenzyme A 3-O-methyltransferase (function:disease resistance) (promoter up to next ORF) SEQ ID NO:  
776

catgtctcttgagtctcgtgggttggtgcaaatgttcgttggtataaacgagagatgt  
atgtcaatatatatattggcttctggtcaaactaattgagctactaataagaccccaat  
taaggactaacacaccaattgatcttatccatgacttttcaaccatgggactagaaaat  
caattatctagacagtacttgatgcgaatatattaacgttttatgtttcttaaggatttt

FIG. 2B

SUBSTITUTE SHEET (RULE 26)



4/12

ttttctctcttaagggttgcatatacaaatggtgaaatgatgcaagcaggcgaacagtttgca  
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tatagtatagaattatttaaagaatatatcaaattgaagggtactaaaaaacggatttg  
aattcgaatgctaataacgaataaccagcataaatctccaaagatgattcaaattttg  
cagtttcaatccctcaatccgcttcaacggatgaaacaataataattcaacatgttc  
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tgatgtggcataggagattgggcatcctcatcatcaagatccctaaatgacgaaatgat  
tttaaaataataattcctaagatttcacatccttaaaccttattaagtcctaacttc  
gaaaatacacacacattcatttgatttaatttaaatttttatattaacttctctattttc  
attaaaaattgtaaaataatttttttattgtcgtaaaatgttttacttttctatttccat  
taaagttgtaaatatgttttattaacgtcgtaaaatgttatttttttaataaaaaatat  
ctggtgggccaaga

17653 (similarity to DNA damage inducible)  
(promoter up to next ORF)

SEQ ID NO:  
777

acaataatttccataattcaaattgctttcagaaaggatttctcaatacagggttaaaaat  
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aaacaaatctcaaattttgtggctataccaccattttcattgaaactaactactcaatt  
aacggtctgaaagaggacaaaaagattttcacaaagtgtacaccaataaaaagaaaatcgt  
ttttttcccttataaaaatgacaaaaattaccaagaaattaaatggaacataacttacga  
cgaaatttacctgacgattttttttccttactgaaaattaccaagaaatcgcggtggaag  
tcggaaatgttacataactttttctttgtaactacactgcgaaagcaaaaaaaaaaacat  
aaagtcaaccttttgggaaaattgtcgtctttgacatcagaagagattcaaactaaaat  
gaatgagtacgttacttgcggttatgggtgggttttcttttttaatttttagaaacttttc  
ttacttatattttgaatcaacagttgataacacaagtataaattattattttcgccatc  
acactggagtcaggtcgagagagacttgtttcttaatttaattcataaacttgtttcg  
acagtgaatatatacatcttcgaagaaataacaccattgacttaaaaccaaataaata  
acaatagtcttataattttatattttcacacttaaaattacaatacaagtcttttcaa  
agtcttttaatttatataaacaatagaagtctttttcattgtctctttttgactaattaa  
taaagaccatgaaaagacttgattgtaagttttgagtgtaaatgtaataaattacta  
tggttttggttggttttatatttctgccatctaaataattacattatatgataaaaataat  
taccctagcgacaaatgacagctagaaatgtaataagaacaccaactaaataattatgc  
aggttaataatggagcaagtgatgttctttctatatactgtacattttcttttttaaaaa  
attatgtaatttgcgagaagagaaaagaaaaacacgtgggtgattagagagtagtataaa  
gatagttgggtgggttctgtttttttctgtatctcgaggcgccaaaaacaacaaaa  
aaaacttcagagcggtgatcagattcaccgattttttctcaaaatg

FIG. 2C

SUBSTITUTE SHEET (RULE 26)

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17008 putative tyrosine aminotransferase

SEQ ID NO:  
778

cataggactactacaatcagTTGAGAgagacgacgatctgggttaatggcatggccactg  
agtttgatagcttccttggagatggcatgacgatcatagaaaccttttagtcTGTCAAa  
tatttcttgtaccactgattcgtcgggttcctatcgatatacctcaccgaattctctgccc  
ctagagccactcctaaaaatttcaacacaaaataaatataaataagtaataaaaaaag  
attgatcataattaacgatgcaaatttataaattaaaatcatatgtaagaagattgacta  
tgggagccccaagttcttaagatggttgatatattgttaaagagatcaatacctgggtataa  
ggataagactctcctcactaactagcttcgTGACGaaatcaaaatcatttttgatatta  
ttcaacattgatgTGTCAAgcttcaactgtaaaataaatcgtttaagctaatacatttat  
tattataagcaaaatatggagcatccaatagcaaaaaaaaaatctagaaaaccaagaatc  
caagaaaaagaattaaagtaccataaaataagaacaagattcggggtttcttgggacaaa  
agagacaaggaatatccttgagcctctcacatgaaagctcgACGTtgcgctctcatggct  
ttgatcttcttctcgaagaactctttaggtgttttctccaatatatcaggaagtgttc  
ctatcaaaatccataataatctcacattatttagagaaccaaaacttatagcttacgat  
gatagtgagagattacaaacctggagaataaatgaaggctgtggagttaaatacaagaaa  
atcctctattgcttgaactacctgttggtgaacgaaaggcccatatattagttagaatc  
ttcttaattggtgcggtaatcttatttttaagtaaaaactatagtgtttagaagTGACTg  
accctgtagatacaaagataaccattaggatcgttcatggcgatccagccaactctcca  
gcctgggTGACCcatcctttggatatggatccgagcgtgatcaccggagctattgatg  
caaacttccccatgggaataaaaggcttgtctccatatacaacatgatcatatacttcg  
tcggatattatcattataccgagttttctagccatctccgcgacctaaagattagtcga  
tatattaccaaaaaACGTtagttgttttacacttcaaaaaaacttatattacattaat

15042 cinnamyl alcohol dehydrogenase-like  
protein (promoter up to BAC end)SEQ ID NO:  
779

cattttttgatgattctttcttctttcttatcttgatctgctgctttcacgcttttgct  
gtttatgtgtgtgtattactatatatatatagagaaagttggaaacgtaacgtatgc  
gtatgtgtgatgaaataattggtgtttctgcatagcacacatttgatggctataattga  
gtgtaaatttggtgtatattattgacaaaatttagtcaaaagcttaaaatcttttttagtc  
gttgaaagatccttctagaaaaagacattttttttcttcttcttttcatacgatggctc  
atggctgtgtagtttattagaatttttaggtgaaaaaaatattagaagccaacaaaactt  
aaatgaaatttatttgcattcataattcattttaccagtttataacaacaacgtaatcc  
aaaaagtaaaatgagaaagaatggaatttggtgtactttgaaaggaagaaaaaccactat  
tgacgtggacacgtcggctaaaggagggtccacgggggttggtgaacaaacaatgtggg  
gtctaatacgtgtgtttgctttgggttaaaatcatgggtggccacgtgttgattcttgac  
ctctctctgacatgaaactgtagcattgacggcccagatcagctgcgagaatacttccc  
acaaccatggaaattttacggcccagatcaacaaagaatcgatttgctctttactattt  
cgaagaacaaagagtgacagttatgaataatagaaaagaaggacaaagagtgtgtgaat  
ggcttcacattaaaacaaaagcccattatgaatgaccattcacatttcacaccagtt  
tgaaaaatcgaccgtccaattaagtaacattcaaaaacccaaaagataaacctctaatt  
cacgaatcacaacagcagcatgagccgtttcatcacgacgttatctcagagtttcttgg  
aaataatttggtgtagcggacttgtggctgtaaatggggccaatgcttaaatttacttg  
tctcgtctcttctacacgtcttctcttcgaccacacccttcattcaattcaacgtctc

FIG. 2D

SUBSTITUTE SHEET (RULE 26)

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12778 Lipase/Acylhydrolase with GDSL-motif family SEQ ID NO:  
(promoter up to next ORF) 780

catcatttagagagagggagaaacagaactgtgaaaagagaagaagattgcttttgtgc  
cttagctcgtagaccgattcgttatatttatattgcaagtactacaatttggcaatgaa  
aataatagttcatttttactatacaaataataacgtgtagcgcgagggttcattttactat  
acacctatttaacgcactagcaaacgattatcgatcaattatattatagttcgttta  
atcacgtctgacgcattactggtttctcttctactttatttttaattctcaacaaaata  
tctattgttactacgagtaccaagaaagatcgtgcttttttttttttgggttcaacaaca  
acttacaattacacaagagtctgaatacacataagctttaacccaatccggcaatatag  
aatacaatttgggatcataattcagaaaagaaagagattccctagcaattctatctgcc  
acacaattcccttctcatcgggtaaaagtcactttaacctcttcgaagtgtgaaaaga  
tcgtgcatttagagggaagaagtagaattaaacatacaaatttcacggaaatatagggt  
gtaatggtaacactaaaccagattcagtaatttctgcagtaaccatttgcataaaaact  
aaattttgctgactagccaaattcaacaaaaaaatttcaacaccaacatatacgtagat  
atgtttatttctgctaaaacttttggataatttacgagtacacaactcgaattaaaata  
tttttaatatcaaaaatacatatcaaatagatatttttaataagtcagattatactgat  
acgatatatgaataatatagatacataaaaatatcactaccagaatagacaagagacgaa  
tatgttcggataattatagataatttggataataattttaataacgttttagataactta  
aatcaattattaaaatttttgcaaaaacaactcatacctatgctaagatatcttttaaaa  
gataaattatagtaatttcttaatcatcctcatcatattattgattaaattacttgaa  
aacaattaaaaaaaacaattaacaatctatattttatcatcatgttaatttttgaaatt  
attttcttaatagtgttttgacaaagattttcgttaattatttacatatttttaatagt  
tcaaatttaataaagaagaataactcaattttgcgttgacacaatcttaatagtatag

|| Subcluster B

20245 glutathione-conjugate transporter  
AtMRP4

SEQ ID NO:  
781

atttttctaataagacttttcttattctcatagactcttcttattcatctttcttaatc  
aattcgaccaactcagtggaagacaaatctcacacgaccctttccactttttggtaact  
ttattattaattttattagtagtggtgtagttcctttctttcttctgctgatctTGTC AAC  
aaaataactaaatttttccctaagcggctgtttatatattattaacaaagggtttccgcgtg  
tctcttgtttaactagtagactaaaaacaaatcgtaaaactcgattttctcaaccaaatt  
tagaagatactacggcatgtaattagctaatagataaaagattcgaattttcgttccaat  
ggatttgtcttttcttttgcccaaaaaccaagaatttgtcttctcttggcagtagtttagc  
tagacaacgcataatagctatatattttgtgtacactGGTCAAggtcgtggatACGTCA  
taataatattatttccaataagtcctattaaaacattaaacaactttgagttttaaaac  
aaacttagtgtaaagaaaataaaaatagcagacagtttacgggtaagactagatgacca  
tatatgattgagtgcataaaaacatcttttttctttcttttttgaaaaagcgaactaa  
aagattattagttgttggaaatcagcttagcgtaatcttcgagaaaaatgactctaattgc  
taaaatactgatttaataatcaatttttctaattggTTGACCCAACagactttttttttttt  
ctatcctctaataatatataatcatatagtagtaattatttagtagataatatgattaa  
cACGTgaatagcaaagtttctatcatttttattcaaaaaaagattcataagtaataaaa  
tgatAGTCAActtttctttttctttttgtgtttggccttttgtTGACGCGTCAttgttg

FIG. 2E

SUBSTITUTE SHEET (RULE 26)



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tacaccaccagtcacactattgtgggatgtgataatcggtaccttttaatgtcaggagc  
ttctttcttacattttccacttcaaacaacccgataattcagaggaattttctcttcct  
ctctctctctcttttttatattttttcactgggaaaaatg

17051 CTF2B involved in hydroxylation  
and oxidation of an aromatic ring

SEQ ID NO:  
782

catagccgcggtccaagaggaGGTCAAgtggattcacttttctataatcaatattaaat  
tgtagtcacaaaattcaagaaacttatatagaccttatttttatttttgaacatcaatag  
ttgtcgttgaaaagtatcttggggatatttagatttagcatatgAGTCAATGTTGgggtc  
cttaagagttgaggctacaaatttataactcagaaaaagtgtatatgccctttaatttt  
tggcctattgggtcttttatggCGTCAactccaatttcagtttgaaaagaaaTGTCAAta  
actaacaatggttcttTGACTttgaaatcttagaagtttegacttacceatttctac  
aagtgttaaatagcactgttattcaaaatcttatatttggttaattgtgcttaatatatt  
ttaaaatttaataacttcattaaaatccaatgttattcaaaactaaattacttttgaaa  
tatgtgtatatgaagtcatttgaaatgaaatctcataaagtttcataagtaaattatta  
gaataaaaacccaaggtaattgtatagattttgaaatccacacaataatatcgaattgt  
aaaatctagagaattcaatttcaattcatgaaggagtgttaataatcatggatttttaa  
agttagttgattgaatataaaaagtaggaaagatgtgggattcatgtgggtgggtttggccc  
atctccatgatctctagtgaatttcagctTGACGcaactttcggttaagatcttacttca  
ttgtgtgttggtgttgagcctcactggattgggtgtgtcggttttttagttcactcagag  
ttaagagtccttcgagtaagactctatcactatttaataaattaatgttaattgagttatg  
ataattcaaattggatctccttcattccatagttgcattTGACAatttttatataaaactt  
gctgattatctaagtcacaaatttgagtccttggttaataattcagtttcaatcatcaggag  
atgtctaataagattaaaaaattaaagatagaaatgtctaattggattgaaatatataaagt  
gactcagccaaaaacatgttaactgaaaatcttgtataaaatggagattctctgataac

19640 putative glutathione S-transferase

SEQ ID NO:  
783

aatgtagttttttctgggttttgtggagttaatcactaccttttagcttggatttatagc  
cttatgggtgttgatgggtcttgtgataaaaacgacgacgaactttgccgttttatatgggc  
ggcagtgatgtaaatgcgaagagtctagaaggaaacagatgTGACTttacaacata  
tttataACGTtccctttataatttttttttatctcttttttagtaagtggagatgtgtc  
ctaattcctaaccttgcccttatccctggagcatgtgtaccTGACTtgatccattcatt  
ttctgaagacaaccccatgcttCGTCAagaatttcttctgcttcccccaattatacccat  
cactttatcgtgggttcttcataattgatccattttgtctgtgtatgaaacatcaacagc  
tttaaaaccatttgtcattctcgtttggttatattgacgcccccaagaaaacaaacaactct  
atagtctgagctataaaaaaagaattagtactaatctgttatattgatgttccttttggc  
atatattaaaaatgttggtgttatataataggcggttggtttttccggtttctccatctacga  
acttggttgctgaattttccttccaacaatgttatataaagtatcgggtgaattttctatgg  
ttacaagactcaccacctcacgataactaaaaatataactaaagaaatttggttatattgtg  
ccgcaacaatatagaccacatgtccggtgtactttcctctgtttacacaacttcttACG  
TgtcgaataacatgttcacatttaacatagttgtgggttttattaagaaggatgggtTTG

FIG. 2F

SUBSTITUTE SHEET (RULE 26)

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ACTaaattatagctttttatctactttttctttcatatgaaaactccagggtttatgaacca  
atttcttatgatttgtaagaaattgaatactactacattttaaagtgtttataataatta  
aTTGACAttagaatttagtaaaaaacactaattgtttcatacaaatgtttcatttattggt  
catacaaaactattataacaagattacacaaacatatagttaacatctactgatcgaaga  
gtatcattggtgtctcttaggctgatttgattctttctacaactttcttcatatg

14248 PAD3\_at member of the PF|00067  
Cytochrome P450 family

SEQ ID NO:  
784

gttctggtcgaaggatttgtcccggaatgccaatggcgattgctagtgtggaactagca  
ttgatgaatttgctttattatgttattgattggagtatgcctgatgggactaaagggtgaaga  
cattgatatggaagaagctggtaatatctctatTGTCAAgaataacctcttcaacttg  
tgctgttcaACGTtattgatgagcaataataagctcgataacatggaaagtgtatg  
aagcaaaaaacataagattcttttagattttgttgtgttatataagaaagaaatgttcca  
ataataaatcaagaaagaataacttttgttcatcttacttaaaaaactagatcataatcaa  
cacggattaagatctttttcattcaacaaaattctaaattttgttttttaagtaaaaa  
atgttatagcataaatgttcagatttttatgtcgtatttatattgaattaaatataggac  
aaagaaaaataagatacagaacaaagagaaattttgatccaaaaaaaaaagaaagaga  
aataagatctagaacaaaaacgatacattcagattgattattgaaatcaaataatcgaa  
tttataattgaatttgatggaatttataatgtattttttgtcatggaaataataaagtt  
tgttaatatagtaggcacgatcgaatctggagcttcaattttttttaactaattgtta  
tggaagatgctggaatgatctctttttacaagaaagctcctctcattcttggtccggtt  
aacaccattaatgacatcggcacacaaaaattcaaacaccggtgaagattgtttgcta  
tactttatttttatcaataataagttgcggtacttggttaactgtatACGTacttctat  
ttcttatagttgtgcgataattaccacaagtccaaaaaagtaaaatatgaatttgataa  
agcagtgtaaacctgagattttcaagatttgggcctaaaccattagagaatgctACGT  
agagaaccattgggcccataaacttattttattcccgcgaagcctgagtggaattcgaa  
cactaccacaaaaagtaagagtttgggttatttgattttaatcattcactttgaattat  
tatagacaccggacagtgaacttatgataaagagatttttaacctttaaaactaaaacac  
taaaatacataatccaaagaagacggaacaaaaaacaaaaacagagccaggaataatg

17500 athcallga\_s\_at calmodulin-like protein  
(promoter up to next ORF)

SEQ ID NO:  
785

catcaaactaattttgggttattcttgagattaggaatgtgtgttcacctaaaagctagta  
attgattactaaaatgtaatgcatgcaacaagaagagtcaatcgaatttttatagagata  
agtcatataaaaatgattaattatcgctagaggaagctgcatgaaatttcttacagctt  
ttgtcttttaccatctaatcatttaattctctgagcctacgccatcacacatatctaaa  
agcaccttcttcgaaattcccttgaggacaaaacatggacctctttttgttcaacttg  
gattttctcggaatatgacttgcatgtcttcttactatattttatgtatcccttcattc  
tatactttttcgaaattctaatttaactctacatataatcccactcccaccagctaaag  
tttagacatgacaagtattttatcaaatgctccttcaattcaaactactgaatattggt  
tggaataagtactttttggagacgtaagctatattttccaatccgaaatgaatgaaccaa  
atgtccatagttctgttttttttctcctaaagtgaatatattaagagacactaaatt  
ctagaaaatatgtttaaaataataataatcagtaattgtccaaaaaatgtgaataactta

FIG. 2G

SUBSTITUTE SHEET (RULE 26)

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aatcaaaatcaggatacgaattgtcacaagaaacaaactttcctagataatgtatatatttt  
atattattatcatattatgtatgcacttaagacatctccatccatgagaaacctacaaa  
gtttttcaaacaaaaaaaatattaatattatattataatttgattatttttattaaaaa  
agtatttttgttaaaaaaattaaaccaatagtaagatgagaattgtcatgatgggttgta  
caaagtatctcagagtatctcagagtttctcacttgagaaactttctacactctctctc  
cttcattttttattattttttatttttttaattgtgagaaattcttatgagatacccacaa  
tagagatgggtcttataaaatttatcaacatgggtgaatctctcatgttatatatagagggtg  
atttaaaggctaaatagaataacacactacagcatataaactcaatgatatg

18928 putative endochitinase (promoter up to next repeat region) SEQ ID NO: 786

catttttgtgtatggagggtgttgtgtgaagaaatgaagaagggtgtgttgatgtattttat  
agtgtaaatttgggtctattcaaattgaaatattgatcagtggttagacatctttcacgat  
tattgattggctttttctgagtc aaagtcaatgccactttgtaccacttaacaaaagtc  
aatgacacagttttttctcttgctggttatgagaaattccatgtcggtcatagatcagat  
caaaaacgaatatgtaatcaaaattttaaagagccaagttacttggatgaaaatcattc  
tcataaaaacttgattgagataatcaagtttagattagttcaaacgtttgagatttttc  
tattgaatagttccaagtttttggttaattagctcaaacgatattgttagctaatatagc  
attttttttgggtcaactaatatagcatttagaacggtcttttaaagtcttactttgatt  
tttaacaaaaattgtatggaattgtgagaaaaatgactagtgaagccaaaatgtttcta  
tttataaatcaaaatcaaccaaattagaaaaatccaactcaattattgcaatttccaa  
atagtcatgcgtcaaaattaaaccagcatatcaataaaaagcggtttagtcttaccac  
cctgggtctagagactctagaaccatcggagctcaagtgaaaaacgacgccgttaagctg  
catctttcaagatagataaaaaacttttgcgatcgttcatctctcacagagtttcggc  
tcctccggtgtgtttcaggacgacgcaaaggggaaaaaaaattgaattctttctctcca  
agcgaaactagggtttcgaaagtctctgtctcatcaaagcttcgaaaaggtagatttat  
ggtttcttactctcctttctctatgatattccaatttcttgcgagcttgctcagtggtc  
ttaccttatatttaccgaaccagtgcctttatattctatcacattcgaagttattgggt  
tctgggttacttatattgcttattgttctatgactacgatataattatcccaaagatttg  
ttcttttctccgaatttggattagaaatggatataactcaaattctgaacatgcccgaa  
gaatcct

14614 putative glucosyltransferase (promoter up to next repeat region) SEQ ID NO: 787

ttaatttatccacacctcaacgaaaatttccggttggtgcgctaacgaattcaggctgtg  
aagttaaaagaaaaataacaaaattatagcttcacataagcgatcgatcttcaaactct  
acacatgacagaagcaaataactaaattaaatagcgtaaattttgtataataactagaa  
aacctaaaaaccaaattgtaaaaaaccttatgggaaaaaatgtgataaagcacctaaacc  
atagaataacttaaaatttcaatttcccaatcaagggtatgatataaaaacccatggaaaa  
caaattctcagccatatttctatctgaccgagtcctttttcaaaataatatatagacgggt  
agagtccttatatagtaaaaaacatttttttaaaactaatttatcttctcatatgaaaatg  
aatgcaaataaaaatgaccatataatgctgtaatgatattcaaggaagagatatcacaac  
aagggtcgaagaaatatacaatatctgaaagtcgactatatgggtccactttccaaattag

FIG. 2H

SUBSTITUTE SHEET (RULE 26)



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agatggaaagaagaacgattatgcagcaaaccattgatcggacgaagaagaataaa  
tatggaggcccatctactatagtagtatttggccttgaaatattttgggtccgagaaataataa  
ataaacagttatggcttttcggatttgggttgctttcaattttctcaaagtgttggacaa  
gtgttattacactcacctaaaacaggatcattccaatttcttgggctcagagtctgtac  
tttcttcttctttaaaccaaggctcttataagtattctctaaaccaagtcactaaacaat  
aattgggtcttgggtctgggtcaaacttggatcaatgttgccacatagccattagccaca  
caaaacaaaaattgtcttgcctttatatggaatgaagaaaaatcgaattttgtaaccat  
ttttgactttaaagtcacactcgccgtatacggcacaccaaatagacaaaaaacatttga  
ccaccaactttgctttaatgttaaaaacttttttttgcacccactactctcttcttca  
cctcctcaagtcacagtgaccaaatacacacacttcacaagaacaacctatg

||| Additional genes showing early and transient RPP-triggered  
expression

13176 Contains Myb DNA-binding domain  
repeat signatures

SEQ ID NO:  
788

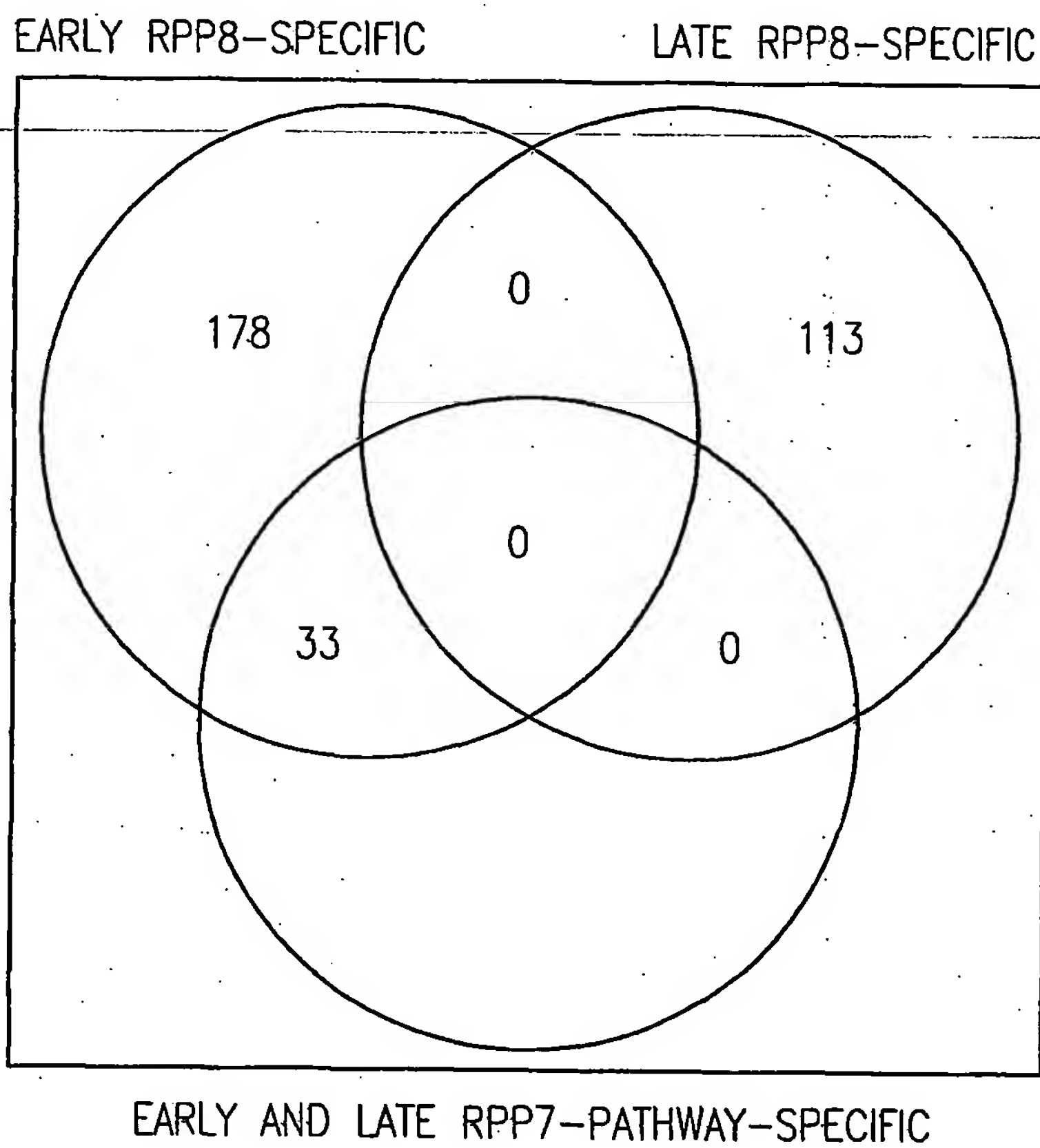
ttccaaaacttaaacctttaaaccttaaatgaacttcaatctacaccatataaagagga  
agagatataccttcgccatCGTCAAttggcccaaagaacaaaatgtacatactttacaag  
aggaatcaatattaaagtgtatataaccaatgacaagggtccaataatatcttctttgt  
cgtaattggagatcttctgaacatgacagtggaaggtatacaatgggctagttccaata  
tcaccaataacaacccaagtgtctgcaaagcaagtatgagtttcttctcctataaccagt  
gtcctgaaaaaacacattaccaagttcaacaactcaatcagatcgaaaagtaacaaca  
tgaagaagaagaagaacattcacacacaaatgctaacctcgatttcgtttttctgagtt  
ccaggaatctcaagagcatctacatcgaaagAGTCAAcggcagggctagtgcgaaatcaa  
acgctgctccacattgtcatcctcctcatcggaatccatttccgggtgattatgctcat  
catatccatcatcgctcgtaatcttcattaacctcataatcatcttctcatcgaaacacc  
catcgcgacaaTGACGTcgttgaatcgctctccgccaaactcctcatcaatctcagaccc  
atcgctccactgctttcttcttccACGTgaaacatcaatcacggttggaacactga  
agatctcgagattgtgattcagattcgatctctgatccaaggaaacaggattggaatt  
gggtgtttttgagagattgagagatggaagagagagattgatctacataactggagagg  
acctggcacgaatgagaaagaagcttacACGTgtccaatcatgattggattcgagactc  
acggtttaaggaaaaacaaaccagaccaaattaggcttaaccgctaaaaaacgggttc  
tcgttttgaaagattgagagagacgatctacaaaggaggacaggacccggcacgaatga  
gaagaagcttacACGTgtccaatcaggattgaacgatttaataagcttaaccgtatgt  
aaaccggatttttagctgggtccacaagtAGTCAAatatagatttttttaataAGTCAAata  
attttcataggggcgaagttcaagatgagttactacactcatcaaagctcacaaaaaga  
gaagagaagagacgaggatcaatcaccattctcatg

FIG. 21

SUBSTITUTE SHEET (RULE 26)

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26 *Peronospora* (Hiks1 and Emco5) induced  
RPP7, EDM1,2,3 and RPP8-Dependent genes

**FIG. 3**

RPP4-pathway, RPP7-pathway and  
RPP8-up-regulated transcription factor genes

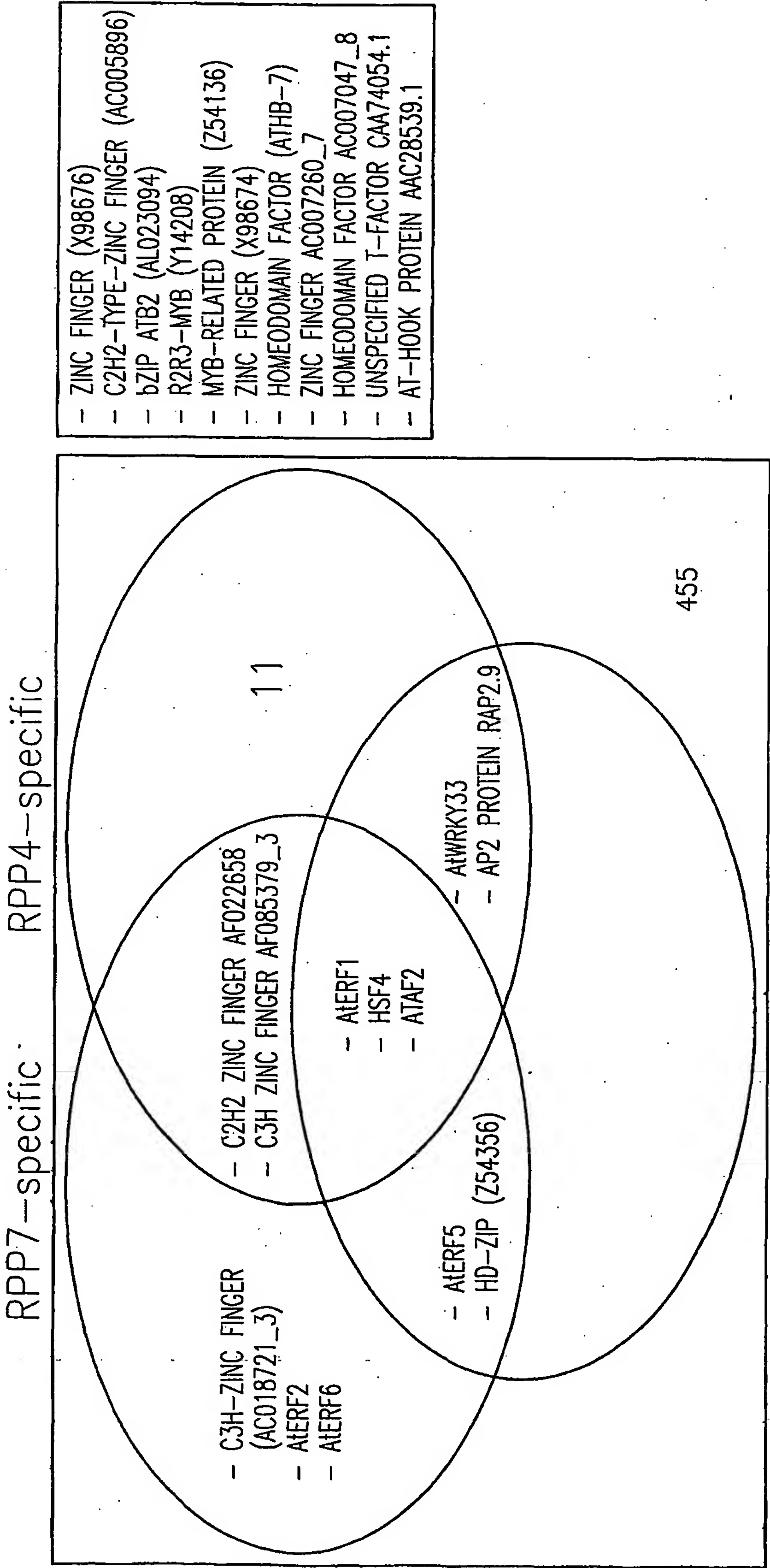


FIG. 4



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- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☒ **LINES OR MARKS ON ORIGINAL DOCUMENT**
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- ☐ **OTHER:** \_\_\_\_\_

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